

(12) DEMANDE INTERNATIONALE PUBLIÉE EN VERTU DU TRAITÉ DE COOPÉRATION
EN MATIÈRE DE BREVETS (PCT)

(19) Organisation Mondiale de la Propriété
Intellectuelle
Bureau international



(43) Date de la publication internationale
28 novembre 2002 (28.11.2002)

PCT

(10) Numéro de publication internationale
WO 02/094867 A2

(51) Classification internationale des brevets⁷ :
C07K 14/195

(21) Numéro de la demande internationale :
PCT/IB02/03040

(22) Date de dépôt international : 7 février 2002 (07.02.2002)

(25) Langue de dépôt : français

(26) Langue de publication : français

(30) Données relatives à la priorité :
0101659 7 février 2001 (07.02.2001) FR

(71) Déposants (pour tous les États désignés sauf US) : IN-
STITUT PASTEUR [FR/FR]; 28, rue du Docteur Roux,
F-75015 Paris (FR). CENTRE NATIONAL DE LA
RECHERCHE SCIENTIFIQUE (CNRS) [FR/FR]; 3,
rue Michel-Ange, F-75794 Paris Cedex 16 (FR).

(72) Inventeurs; et

(75) Inventeurs/Déposants (pour US seulement) :
DUCHAUD, Eric [FR/FR]; 55, rue Traversière,
F-75012 Paris (FR). TAOURIT, Sead [FR/FR]; 22,
allée Sainte-Anne, F-93320 Les Pavillons-sous-Bois (FR).
GLASER, Philippe [FR/FR]; 72, rue de la Glacière,
F-75013 Paris (FR). FRANGEUL, Lionel [FR/FR];
2, rue Mouton-Duvernet, F-75014 Paris (FR). KUNST,
Frederik [FR/FR]; 46, rue Barbès, F-94200 Ivry-sur-Seine
(FR). DANCHIN, Antoine [FR/FR]; 108 bis, boulevard
Blanqui, F-75013 Paris (FR). BUCHRIESER, Carmen
[AT/FR]; 11, rue de l'Amiral Mouchez, F-75013 Paris
(FR).

(74) Mandataires : MARTIN, Jean-Jacques etc.; Cabinet
Regimbeau, 20, rue de Chazelles, F-75847 Paris Cedex 17
(FR).

(81) États désignés (national) : AE, AG, AL, AM, AT, AU, AZ,
BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ,
DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM,
HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,
MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI,
SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW.

(84) États désignés (régional) : brevet ARIPO (GH, GM, KE,
LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), brevet
eurasien (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), brevet
européen (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR,
IE, IT, LU, MC, NL, PT, SE, TR), brevet OAPI (BF, BJ,
CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN,
TD, TG).

Publiée :

- sans rapport de recherche internationale, sera republiée
dès réception de ce rapport
- avec la partie réservée au listage des séquences de la de-
scription publiée séparément sous forme électronique et
disponible sur demande auprès du Bureau international

En ce qui concerne les codes à deux lettres et autres abrégia-
tions, se référer aux "Notes explicatives relatives aux codes et
abréviations" figurant au début de chaque numéro ordinaire de
la Gazette du PCT.

WO 02/094867 A2

(54) Title: SEQUENCE OF THE <I>PHOTORHABDUS LUMINESCENS</I> STRAIN TTO1 GENOME AND USES

(54) Titre : SEQUENCE DU GENOME DE PHOTORHABDUS LUMINESCENS SOUCHE TTO1 ET UTILISATIONS

(57) Abstract: The invention concerns the genomic sequence and nucleotide sequences coding for polypeptides of *Photobacterium luminescens*, such as polypeptides involved in operons of biosynthesis of antibiotics, or of toxins, or polypeptides exhibiting a toxin or antibiotic type activity capable of being used as pesticide, bactericide or fungicide as well as vectors comprising said sequences and cells or animals transformed by said vectors.

(57) Abrégé : L'invention a pour objet la séquence génomique et des séquences nucléotidiques codant pour des polypeptides de *Photobacterium luminescens*, tels que des polypeptides impliqués dans des opérons de biosynthèse d'antibiotiques, ou de toxines, ou des polypeptides à activité de type toxine ou antibiotique pouvant être utilisés comme pesticide, bactéricide ou fongicide ainsi que des vecteurs incluant lesdites séquences et des cellules ou animaux transformés par ces vecteurs.

SEQUENCE DU GÉNOME DE *PHOTORHABDUS LUMINESCENS* SOUCHE TT01 ET UTILISATIONS

L'invention a pour objet la séquence génomique et des séquences nucléotidiques
5 codant pour des polypeptides de *Photorhabdus luminescens*, tels que des polypeptides
impliqués dans des opérons de biosynthèse d'antibiotiques, ou de toxines, ou des
polypeptides à activité de type toxine ou antibiotique pouvant être utilisés comme
pesticide, bactéricide ou fongicide ainsi que des vecteurs incluant lesdites séquences et
des cellules ou animaux transformés par ces vecteurs.

10 *Photorhabdus luminescens* est une bactérie entomopathogène, commensale
intestinal d'un nématode et parasite d'insecte. Cette bactérie est à la fois un modèle pour
l'étude des interactions hôte-parasite et une bactérie dont les applications industrielles
sont nombreuses en raison de sa capacité à synthétiser de nombreuses toxines
(insecticides, bactéricides et fongicides) et à sécréter de nombreuses enzymes.

15 Afin d'appréhender de manière globale les déterminants génétiques impliqués
dans ces processus, le séquençage du génome *Photorhabdus luminescens* a été réalisé.

Le choix de la souche TT01 *Photorhabdus luminescens*, sous-espèce laumondii
dont le séquençage du génome a été réalisé dans la présente invention, est très important
car cette souche présente plusieurs avantages :

20 - son génome est stable ;
- elle peut être cultivée sur boîte de Pétri ;
- elle est centrale dans l'arbre phylogénétique, donc représentative de l'espèce ;
et

- son nématode associé est connu et cultivé (*Heterorhabditis bacteriophora*
25 HP88, Trinidad).

La présente invention concerne ainsi les séquences nucléotidiques et
polypeptidiques de *Photorhabdus luminescens* souche TT01.

Ainsi, c'est un objet de la présente invention que de divulguer la séquence du
génome de *Photorhabdus luminescens*, souche TT01 contenue dans la banque
30 génomique préparée à partir du génome de cette souche et déposée à la CNCM le 12
mai 2000 sous le numéro I-2478 ainsi que de tous les gènes et séquences régulatrices
non codantes contenus dans ledit génome.

La souche *Photorhabdus luminescens* TT01 est également identifiée dans la
présente demande par *Photorhabdus luminescens*, de manière interchangeable.

L'invention concerne également de nouveaux outils pour le typage des souches de *Phototrhhabdus*. Ces outils pourraient être du type "puce" à ADN ou d'un autre type. Les caractéristiques nouvelles de ces outils de typage seront les suivantes :

- * rapidité et simplicité d'utilisation ;
- 5 * haut pouvoir de discrimination entre les souches ; et
- * possibilité de fournir des informations sur le contenu génomique de la souche analysée.

La présente invention concerne donc une séquence nucléotidique isolée issue du génome de *Phototrhhabdus luminescens*, caractérisée en ce qu'elle comprend une
10 séquence choisie parmi les séquences SEQ ID N° 1 à SEQ ID N° 41 et les séquences SEQ ID N° 5826 à SEQ ID N° 5834.

Les séquences SEQ ID N° 1 à SEQ ID N° 41 représentent les séquences de 41 contigs dont l'ensemble recouvre la séquence génomique de *Phototrhhabdus luminescens* TT01.

15 Ces séquences SEQ ID N° 1 à SEQ ID N° 41 ont pu être réassemblées et relissées en 9 nouveaux contigs dont l'ensemble recouvre également la séquence génomique de *Phototrhhabdus luminescens* TT01. Les séquences SEQ ID N° 5826 à SEQ ID N° 5834 représentent les séquences de ces 9 contigs

Les séquences nucléotidiques SEQ ID N° 1 à SEQ ID N° 41 et SEQ ID N° 5826
20 à SEQ ID N° 5834 ont été obtenues par séquençage du génome de *Phototrhhabdus luminescens* TT01 par la technique dite de shot-gun (cf. Exemples). Malgré la grande précision de ces séquences SEQ ID N° 1 à SEQ ID N° 41 ou SEQ ID N° 5826 à SEQ ID N° 5834, il est possible que celles-ci ne représentent pas de manière parfaite à 100 % après assemblage la séquence nucléotidique du génome de *Phototrhhabdus luminescens*
25 TT01 et que quelques rares erreurs de séquençage ou indéterminations subsistent dans ces séquences. Dans la présente invention, la présence d'une indétermination d'un acide aminé est désignée par « Xaa » et celle d'un nucléotide est désignée par « N » ou « n » dans la liste des séquences ci-après. Ces quelques rares erreurs ou indéterminations pourraient facilement être mises en évidence et corrigées par l'homme de l'art à partir
30 du chromosome entier et/ou de ses fragments représentatifs selon l'invention et des méthodes standards d'amplification, de clonage et de séquençage, les séquences obtenues pouvant facilement être comparées, en particulier au moyen d'un logiciel informatique et en utilisant des supports d'enregistrement des séquences selon l'invention lisibles par un ordinateur tels que décrits par exemple ci-après. Après

correction de ces éventuelles rares erreurs ou indéterminations, la séquence nucléotidique corrigée obtenue comporterait encore au moins 97 %, de préférence au moins 98 %, 98,5 %, 99 % ou 99,9 % d'identité avec la séquence génomique obtenue après assemblage de ces séquences nucléotidiques SEQ ID N° 1 à SEQ ID N° 41 ou
5 SEQ ID N° 5826 à SEQ ID N° 5834.

La présente invention concerne également une séquence nucléotidique isolée issue du génome *Photorhabdus luminescens*, caractérisée en ce qu'elle est choisie parmi :

- a) une séquence nucléotidique comportant au moins 75 %, 80 %, 85 %, 90 %, 95 %, 98 % ou 99 % d'identité avec une séquence choisie parmi les séquences SEQ ID N° 1 à SEQ ID N° 41 ou SEQ ID N° 5826 à SEQ ID N° 5834 ;
10
- b) une séquence nucléotidique comprenant un fragment représentatif d'une séquence choisie parmi les séquences SEQ ID N° 1 à SEQ ID N° 41 ou SEQ ID N° 5826 à SEQ ID N° 5834 ;
- 15 c) une séquence nucléotidique complémentaire d'une séquence nucléotidique telle que définie en a) ou b) ;
- d) une séquence nucléotidique de l'ARN correspondant à l'une des séquences telles que définies en a), b) ou c) ;
- e) une séquence nucléotidique telle que définie en a), b), c) ou d) modifiée ;
- 20 f) une séquence nucléotidique hybridant dans des conditions de forte stringence avec une séquence choisie parmi SEQ ID N° 1 à SEQ ID N° 41 ou SEQ ID N° 5826 à SEQ ID N° 5834, et comportant au moins 20 nucléotides, de préférence au moins 25, 30, 50, 75, 100, 150, 200, 250, 500, 750, 1000, 1500, 2000 ou 2500 nucléotides.

De façon plus particulière, la présente invention a également pour objet une
25 séquence nucléotidique comprise dans une des séquences SEQ ID N° 1 à SEQ ID N° 41 ou une des séquences SEQ ID N° 5826 à SEQ ID N° 5834, et en ce qu'elle code pour un polypeptide choisi parmi les polypeptides de séquence SEQ ID N° 42 à SEQ ID N° 3855 ou parmi les polypeptides codés par une séquence SEQ ID N° 5835 à SEQ ID N° 10784 .

30 De préférence les polypeptides codés par une des séquence SEQ ID N° 5835 à SEQ ID N° 10784, sont les polypeptides dont la séquence d'au moins 5 acides aminés est obtenue en prenant comme cadre de lecture le premier nucléotide des séquences SEQ ID N° 5835 à SEQ ID N° 10784.

De manière très préférée, l'invention a également pour objet une séquence nucléotidique, caractérisée en ce qu'elle code pour un polypeptide dont la fonction annotée au tableau I ci-après, dernière colonne ou au tableau II ci-après, avant-dernière colonne, correspond à une activité de type toxine et/ou antibiotique, ou à un opéron
 5 impliqué dans la synthèse de toxine et/ou d'antibiotique, polypeptide choisi de préférence parmi :

- a) les polypeptides de séquences SEQ ID N° 61, SEQ ID N° 62, SEQ ID N° 67, SEQ ID N° 171, SEQ ID N° 221, SEQ ID N° 268, SEQ ID N° 288, SEQ ID N° 380, SEQ ID N° 426, SEQ ID N° 438, SEQ ID N° 448, SEQ ID N° 453, SEQ ID N° 455, SEQ ID N°
 10 456, SEQ ID N° 458, SEQ ID N° 501, SEQ ID N° 516, SEQ ID N° 530, SEQ ID N° 542, SEQ ID N° 551, SEQ ID N° 720, SEQ ID N° 761, SEQ ID N° 762, SEQ ID N° 814, SEQ ID N° 859, SEQ ID N° 860, SEQ ID N° 861, SEQ ID N° 862, SEQ ID N° 869, SEQ ID N° 1079, SEQ ID N° 1168, SEQ ID N° 1174, SEQ ID N° 1176, SEQ ID N° 1413, SEQ ID N° 1414, SEQ ID N° 1415, SEQ ID N° 1416, SEQ ID N° 1417, SEQ ID N° 1457, SEQ ID N° 1651, SEQ ID N° 1856, SEQ ID N° 1869, SEQ ID N° 2021,
 15 SEQ ID N° 2080, SEQ ID N° 2152, SEQ ID N° 2162, SEQ ID N° 2173, SEQ ID N° 2251, SEQ ID N° 2295, SEQ ID N° 2306, SEQ ID N° 2317, SEQ ID N° 2328, SEQ ID N° 2340, SEQ ID N° 2342, SEQ ID N° 2351, SEQ ID N° 2500, SEQ ID N° 3228, SEQ ID N° 3230, SEQ ID N° 3311, SEQ ID N° 3317, SEQ ID N° 3318, SEQ ID N° 3319, SEQ ID N° 3320, SEQ ID N° 3322, SEQ ID N° 3323, SEQ ID N° 3326, SEQ ID N° 3327, SEQ ID N° 3328, SEQ ID N° 3375, SEQ ID N° 3376, SEQ ID N° 3377, SEQ ID N° 3378, SEQ ID N° 3422, SEQ ID N° 3489, SEQ ID N° 3503, SEQ ID N° 3609, SEQ ID N° 3623, SEQ ID N° 3624, SEQ ID N° 3772, SEQ ID N° 3783, SEQ ID N° 3788 et SEQ ID N° 3794 ; ou
 20
 25 b) parmi les polypeptidiques codées par les séquences SEQ ID N° 5835 à SEQ ID N° 10784 homologues aux séquences telles que définies en a) ci-avant, comme indiqué à la dernière colonne du tableau II.

Ces 82 polypeptides de séquence telle que défini dans le paragraphe a) ci-avant dont la fonction est associée à une activité de type toxine ou antibiotique, ou leur
 30 polypeptide homologue du tableau II tel que défini dans le paragraphe b) ci-avant, ont pu être identifiés, par exemple, par la présence d'un motif consensus liée à ces fonctions ou par la présence de séquences les jouxtant sur le génome et impliquées dans ce type d'activité.

La présente invention concerne aussi de façon plus générale les séquences nucléotidiques issues de SEQ ID N° 1 à SEQ ID N° 41 ou SEQ ID N° 5826 à SEQ ID N° 5834, et codant pour un polypeptide de *P. luminescens*, telles qu'elles peuvent être isolées à partir de SEQ ID N° 1 à SEQ ID N° 41 ou SEQ ID N° 5826 à SEQ ID N° 5834.

De plus, les séquences nucléotidiques caractérisées en ce qu'elles comprennent une séquence nucléotidique choisie parmi :

- a) une séquence nucléotidique codant pour un polypeptide choisi parmi les séquences SEQ ID N° 42 à SEQ ID N° 3855 ou parmi les polypeptides codés par les séquences SEQ ID N° 5835 à SEQ ID N° 10784, de préférence parmi les 82 séquences de polypeptides ci-avant sélectionnés pour leur fonction associée à une activité de type toxine ou antibiotique ou leur peptide homologue tel que défini dans le tableau II à la dernière colonne ;
 - b) une séquence nucléotidique comportant au moins 75 % d'identité avec une séquence nucléotidique telle que définie en a), de préférence d'au moins 80 %, 85 %, 90 %, 95 %, 98 % ou 99 % d'identité ;
 - c) une séquence nucléotidique complémentaire ou d'ARN correspondant à une séquence telle que définie en a) ou b) ;
 - d) une séquence nucléotidique d'un fragment représentatif d'une séquence telle que définie en a) ou c) ; et
 - e) une séquence telle que définie en a), ou c) modifiée,
- sont également des objets de l'invention.

Par acide nucléique, séquence nucléique ou d'acide nucléique, polynucléotide, oligonucléotide, séquence de polynucléotide, séquence nucléotidique, termes qui seront employés indifféremment dans la présente description, on entend désigner un enchaînement précis de nucléotides, modifiés ou non, permettant de définir un fragment ou une région d'un acide nucléique, comportant ou non des nucléotides non naturels, et pouvant correspondre aussi bien à un ADN double brin, un ADN simple brin qu'à des produits de transcription desdits ADNs. Ainsi, les séquences nucléiques selon l'invention englobent également les PNA (Peptid Nucleic Acid).

Il doit être compris que la présente invention ne concerne pas les séquences nucléotidiques dans leur environnement chromosomique naturel, c'est-à-dire à l'état naturel. Il s'agit de séquences qui ont été isolées et/ou purifiées, c'est-à-dire qu'elles ont

été prélevées directement ou indirectement, par exemple par copie, leur environnement ayant été au moins partiellement modifié. On entend ainsi également désigner les acides nucléiques obtenus par synthèse chimique.

5 Par « pourcentage d'identité » entre deux séquences d'acides nucléiques ou d'acides aminés au sens de la présente invention, on entend désigner un pourcentage de nucléotides ou de résidus d'acides aminés identiques entre les deux séquences à comparer, obtenu après le meilleur alignement, ce pourcentage étant purement statistique et les différences entre les deux séquences étant réparties au hasard et sur toute leur longueur. On entend désigner par "meilleur alignement" ou "alignement optimal", l'alignement pour lequel le pourcentage d'identité déterminé comme ci-après
10 est le plus élevé. Les comparaisons de séquences entre deux séquences d'acides nucléiques ou d'acides aminés sont traditionnellement réalisées en comparant ces séquences après les avoir alignées de manière optimale, ladite comparaison étant réalisée par segment ou par « fenêtre de comparaison » pour identifier et comparer les régions locales de similarité de séquence. L'alignement optimal des séquences pour la
15 comparaison peut être réalisé, outre manuellement, au moyen de l'algorithme d'homologie locale de Smith et Waterman (1981, Ad. App. Math., 2:482), au moyen de l'algorithme d'homologie locale de Neddleman et Wunsch (1970, J. Mol. Biol., 48:443), au moyen de la méthode de recherche de similarité de Pearson et Lipman (1988, Proc. Natl. Acad. Sci. USA, 85:2444), au moyen de logiciels informatiques
20 utilisant ces algorithmes (GAP, BESTFIT, BLAST P, BLAST N, FASTA et TFASTA dans le Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI). Afin d'obtenir l'alignement optimal, on utilise de préférence le programme BLAST, avec la matrice BLOSUM 62. On peut également utiliser les
25 matrices PAM ou PAM250.

Le pourcentage d'identité entre deux séquences d'acides nucléiques ou d'acides aminés est déterminé en comparant ces deux séquences alignées de manière optimale, la séquence d'acides nucléiques ou d'acides aminés à comparer pouvant comprendre des additions ou des délétions par rapport à la séquence de référence pour un alignement
30 optimal entre ces deux séquences. Le pourcentage d'identité est calculé en déterminant le nombre de positions identiques pour lesquelles le nucléotide ou le résidu d'acide aminé est identique dans les deux séquences, en divisant ce nombre de positions identiques par le nombre total de positions comparées et en multipliant le résultat obtenu par 100 pour obtenir le pourcentage d'identité entre ces deux séquences.

Par séquences nucléiques présentant un pourcentage d'identité d'au moins 75 %, de préférence 80 %, 85 %, 90 %, 95 %, 98 % ou 99 %, après alignement optimal avec une séquence de référence, on entend désigner les séquences nucléiques présentant, par rapport à la séquence nucléique de référence, certaines modifications comme en particulier une délétion, une troncation, un allongement, une fusion chimérique et/ou une substitution, notamment ponctuelle, et dont la séquence nucléique présente au moins 75 %, de préférence 80 %, 85 %, 90 %, 95 %, 98 % ou 99 %, d'identité après alignement optimal avec la séquence nucléique de référence. Il s'agit de préférence de séquences dont les séquences complémentaires sont susceptibles de s'hybrider spécifiquement avec les séquences de référence. De préférence, les conditions d'hybridation spécifiques ou de forte stringence seront telles qu'elles assurent au moins 75 %, de préférence 80 %, 85 %, 90 %, 95 %, 98 % ou 99 % d'identité après alignement optimal entre l'une des deux séquences et sa séquence complémentaire.

Une hybridation dans des conditions de forte stringence signifie que les conditions de température et de force ionique sont choisies de telle manière qu'elles permettent le maintien de l'hybridation entre deux fragments d'ADN complémentaires. A titre illustratif, des conditions de forte stringence de l'étape d'hybridation aux fins de définir les fragments polynucléotidiques décrits ci-dessus, sont avantageusement les suivantes.

L'hybridation ADN-ADN ou ADN-ARN est réalisée en deux étapes : (1) préhybridation à 42°C pendant 3 heures en tampon phosphate (20 mM, pH 7,5) contenant 5 x SSC (1 x SSC correspond à une solution 0,15 M NaCl + 0,015 M citrate de sodium), 50 % de formamide, 7 % de sodium dodécyl sulfate (SDS), 10 x Denhardt's, 5 % de dextran sulfate et 1 % d'ADN de sperme de saumon ; (2) hybridation proprement dite pendant 20 heures à une température dépendant de la taille de la sonde (i.e. : 42°C, pour une sonde de taille > 100 nucléotides) suivie de 2 lavages de 20 minutes à 20°C en 2 x SSC + 2 % SDS, 1 lavage de 20 minutes à 20°C en 0,1 x SSC + 0,1 % SDS. Le dernier lavage est pratiqué en 0,1 x SSC + 0,1 % SDS pendant 30 minutes à 60°C pour une sonde de taille > 100 nucléotides. Les conditions d'hybridation de forte stringence décrites ci-dessus pour un polynucléotide de taille définie, peuvent être adaptées par l'homme du métier pour des oligonucléotides de taille plus grande ou plus petite, selon l'enseignement de Sambrook et al. (1989, Molecular cloning : a laboratory manual. 2nd Ed. Cold Spring Harbor).

De plus, par fragment représentatif de séquences selon l'invention, on entend désigner tout fragment nucléotidique présentant au moins 15 nucléotides, de préférence au moins 20, 25, 30, 50, 75, 100, 150, 200, 300 et 450 nucléotides consécutifs de la séquence dont il est issu.

5 Par fragment représentatif, on entend en particulier une séquence nucléique codant pour un fragment biologiquement actif d'un polypeptide, tel que défini plus loin.

Par fragment représentatif, on entend également les séquences intergéniques, et en particulier les séquences nucléotidiques portant les signaux de régulation (promoteurs, terminateurs, voire enhanceurs, ...).

10 Parmi lesdits fragments représentatifs, on préfère ceux ayant des séquences nucléotidiques correspondant à des cadres ouverts de lecture, dénommés séquences ORFs (ORF pour « Open Reading Frame »), compris en général entre un codon d'initiation et un codon stop, ou entre deux codons stop, et codant pour des polypeptides, de préférence d'au moins 100 acides aminés, tels que par exemple, sans
15 s'y limiter, les séquences ORFs qui seront décrites par la suite.

La numérotation des séquences nucléotidiques ORFs qui sera utilisée par la suite dans la présente description correspond à la numérotation des séquences d'acides aminés des protéines codées par lesdites ORFs pour les les séquences SEQ ID N° 42 à SEQ ID N° 3855. La numérotation des séquences nucléotidiques ORFs SEQ ID N°
20 5835 à SEQ ID N° 10784 sera utilisée par la suite dans la présente description pour la numérotation des séquences d'acides aminés des protéines codées par lesdites ORFs SEQ ID N° 5835 à SEQ ID N° 10784.

Les fragments représentatifs selon l'invention peuvent être obtenus par exemple par amplification spécifique telle que la PCR ou après digestion par des enzymes de
25 restriction appropriées de séquences nucléotidiques selon l'invention, cette méthode étant décrite en particulier dans l'ouvrage de Sambrook et al.. Lesdits fragments représentatifs peuvent également être obtenus par synthèse chimique lorsque leur taille n'est pas trop importante, selon des méthodes bien connues de l'homme du métier.

Parmi les séquences contenant des séquences de l'invention, ou des fragments
30 représentatifs, on entend également les séquences qui sont naturellement encadrées par des séquences qui présentent au moins 75 %, 80 %, 85 %, 90 %, 95 %, 98 % ou 99 % d'identité avec les séquences selon l'invention.

Par séquence nucléotidique modifiée, on entend toute séquence nucléotidique obtenue par mutagenèse selon des techniques bien connues de l'homme du métier, et

comportant des modifications par rapport aux séquences normales, de préférence au plus 10 % de nucléotides modifiés par rapport à ces séquences normales, par exemple des mutations dans les séquences régulatrices et/ou promotrices de l'expression du polypeptide, notamment conduisant à une modification du taux d'expression ou de l'activité dudit polypeptide.

Par séquence nucléotidique modifiée, on entend également toute séquence nucléotidique codant pour un polypeptide modifié tel que défini ci-après.

Les fragments représentatifs selon l'invention peuvent également être des sondes ou amorces, qui peuvent être utilisées dans des procédés de détection, d'identification, de dosage ou d'amplification de séquences nucléiques.

Une sonde ou amorce se définit, au sens de l'invention, comme étant un fragment d'acides nucléiques simple brin ou un fragment double brin dénaturé comprenant par exemple de 12 bases à quelques kb, notamment de 15 à quelques centaines de bases, de préférence de 15 à 50 ou 100 bases, et possédant une spécificité d'hybridation dans des conditions déterminées pour former un complexe d'hybridation avec un acide nucléique cible.

Les sondes et amorces selon l'invention peuvent être marquées directement ou indirectement par un composé radioactif ou non radioactif par des méthodes bien connues de l'homme du métier, afin d'obtenir un signal détectable et/ou quantifiable (brevet FR 78 10975 et bDNA de Chiron EP 225 807 et EP 510 085).

Les séquences non marquées de polynucléotides selon l'invention peuvent être utilisées directement comme sonde ou amorce.

Les séquences sont généralement marquées pour obtenir des séquences utilisables pour de nombreuses applications. Le marquage des amorces ou des sondes selon l'invention est réalisé par des éléments radioactifs ou par des molécules non radioactives.

Parmi les isotopes radioactifs utilisés, on peut citer le ^{32}P , le ^{33}P , le ^{35}S , le ^3H ou le ^{125}I . Les entités non radioactives sont sélectionnées parmi les ligands tels la biotine, l'avidine, la streptavidine, la dioxygénine, les haptènes, les colorants, les agents luminescents tels que les agents radioluminescents, chémoluminescents, bioluminescents, fluorescents, phosphorescents.

Les polynucléotides selon l'invention peuvent ainsi être utilisés comme amorce et/ou sonde dans des procédés mettant en oeuvre notamment la technique de PCR (amplification en chaîne par polymérase) (Rolfes et al., 1991, Berlin : Springer-Verlag).

Cette technique nécessite le choix de paires d'amorces oligonucléotidiques encadrant le fragment qui doit être amplifié. On peut, par exemple, se référer à la technique décrite dans le brevet américain U.S. N° 4,683,202. Les fragments amplifiés peuvent être identifiés, par exemple après une électrophorèse en gel d'agarose ou de polyacrylamide, ou après une technique chromatographique comme la filtration sur gel ou la chromatographie échangeuse d'ions, puis séquencés. La spécificité de l'amplification peut être contrôlée en utilisant les séquences nucléotidiques de polynucléotides de l'invention comme matrice, des plasmides contenant ces séquences ou encore les produits d'amplification dérivés. Les fragments nucléotidiques amplifiés peuvent être utilisés comme réactifs dans des réactions d'hybridation afin de mettre en évidence la présence, dans un échantillon biologique, d'un acide nucléique cible de séquence complémentaire à celle desdits fragments nucléotidiques amplifiés.

L'invention vise également les acides nucléiques susceptibles d'être obtenus par amplification à l'aide d'amorces selon l'invention.

D'autres techniques d'amplification de l'acide nucléique cible peuvent être avantageusement employées comme alternative à la PCR (PCR-like) à l'aide de couple d'amorces de séquences nucléotidiques selon l'invention. Par PCR-like on entend désigner toutes les méthodes mettant en œuvre des reproductions directes ou indirectes des séquences d'acides nucléiques, ou bien dans lesquelles les systèmes de marquage ont été amplifiés, ces techniques sont bien entendu connues. En général, il s'agit de l'amplification de l'ADN par une polymérase ; lorsque l'échantillon d'origine est un ARN il convient préalablement d'effectuer une transcription reverse. Il existe actuellement de très nombreux procédés permettant cette amplification, comme par exemple la technique SDA (Strand Displacement Amplification) ou technique d'amplification à déplacement de brin (Walker et al., 1992, Nucleic Acids Res., 20:1691), la technique TAS (Transcription-based Amplification System) décrite par Kwoh et al. (1989, Proc. Natl. Acad. Sci. USA, 86, 1173), la technique 3SR (Self-Sustained Sequence Replication) décrite par Guatelli et al. (1990, Proc. Natl. Acad. Sci. USA, 87: 1874), la technique NASBA (Nucleic Acid Sequence Based Amplification) décrite par Kievitis et al. (1991, J. Virol. Methods, 35, 273), la technique TMA (Transcription Mediated Amplification), la technique LCR (Ligase Chain Reaction) décrite par Landegren et al. (1988, Science, 241, 1077), la technique de RCR (Repair Chain Reaction) décrite par Segev (1992, Kessler C. Springer Verlag, Berlin, New-York, 197-205), la technique CPR (Cycling Probe Reaction) décrite par Duck et al.

(1990, Biotechniques, 9, 142), la technique d'amplification à la Q-béta-réplacase décrite par Miele et al. (1983, J. Mol. Biol., 171, 281). Certaines de ces techniques ont depuis été perfectionnées.

Dans le cas où le polynucléotide cible à détecter est un ARNm, on utilise
5 avantageusement, préalablement à la mise en oeuvre d'une réaction d'amplification à l'aide des amorces selon l'invention ou à la mise en oeuvre d'un procédé de détection à l'aide des sondes de l'invention, une enzyme de type transcriptase inverse afin d'obtenir un ADNc à partir de l'ARNm contenu dans l'échantillon biologique. L'ADNc obtenu
servira alors de cible pour les amorces ou les sondes mises en oeuvre dans le procédé
10 d'amplification ou de détection selon l'invention.

La technique d'hybridation de sondes peut être réalisée de manières diverses (Matthews et al., 1988, Anal. Biochem., 169, 1-25). La méthode la plus générale consiste à immobiliser l'acide nucléique extrait des cellules de différents tissus ou de
cellules en culture sur un support (tels que la nitrocellulose, le nylon, le polystyrène) et
15 à incubé, dans des conditions bien définies, l'acide nucléique cible immobilisé avec la sonde. Après l'hybridation, l'excès de sonde est éliminé et les molécules hybrides formées sont détectées par la méthode appropriée (mesure de la radioactivité, de la fluorescence ou de l'activité enzymatique liée à la sonde).

Selon un autre mode de mise en oeuvre des sondes nucléiques selon l'invention,
20 ces dernières peuvent être utilisées comme sondes de capture. Dans ce cas, une sonde, dite « sonde de capture », est immobilisée sur un support et sert à capturer par hybridation spécifique l'acide nucléique cible obtenu à partir de l'échantillon biologique à tester et l'acide nucléique cible est ensuite détecté grâce à une seconde sonde, dite « sonde de détection », marquée par un élément facilement détectable.

25 Parmi les fragments d'acides nucléiques intéressants, il faut ainsi citer en particulier les oligonucléotides anti-sens, c'est-à-dire dont la structure assure, par hybridation avec la séquence cible, une inhibition de l'expression du produit correspondant. Il faut également citer les oligonucléotides sens qui, par interaction avec des protéines impliquées dans la régulation de l'expression du produit correspondant,
30 induiront soit une inhibition, soit une activation de cette expression.

De façon préférée, les sondes ou amorces selon l'invention sont immobilisées sur un support, de manière covalente ou non covalente. En particulier, le support peut être une puce à ADN ou un filtre à haute ou moyenne densité, également objet de la

présente invention (brevets WO 97/29212, WO 98/27317, WO 97/10365 et WO 92/10588).

On entend désigner par puce à ADN ou filtre haute densité, un support sur lequel sont fixées des séquences d'ADN, chacune d'entre elles pouvant être repérée par sa localisation géographique. Ces puces ou filtres diffèrent principalement par leur taille, le
5 matériau du support, et éventuellement le nombre de séquences d'ADN qui y sont fixées.

On peut fixer les sondes ou amorces selon la première invention sur des supports solides, en particulier les puces à ADN, par différents procédés de fabrication. En
10 particulier, on peut effectuer une synthèse *in situ* par adressage photochimique ou par jet d'encre. D'autres techniques consistent à effectuer une synthèse *ex situ* et à fixer les sondes sur le support de la puce à ADN par adressage mécanique, électronique ou par jet d'encre. Ces différents procédés sont bien connus de l'homme du métier.

Une séquence nucléotidique (sonde ou amorce) selon l'invention permet donc la
15 détection et/ou l'amplification de séquences nucléiques spécifiques. En particulier, la détection de cesdites séquences est facilitée lorsque la sonde est fixée sur une puce à ADN, ou à un filtre haute densité.

L'utilisation de puces à ADN ou de filtres à haute densité permet en effet de déterminer l'expression de gènes dans un organisme présentant une séquence
20 génomique proche de *P. luminescens* et le typage de la souche en cause.

La séquence génomique de *P. luminescens*, complétée par l'identification des gènes de ces organismes, telles que présentée dans la présente invention, servent de base à la construction de ces puces à ADN ou filtre.

La préparation de ces filtres ou puces consiste à synthétiser des oligonucléotides,
25 correspondant aux extrémités 5' et 3' des gènes ou à des fragments plus internes pour amplifier des fragments d'une taille adaptée, par exemple comprise environ entre 300 et 800 bases. Ces oligonucléotides sont choisis en utilisant la séquence génomique et ses annotations divulguées par la présente invention. La température d'appariement de ces oligonucléotides aux places correspondantes sur l'ADN doit être approximativement la
30 même pour chaque oligonucleotide. Ceci permet de préparer des fragments d'ADN correspondant à chaque gène par l'utilisation de conditions de PCR appropriées dans un environnement hautement automatisé. Les fragments amplifiés sont ensuite immobilisés sur des filtres ou des supports en verre, silicium ou polymères synthétiques et ces milieux sont utilisés pour l'hybridation.

La disponibilité de tels filtres et/ou puces et de la séquence génomique correspondante annotée permet d'étudier l'expression de grands ensembles, voire de la totalité des gènes de *Photorhabdus luminescens*, notamment de *P. luminescens* TT01, en préparant les ADN complémentaires, et en les hybridant à l'ADN ou aux oligonucléotides immobilisés sur les filtres ou les puces. De même, les filtres et/ou les puces permettent d'étudier la variabilité des souches ou des espèces, en préparant l'ADN de ces organismes et en les hybridant à l'ADN ou aux oligonucléotides immobilisés sur les filtres ou les puces.

Les différences entre les séquences génomiques des différentes souches ou espèces peuvent grandement affecter l'intensité de l'hybridation et, par conséquent, perturber l'interprétation des résultats. Il peut donc être nécessaire d'avoir la séquence précise des gènes de la souche que l'on souhaite étudier. La méthode de détection des gènes décrite plus loin en détail, impliquant la détermination de la séquence de fragments aléatoires d'un génome, et les organisant d'après la séquence du génome de *P. luminescens*, notamment de *P. luminescens* TT01, divulguée dans la présente invention, peut être très utile.

Les séquences nucléotidiques selon l'invention peuvent être utilisées dans des puces à ADN pour effectuer l'analyse de mutations. Cette analyse repose sur la constitution de puces capables d'analyser chaque base d'une séquence nucléotidique selon l'invention. On pourra notamment à cette fin mettre en œuvre les techniques de microséquençage sur puce à ADN. Les mutations sont détectées par extension d'amorces immobilisées hybridant à la matrice des séquences analysées, juste en position adjacente de celle du nucléotide muté recherché. Une matrice simple brin, ARN ou ADN, des séquences à analyser sera avantageusement préparée selon des méthodes classiques, à partir de produits amplifiés selon les techniques de type PCR. Les matrices d'ADN simple brin, ou d'ARN ainsi obtenues sont alors déposées sur la puce à ADN, dans des conditions permettant leur hybridation spécifique aux amorces immobilisées. Une polymérase thermostable, par exemple la Tth ou la Taq ADN polymérase, étend spécifiquement l'extrémité 3' de l'amorce immobilisée avec un analogue de nucléotide marqué complémentaire du nucléotide en position du site variable ; par exemple, un cyclage thermique est réalisé en présence des didéoxyribonucléotides fluorescents. Les conditions expérimentales seront adaptées notamment aux puces employées, aux amorces immobilisées, aux polymérases employées, et au système de marquage choisi. Un avantage du microséquençage, par rapport aux techniques basées sur l'hybridation

de sondes, est qu'il permet d'identifier tous les nucléotides variables avec une discrimination optimale dans des conditions de réactions homogènes ; utilisé sur des puces à ADN, il permet une résolution et une spécificité optimales pour la détection routinière et industrielle de mutations en multiplex.

- 5 Une puce à ADN ou un filtre peut être un outil extrêmement intéressant pour la détermination, la détection et/ou l'identification d'un micro-organisme. Ainsi, on préfère également les puces à ADN selon l'invention qui contiennent en outre au moins une séquence nucléotidique d'un micro-organisme autre que *Photorhabdus luminescens*, immobilisée sur le support de ladite puce. De préférence, le micro-organisme choisi l'est parmi les bactéries du genre *Photorhabdus* (ci-après désignées
10 comme bactéries associées à *P. luminescens*), ou les variants de *Photorhabdus luminescens* TT01.

- Une puce à ADN ou un filtre selon l'invention est un élément très utile de certains kits ou nécessaires pour la détection et/ou l'identification de micro-organismes,
15 en particulier les bactéries appartenant à l'espèce *Photorhabdus luminescens*, également objet de l'invention.

- Par ailleurs, les puces à ADN ou les filtres selon l'invention, contenant des sondes ou amorces spécifiques de *Photorhabdus luminescens*, sont des éléments très avantageux de kits ou nécessaires pour la détection et/ou la quantification de
20 l'expression de gènes de *Photorhabdus luminescens*.

- En effet, le contrôle de l'expression des gènes est un point critique pour optimiser la croissance et le rendement d'une souche, soit en permettant l'expression d'un ou plusieurs gènes nouveaux, soit en modifiant l'expression de gènes déjà présents dans la cellule. La présente invention fournit l'ensemble des séquences naturellement
25 actives chez *P. luminescens* permettant l'expression des gènes. Elle permet ainsi la détermination de l'ensemble des séquences exprimées chez *P. luminescens*. Elle fournit également un outil permettant de repérer les gènes dont l'expression suit un schéma donné. Pour réaliser cela, l'ADN de tout ou partie des gènes de *P. luminescens* peut être amplifié grâce à des amorces selon l'invention, puis fixé à un support comme par
30 exemple le verre ou le nylon ou une puce à ADN, afin de construire un outil permettant de suivre le profil d'expression de ces gènes. Cet outil, constitué de ce support contenant les séquences codantes sert de matrice d'hybridation à un mélange de molécules marquées reflétant les ARNs messagers exprimés dans la cellule (en particulier les sondes marquées selon l'invention). En répétant cette expérience à différents instants et

en combinant l'ensemble de ces données par un traitement approprié, on obtient alors les profils d'expression de l'ensemble de ces gènes. La connaissance des séquences qui suivent un schéma de régulation donné peut aussi être mise à profit pour rechercher de manière dirigée, par exemple par homologie, d'autres séquences suivant globalement, mais de manière légèrement différente le même schéma de régulation. En complément, il est possible d'isoler chaque séquence de contrôle présente en amont des segments servant de sondes et d'en suivre l'activité à l'aide de moyen approprié comme un gène rapporteur (luciférase, β -galactosidase, GFP). Ces séquences isolées peuvent ensuite être modifiées et assemblées par ingénierie métabolique avec des séquences d'intérêt en vue de leur expression optimale.

L'invention concerne également les polypeptides codés par une séquence nucléotidique selon l'invention, de préférence, par un fragment représentatif des séquences précédentes et correspondant à une séquence ORF. En particulier, les polypeptides de *Photorhabdus luminescens* TT01 de SEQ ID N° 42 à SEQ ID N° 3855 ou codés par les SEQ ID N° 5835 à SEQ ID N° 10784 sont objet de l'invention.

L'invention comprend également les polypeptides caractérisés en ce qu'ils comprennent un polypeptide choisi parmi :

- a) un polypeptide de séquence SEQ ID N° 42 à SEQ ID N° 3855 ou codé par une séquence SEQ ID N° 5835 à SEQ ID N° 10784 ;
- b) un polypeptide présentant au moins 80 % de préférence 85 %, 90 %, 95 % et 98 % d'identité avec un polypeptide selon l'invention ;
- c) un fragment d'au moins 5 acides aminés d'un polypeptide tel que défini en a) ;
- d) un fragment biologiquement actif d'un polypeptide tel que défini en a) ; et
- e) un polypeptide tel que défini en a), b), c) ou d) modifié.

Les séquences nucléotidiques codant pour les polypeptides décrits précédemment sont également objet de l'invention.

Dans la présente description, les termes polypeptides, séquences polypeptidiques, peptides et protéines sont interchangeable. Le terme polypeptide comprend toute séquence d'acides aminés permettant de générer une réponse anticorps.

Il doit être compris que l'invention ne concerne pas les polypeptides sous forme naturelle, c'est-à-dire qu'ils ne sont pas pris dans leur environnement naturel. En revanche, elle concerne ceux qui ont pu être isolés ou obtenus par purification à partir de sources naturelles, ou bien obtenus par recombinaison génétique, ou par synthèse

chimique, et qu'ils peuvent alors comporter des acides aminés non naturels comme cela sera décrit plus loin.

Par polypeptide présentant un certain pourcentage d'identité avec un autre, que l'on désignera également par polypeptide homologue, on entend désigner les polypeptides présentant par rapport aux polypeptides naturels, certaines modifications, en particulier une délétion, addition ou substitution d'au moins un acide aminé, une troncation, un allongement, une solution chimérique et/ou une mutation, ou les polypeptides présentant des modifications post-traductionnelles. Parmi les polypeptides homologues, on préfère ceux dont la séquence d'acides aminés présente au moins 80 %, de préférence 85 %, 90 %, 95 %, 98 % ou 99 % d'identité après alignement optimal avec les séquences d'acides aminés des polypeptides selon l'invention. Dans le cas d'une substitution, un ou plusieurs acide(s) aminé(s) consécutif(s) ou non consécutif(s) peuvent être remplacés par des acides aminés « équivalents ». L'expression « acides aminés équivalents » vise ici à désigner tout acide aminé susceptible d'être substitué à l'un des acides aminés de la structure de base sans cependant modifier essentiellement les activités biologiques des peptides correspondant telles qu'elles seront définies par la suite.

Ces acides aminés équivalents peuvent être déterminés soit en s'appuyant sur leur homologie de structure avec les acides aminés auxquels ils se substituent, soit sur des résultats d'essais comparatifs d'activité biologique entre les différents polypeptides susceptibles d'être effectués.

A titre d'exemple, on mentionne les possibilités de substitution susceptibles d'être effectuées sans qu'il résulte en une modification approfondie de l'activité biologique du polypeptide modifié correspondant. On peut remplacer ainsi la leucine par la valine ou l'isoleucine, l'acide aspartique par l'acide glutamine, la glutamine par l'asparagine, l'arginine par la lysine, etc., les substitutions inverses étant naturellement envisageables dans les mêmes conditions.

Les polypeptides homologues correspondent également aux polypeptides codés par les séquences nucléotidiques présentant un certain pourcentage d'identité avec les séquences nucléotidiques de l'invention ou identiques, telles que définies précédemment et comprennent ainsi dans la présente définition des polypeptides mutés ou correspondant à des variations inter ou intra espèces, pouvant exister chez *Photorhabdus*, et qui correspondent notamment à des troncatures, substitutions, délétions et/ou additions, d'au moins un résidu d'acides aminés.

Il est entendu que l'on calcule le pourcentage d'identité entre deux polypeptides de la même façon qu'entre deux séquences d'acides nucléiques. Ainsi, le pourcentage d'identité entre deux polypeptides est calculé après alignement optimal de ces deux séquences, sur une fenêtre d'homologie maximale. Pour définir ladite fenêtre
5 d'homologie maximale, on peut utiliser les mêmes algorithmes que pour les séquences d'acide nucléique.

Par fragment biologiquement actif d'un polypeptide selon l'invention, on entend désigner en particulier un fragment de polypeptide, tel que défini ci-après, présentant au moins une des caractéristiques biologiques des polypeptides selon l'invention,
10 notamment en ce qu'il est capable d'exercer de manière générale une activité même partielle, telle que par exemple :

- une activité enzymatique (métabolique), une activité pouvant être impliquée dans la biosynthèse ou la biodégradation de composés organiques ou inorganiques, ou de préférence une activité toxique ou antibiotique, notamment pour les insectes ou
15 micro-organismes (bactéries ou champignons), ou encore une activité impliquée dans la biosynthèse de ces toxines ou antibiotiques ; de telles protéines à activité enzymatique pourront notamment être utilisées dans des procédés de criblage et/ou de sélection de composés capables de modifier cette activité, en particulier de l'inhiber.

- une activité structurale (enveloppe cellulaire, molécule chaperonne, ribosome). Les protéines correspondant notamment à des protéines extramembranaires
20 pourront être en particulier utilisées comme immunogène pour la production d'anticorps, mono- ou polyclonaux dirigés spécifiquement contre ces protéines extramembranaires ;

- une activité de transport (d'énergie, d'ion) ; ou dans la sécrétion de protéine ;
25 - une activité dans le processus de réplication, amplification, préparation, transcription, traduction ou maturation, notamment de l'ADN, de l'ARN ou des protéines.

Par fragment de polypeptide selon l'invention, on entend désigner un polypeptide comportant au minimum 5 acides aminés, de préférence 10, 15, 25, 50, 100
30 et 150 acides aminés.

Les fragments de polypeptides peuvent correspondre à des fragments isolés ou purifiés naturellement présents dans les souches de *Photothabdus*, ou à des fragments qui peuvent être obtenus par clivage dudit polypeptide par une enzyme protéolytique telle que la trypsine ou la chymotrypsine ou la collagénase, par un réactif chimique

(bromure de cyanogène, CNBr) ou en plaçant ledit polypeptide dans un environnement très acide (par exemple à pH = 2,5). Des fragments polypeptidiques peuvent également être préparés par synthèse chimique, à partir d'hôtes transformés par un vecteur d'expression selon l'invention qui contiennent un acide nucléique permettant
5 l'expression dudit fragment, et placé sous le contrôle des éléments de régulation et/ou d'expression appropriés.

Par « polypeptide modifié » d'un polypeptide selon l'invention, on entend désigner un polypeptide obtenu par recombinaison génétique ou par synthèse chimique comme décrit plus loin, qui présente au moins une modification par rapport à la
10 séquence normale et de préférence au plus 10 % d'acides aminés modifiés par rapport à la séquence normale. Ces modifications peuvent être notamment portées sur des acides aminés nécessaires pour la spécificité ou l'efficacité de l'activité, ou à l'origine de la conformation structurale, de la charge, ou de l'hydrophobicité du polypeptide selon l'invention. On peut ainsi créer des polypeptides d'activité équivalente, augmentée ou
15 diminuée, ou de spécificité équivalente, plus étroite ou plus large. Parmi les polypeptides modifiés, il faut citer les polypeptides dans lesquels jusqu'à cinq acides aminés peuvent être modifiés, tronqués à l'extrémité N ou C-terminale, ou bien délétés, ou ajoutés.

Comme cela est indiqué, les modifications d'un polypeptide ont pour objectif
20 notamment :

- de permettre sa mise en œuvre dans des procédés de biosynthèse ou de biodégradation de composés organiques ou inorganiques, dans la biosynthèse de toxines ou d'antibiotiques,
- de permettre sa mise en œuvre dans des procédés de réplication,
25 d'amplification, de réparation et règle de transcription, de traduction, ou de maturation notamment de l'ADN, l'ARN, ou de protéines ; de permettre sa sécrétion améliorée,
- de modifier sa solubilité, l'efficacité ou la spécificité de son activité, ou encore de faciliter sa purification.

La synthèse chimique présente également l'avantage de pouvoir utiliser des
30 acides aminés non naturels ou des liaisons non peptidiques. Ainsi, il peut être intéressant d'utiliser des acides aminés non naturels, par exemple sous forme D, ou des analogues d'acides aminés, notamment des formes soufrées.

L'invention concerne en outre les séquences nucléiques ou peptidiques selon la présente invention à l'exception des séquences nucléiques ou peptidiques décrites dans

les documents WO 99/54472, WO 99/42589, WO 99/03328, WO 98/08932 et EP 0 823 215.

La présente invention fournit la séquence nucléotidique du génome de *Photorhabdus luminescens* TT01 sous forme de 41 contigs ou sous forme de 9 contigs, ainsi que certaines séquences polypeptidiques.

Les séquences nucléiques ou peptidiques ci-après caractérisées par leur fonction peuvent être également identifiées par leur séquence nucléotidique et d'acides aminés en se reportant au tableau I.

D'une manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 à activité de type toxine et/ou antibiotique, ou impliqué dans la synthèse de ces toxines et/ou antibiotiques.

D'une manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans la biosynthèse des acides aminés.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans la biosynthèse des cofacteurs, groupes prosthétiques et transporteurs.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide d'enveloppe cellulaire ou présent à la surface de *Photorhabdus luminescens* TT01 ou pour un de ses fragments.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans la machinerie cellulaire.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le métabolisme intermédiaire central.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le métabolisme énergétique.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le métabolisme des acides gras et des phospholipides.

- 5 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le métabolisme des nucléotides, des purines, des pyrimidines ou nucléosides.

- De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans les fonctions de régulation.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le processus de réplication.

- 15 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le processus de transcription.

- De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le processus de traduction.

- 20 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le processus de transport et de liaison des protéines.

- 25 De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans l'adaptation aux conditions atypiques.

- De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments dans la sensibilité aux médicaments et analogues.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide de *Photorhabdus*

luminescens TT01 ou un de ses fragments impliqué dans les fonctions relatives aux transposons.

De manière préférée, l'invention est relative à une séquence nucléotidique selon l'invention, caractérisée en ce qu'elle code pour un polypeptide spécifique de
5 *Photorhabdus luminescens* TT01 ou un de ses fragments.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments activité de type toxine et/ou antibiotique, ou impliqué dans la synthèse de ces toxines et/ou antibiotiques.

10 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans la biosynthèse des acides aminés.

Sous un autre aspect, de manière préférée, l'invention a pour objet un
15 polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans la biosynthèse des cofacteurs, groupes prosthétiques et transporteurs.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide
20 d'enveloppe cellulaire ou de surface de *Photorhabdus luminescens* TT01 ou un de ses fragments.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans la machinerie
25 cellulaire.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le métabolisme intermédiaire central.

30 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le métabolisme énergétique.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le métabolisme des acides gras et des phospholipides.

- 5 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le métabolisme des nucléotides, des purines, des pyrimidines ou nucléosides.

- 10 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans les fonctions de régulation.

- 15 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le processus de réplication.

- 20 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le processus de transcription.

- 25 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le processus de traduction.

- 30 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans le processus de transport et de liaison des protéines.

- 30 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans l'adaptation aux conditions atypiques.

 Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de

Photorhabdus luminescens TT01 ou un de ses fragments dans la sensibilité aux médicaments et analogues.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide de
5 *Photorhabdus luminescens* TT01 ou un de ses fragments impliqué dans les fonctions relatives aux transposons.

Sous un autre aspect, de manière préférée, l'invention a pour objet un polypeptide selon l'invention, caractérisé en ce qu'il s'agit d'un polypeptide spécifique de *Photorhabdus luminescens* TT01 ou un de ses fragments.

10 L'invention a également pour objet les opérons impliqués dans la synthèse d'antibiotiques et/ou de toxines.

Le tableau I fournit la liste de certains polypeptides selon l'invention, ainsi que leur localisation dans les contigs représentés par SEQ ID N° 1 à SEQ ID N° 41, et les analogies observées après comparaison dans les bases de données.

15 Le tableau II fournit la liste de certains polypeptides selon l'invention, ainsi que leur localisation dans les contigs représentés par SEQ ID N° 5826 à SEQ ID N° 5834, et les analogies observées après comparaison dans les bases de données. Dans le tableau II, les contig 1 à 9 sont identifiées par les séquences SEQ ID N° 5826 à SEQ ID N° 5834.

20 De manière tout à fait préférée, l'invention a également pour objet les polypeptides dont les fonctions annotées au tableau I, dernière colonne, ou dont les fonctions annotées au tableau II, avant-dernière colonne, correspondent à des activités de type toxine et/ou antibiotique, ou à polypeptides impliqués dans la synthèse de ces toxines et/ou antibiotiques, polypeptides de préférence choisis parmi :

25 a) les polypeptides de séquence SEQ ID N° 61, SEQ ID N° 62, SEQ ID N° 67, SEQ ID N° 171, SEQ ID N° 221, SEQ ID N° 268, SEQ ID N° 288, SEQ ID N° 380, SEQ ID N° 426, SEQ ID N° 438, SEQ ID N° 448, SEQ ID N° 453, SEQ ID N° 455, SEQ ID N° 456, SEQ ID N° 458, SEQ ID N° 501, SEQ ID N° 516, SEQ ID N° 530, SEQ ID N° 542, SEQ ID N° 551, SEQ ID N° 720, SEQ ID N° 761, SEQ ID N° 762, SEQ ID N°
30 814, SEQ ID N° 859, SEQ ID N° 860, SEQ ID N° 861, SEQ ID N° 862, SEQ ID N° 869, SEQ ID N° 1079, SEQ ID N° 1168, SEQ ID N° 1174, SEQ ID N° 1176, SEQ ID N° 1413, SEQ ID N° 1414, SEQ ID N° 1415, SEQ ID N° 1416, SEQ ID N° 1417, SEQ ID N° 1457, SEQ ID N° 1651, SEQ ID N° 1856, SEQ ID N° 1869, SEQ ID N° 2021, SEQ ID N° 2080, SEQ ID N° 2152, SEQ ID N° 2162, SEQ ID N° 2173, SEQ ID N°

2251, SEQ ID N° 2295, SEQ ID N° 2306, SEQ ID N° 2317, SEQ ID N° 2328, SEQ ID N° 2340, SEQ ID N° 2342, SEQ ID N° 2351, SEQ ID N° 2500, SEQ ID N° 3228, SEQ ID N° 3230, SEQ ID N° 3311, SEQ ID N° 3317, SEQ ID N° 3318, SEQ ID N° 3319, SEQ ID N° 3320, SEQ ID N° 3322, SEQ ID N° 3323, SEQ ID N° 3326, SEQ ID N° 3327, SEQ ID N° 3328, SEQ ID N° 3375, SEQ ID N° 3376, SEQ ID N° 3377, SEQ ID N° 3378, SEQ ID N° 3422, SEQ ID N° 3489, SEQ ID N° 3503, SEQ ID N° 3609, SEQ ID N° 3623, SEQ ID N° 3624, SEQ ID N° 3772, SEQ ID N° 3783, SEQ ID N° 3788 et SEQ ID N° 3794 ;

ou

- 10 b) les polypeptides codées par les séquences SEQ ID N° 5835 à SEQ ID N° 10784 homologues aux séquences telles que définies en a) comme indiquées à la dernière colonne du tableau II.

15 La présente invention a également pour objet les séquences nucléotidiques et/ou de polypeptides selon l'invention, caractérisées en ce que lesdites séquences sont enregistrées sur un support d'enregistrement dont la forme et la nature facilitent la lecture, l'analyse et/ou l'exploitation de ladite ou desdites séquence(s). Ces supports peuvent également contenir d'autres informations extraites de la présente invention, notamment les analogies avec des séquences déjà connues, et/ou des informations
20 concernant les séquences nucléotidiques et/ou de polypeptides d'une cellule de plante, d'un animal ou d'un micro-organisme autre que *P. luminescens*, notamment une cellule ou micro-organisme sensible à une toxine ou un antibiotique produit par *P. luminescens*, une bactérie du genre *Photorhabdus*, ou un variant de *P. luminescens*, ceci afin de faciliter l'analyse comparative et l'exploitation des résultats obtenus.

25 Parmi cesdits supports d'enregistrement, on préfère en particulier les supports lisibles par un ordinateur, tels les supports magnétiques, optiques, électriques ou hybrides, en particulier les disquettes informatiques, les CD-ROM, les serveurs informatiques. De tels supports d'enregistrement sont également objet de l'invention.

30 Les supports d'enregistrement selon l'invention, avec les informations apportées, sont très utiles pour le choix d'amorces ou de sondes nucléotidiques pour la détermination de gènes dans *Photorhabdus luminescens* TT01 ou souches proches de cet organisme. De même, l'utilisation de ces supports pour l'étude du polymorphisme génétique de souches proches de *Photorhabdus luminescens* TT01, en particulier par la détermination des régions de colinéarité, est très utile dans la mesure où ces supports

fournissent non seulement la séquence nucléotidique du génome de *Photorhabdus luminescens* TT01, mais également l'organisation génomique dans ladite séquence. Ainsi, les utilisations de supports d'enregistrement selon l'invention sont également des objets de l'invention.

- 5 L'analyse d'homologie entre différentes séquences s'effectue en effet avantageusement à l'aide de logiciels de comparaison de séquences, tels le logiciel Blast, ou les logiciels de la trousse GCG, décrits précédemment.

L'invention vise également les vecteurs de clonage et/ou d'expression, qui contiennent une séquence nucléotidique selon l'invention.

- 10 Les vecteurs selon l'invention comportent de préférence des éléments qui permettent l'expression et/ou la sécrétion des séquences nucléotidiques dans une cellule hôte déterminée.

- Le vecteur doit alors comporter un promoteur, des signaux d'initiation et de terminaison de la traduction, ainsi que des régions appropriées de régulation de la transcription. Il doit pouvoir être maintenu de façon stable dans la cellule hôte et peut éventuellement posséder des signaux particuliers qui spécifient la sécrétion de la protéine traduite. Ces différents éléments sont choisis et optimisés par l'homme du métier en fonction de l'hôte cellulaire utilisé. A cet effet, les séquences nucléotidiques selon l'invention peuvent être insérées dans des vecteurs à réplication autonome au sein de l'hôte choisi, ou être des vecteurs intégratifs de l'hôte choisi.
- 15 transcription. Il doit pouvoir être maintenu de façon stable dans la cellule hôte et peut éventuellement posséder des signaux particuliers qui spécifient la sécrétion de la protéine traduite. Ces différents éléments sont choisis et optimisés par l'homme du métier en fonction de l'hôte cellulaire utilisé. A cet effet, les séquences nucléotidiques selon l'invention peuvent être insérées dans des vecteurs à réplication autonome au sein de l'hôte choisi, ou être des vecteurs intégratifs de l'hôte choisi.
- 20 de l'hôte choisi, ou être des vecteurs intégratifs de l'hôte choisi.

De tels vecteurs sont préparés par des méthodes couramment utilisées par l'homme du métier, et les clones résultant peuvent être introduits dans un hôte approprié par des méthodes standards, telles que la lipofection, l'électroporation, le choc thermique, ou des méthodes chimiques.

- 25 Les vecteurs selon l'invention sont par exemple des vecteurs d'origine plasmidique ou virale. Ils sont utiles pour transformer des cellules hôtes afin de cloner ou d'exprimer les séquences nucléotidiques selon l'invention.

- Parmi ces vecteurs, on préfère également les vecteurs de clonage, et/ou d'expression selon l'invention, caractérisés en ce qu'ils contiennent une séquence nucléotidique choisie parmi les séquences SEQ ID N° 3856 à SEQ ID N° 5825, SEQ ID N° 5835 à SEQ ID N° 10784 ou leur fragment issu du génome de *P. luminescens*, notamment les séquences codant pour les polypeptides à activité toxine, antibiotiques ou impliqués dans ces activités, en particulier ceux précités dont les fonctions annotées au tableau I ci-après correspondent à ces activités.
- 30 nucléotidique choisie parmi les séquences SEQ ID N° 3856 à SEQ ID N° 5825, SEQ ID N° 5835 à SEQ ID N° 10784 ou leur fragment issu du génome de *P. luminescens*, notamment les séquences codant pour les polypeptides à activité toxine, antibiotiques ou impliqués dans ces activités, en particulier ceux précités dont les fonctions annotées au tableau I ci-après correspondent à ces activités.

L'invention comprend également les cellules hôtes transformées par un vecteur selon l'invention.

L'hôte cellulaire peut être choisi parmi des systèmes procaryotes ou eucaryotes, par exemple les cellules bactériennes mais également les cellules de levure ou les
5 cellules animales, en particulier les cellules de mammifères. On peut également utiliser des cellules d'insectes ou des cellules de plantes. Les cellules hôtes préférées selon l'invention sont en particulier les cellules procaryotes, de préférence les bactéries appartenant au genre *Photothabdus* ou à l'espèce *Photothabdus luminescens*, plus particulièrement *Photothabdus luminescens* TT01.

10 L'invention concerne également les végétaux et les animaux, excepté l'Homme, qui comprennent une cellule transformée selon l'invention. Les cellules transformées selon l'invention sont utilisables dans des procédés de préparation de polypeptides recombinants selon l'invention. Les procédés de préparation d'un polypeptide selon l'invention sous forme recombinante, caractérisés en ce qu'ils mettent en œuvre un
15 vecteur et/ou une cellule transformée par un vecteur selon l'invention sont eux-mêmes compris dans la présente invention. De préférence, on cultive une cellule transformée par un vecteur selon l'invention dans des conditions qui permettent l'expression dudit polypeptide et on récupère ledit peptide recombinant.

Ainsi qu'il a été dit, l'hôte cellulaire peut être choisi parmi des systèmes
20 procaryotes ou eucaryotes. En particulier, il est possible d'identifier des séquences nucléotidiques selon l'invention, facilitant la sécrétion dans un tel système procaryote ou eucaryote. Un vecteur selon l'invention portant une telle séquence peut donc être avantageusement utilisé pour la production de protéines recombinantes, destinées à être sécrétées. En effet, la purification de ces protéines recombinantes d'intérêt sera facilitée
25 par le fait qu'elles sont présentes dans le surnageant de la culture cellulaire plutôt qu'à l'intérieur des cellules hôtes.

On peut également préparer les polypeptides selon l'invention par synthèse chimique. Un tel procédé de préparation est également un objet de l'invention. L'homme du métier connaît les procédés de synthèse chimique, par exemple les
30 techniques mettant en œuvre des phases solides (voir notamment Steward et al., 1984, Solid phase peptides synthesis, Pierce Chem. Company, Rockford, 111, 2ème éd., (1984)) ou des techniques utilisant des phases solides partielles, par condensation de fragments ou par une synthèse en solution classique. Les polypeptides obtenus par

synthèse chimique et pouvant comporter des acides aminés non naturels correspondant sont également compris dans l'invention.

Les polypeptides hybrides selon l'invention sont très utiles pour obtenir des anticorps monoclonaux ou polyclonaux, capables de reconnaître spécifiquement les polypeptides selon l'invention.

Ces anticorps polyclonaux ou monoclonaux spécifiques peuvent être obtenus par les méthodes standards bien connues de l'homme de l'art, après immunisation d'un mammifère au moyen de ces polypeptides (ou de leur acide nucléique correspondant) ou par exemple selon la méthode classique de culture d'hybridome décrite par Köhler et Milstein (1975, Nature, 256, 495) pour les anticorps monoclonaux.

De tels anticorps monoclonaux ou polyclonaux, leurs fragments, ou les anticorps chimériques, reconnaissant les polypeptides selon l'invention, sont également objets de l'invention.

Les anticorps selon l'invention sont par exemple des anticorps chimériques, des anticorps humanisés, des fragments Fab, ou $F(ab')^2$. Ils peuvent également se présenter sous forme d'immunoconjugués ou d'anticorps marqués afin d'obtenir un signal détectable et/ou quantifiable.

Ainsi, les anticorps selon l'invention peuvent être employés dans un procédé pour la détection et/ou l'identification de bactéries appartenant au genre *Photothabdus* et/ou à l'espèce *Photothabdus luminescens* dans un échantillon biologique, caractérisé en ce qu'il comprend les étapes suivantes :

- a) mise en contact de l'échantillon biologique avec un anticorps selon l'invention ;
- b) mise en évidence du complexe antigène-anticorps éventuellement formé.

Les anticorps selon la présente invention sont également utilisables afin de détecter une expression d'un gène de *Photothabdus luminescens* TT01. En effet, la présence du produit d'expression d'un gène reconnu par un anticorps spécifique dudit produit d'expression peut être détectée par la présence d'un complexe antigène-anticorps formé après la mise en contact de la souche de *Photothabdus luminescens* TT01 avec un anticorps selon l'invention. La souche bactérienne utilisée peut avoir été « préparée », c'est-à-dire centrifugée, lysée, placée dans un réactif approprié pour la constitution du milieu propice à la réaction immunologique. En particulier, on préfère un procédé de détection de l'expression dans le gène, correspondant à un Western blot, pouvant être effectué après une électrophorèse sur gel de polyacrylamide d'un lysat de la souche bactérienne, en présence ou en l'absence de conditions réductrices (SDS-

PAGE). Après migration et séparation des protéines sur le gel de polyacrylamide, on transfère lesdites protéines sur une membrane appropriée (par exemple en nylon) et on détecte la présence de la protéine ou du polypeptide d'intérêt, par mise en contact de ladite membrane avec un anticorps selon l'invention.

5 Ainsi, la présente invention comprend également les kits ou nécessaires pour la mise en œuvre d'un procédé tel que décrit (de détection de l'expression d'un gène de *Photothabdus luminescens* TT01, ou pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Photothabdus luminescens*), comprenant les éléments suivants :

- a) un anticorps polyclonal ou monoclonal selon l'invention ;
- 10 b) éventuellement, les réactifs pour la constitution du milieu propice à la réaction immunologique ;
- c) éventuellement, les réactifs permettant la mise en évidence des complexes antigène-anticorps produits par la réaction immunologique.

15 Les polypeptides et les anticorps selon l'invention peuvent avantageusement être immobilisés sur un support, notamment une puce à protéines. Une telle puce à protéines est un objet de l'invention, et peut également contenir au moins un polypeptide d'un micro-organisme autre que *Photothabdus luminescens* ou un anticorps dirigé contre un composé d'un micro-organisme autre que *Photothabdus luminescens*.

20 Les puces à protéines ou filtres à haute densité contenant des protéines selon l'invention peuvent être construites de la même manière que les puces à ADN selon l'invention. En pratique, on peut effectuer la synthèse des polypeptides directement fixés sur la puce à protéines, ou effectuer une synthèse *ex situ* suivie d'une étape de fixation sur ladite puce du polypeptide synthétisé. Cette dernière méthode est préférable, lorsque l'on désire fixer des protéines de taille importante sur le support, ces protéines
25 étant avantageusement préparées par génie génétique. Toutefois, si l'on ne désire fixer que des peptides sur le support de ladite puce, il peut être plus intéressant de procéder à la synthèse desdits peptides directement *in situ*.

30 Les puces à protéines selon l'invention peuvent être avantageusement utilisées dans des kits ou nécessaires pour la détection et/ou l'identification de bactéries associées à l'espèce *Photothabdus luminescens* ou à un micro-organisme, ou de façon plus générale dans des kits ou nécessaires pour la détection et/ou l'identification de micro-organismes. Lorsque l'on fixe les polypeptides selon l'invention sur les puces à ADN, on recherche la présence d'anticorps dans les échantillons testés, la fixation d'un

anticorps selon l'invention sur le support de la puce à protéines permettant l'identification de la protéine dont ledit anticorps est spécifique.

De préférence, on fixe un anticorps selon l'invention sur le support de la puce à protéines, et on détecte la présence de l'antigène correspondant, spécifique de

5 *Photorhabdus luminescens*.

Une puce à protéines ci-dessus décrite peut être utilisée pour la détection de produits de gènes, pour établir un profil d'expression desdits gènes, en complément d'une puce à ADN selon l'invention. Les puces à protéines selon l'invention sont également extrêmement utiles pour les expériences de protéomique, qui étudie les
10 interactions entre les différentes protéines d'une cellule de plante, d'un animal, tel qu'un insecte, ou d'un micro-organisme autre que *P. luminescens*.

Ainsi, l'invention comprend également une puce à protéine selon l'invention, caractérisée en ce qu'elle contient en outre au moins un polypeptide d'une cellule de plante, d'un animal ou d'un micro-organisme autre que *P. luminescens*, immobilisé sur
15 le support de ladite puce, de préférence ladite cellule ou micro-organisme autre est choisie parmi une cellule ou micro-organisme sensible à une toxine ou un antibiotique produit par *P. luminescens*.

De façon simplifiée, on fixe des peptides représentatifs des différentes protéines d'un organisme sur un support. Puis, on met ledit support en contact avec des protéines
20 marquées, et après une étape optionnelle de rinçage, on détecte des interactions entre lesdites protéines marquées et les peptides fixés sur la puce à protéines.

Ainsi, les puces à protéines comprenant une séquence polypeptidique selon l'invention ou un anticorps selon l'invention sont objet de l'invention, ainsi que les kits ou nécessaires les contenant.

25 La présente invention couvre également un procédé de détection et/ou d'identification de bactéries appartenant à l'espèce *Photorhabdus luminescens* dans un échantillon biologique, qui met en œuvre une séquence nucléotidique selon l'invention.

Il doit être entendu que le terme échantillon biologique concerne dans la présente invention les échantillons prélevés à partir d'un organisme vivant (en
30 particulier sang, tissus, organes ou autres prélevés à partir d'un mammifère) ou un échantillon contenant du matériel biologique, c'est-à-dire de l'ADN ou de l'ARN. Un tel échantillon biologique comprend aussi les compositions alimentaires contenant des bactéries (par exemple les fromages, les produits laitiers), mais également des compositions alimentaires contenant des levures (bières, pains) ou autres. Le terme

échantillon biologique concerne aussi les bactéries isolées à partir de ces prélèvements ou compositions alimentaires.

Le procédé de détection et/ou d'identification mettant en œuvre les séquences nucléotidiques selon l'invention peut être de diverse nature.

5 On préfère un procédé comportant les étapes suivantes :

- a) éventuellement, isolement de l'ADN à partir de l'échantillon biologique à analyser, ou obtention d'un ADNc à partir de l'ARN de l'échantillon biologique ;
- b) amplification spécifique de l'ADN de bactéries appartenant à l'espèce *Photorhabdus luminescens* à l'aide d'au moins une amorce selon l'invention ;
- 10 c) mise en évidence des produits d'amplification.

Ce procédé est basé sur l'amplification spécifique de l'ADN, en particulier par une réaction d'amplification en chaîne.

On préfère également un procédé comprenant les étapes suivantes :

- a) mise en contact d'une sonde nucléotidique selon l'invention avec un échantillon 15 biologique, l'acide nucléique contenu dans l'échantillon biologique ayant, le cas échéant, préalablement été rendu accessible à l'hybridation, dans des conditions permettant l'hybridation de la sonde à l'acide nucléique d'une bactérie appartenant à l'espèce *Photorhabdus luminescens* ;
- b) mise en évidence de l'hybride éventuellement formé entre la sonde nucléotidique et 20 l'ADN de l'échantillon biologique.

Un tel procédé ne doit pas être limité à la détection de la présence de l'ADN contenu dans l'échantillon biologique à tester, il peut être également mis en œuvre pour détecter l'ARN contenu dans ledit échantillon. Ce procédé englobe en particulier les Southern et Northern blot.

25 Un autre procédé préféré selon l'invention comprend les étapes suivantes :

- a) mise en contact d'une sonde nucléotidique immobilisée sur un support selon l'invention avec un échantillon biologique, l'acide nucléique de l'échantillon, ayant, le cas échéant, été préalablement rendu accessible à l'hybridation, dans des conditions permettant l'hybridation de la sonde à l'acide nucléique d'une bactérie 30 appartenant à l'espèce *Photorhabdus luminescens* ;
- b) mise en contact de l'hybride formé entre la sonde nucléotidique immobilisée sur un support et l'acide nucléique contenu dans l'échantillon biologique, le cas échéant après élimination de l'ADN de l'échantillon biologique n'ayant pas hybridé avec la sonde, avec une sonde nucléotidique marquée selon l'invention ;

c) mise en évidence du nouvel hybride formé à l'étape b).

Ce procédé est avantageusement utilisé avec une puce à ADN selon l'invention, l'acide nucléique recherché s'hybridant avec une sonde présente à la surface de ladite puce, et étant détecté par l'utilisation d'une sonde marquée. Ce procédé est
5 avantageusement mis en œuvre en combinant une étape préalable d'amplification de l'ADN ou de l'ADN complémentaire obtenu éventuellement par transcription inverse, à l'aide d'amorces selon l'invention.

Ainsi, la présente invention englobe également les kits ou nécessaires pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Photorhabdus luminescens*, caractérisé en ce qu'il comprend les éléments suivants :
10

- a) une sonde nucléotidique selon l'invention ;
- b) éventuellement, les réactifs nécessaires à la mise en œuvre d'une réaction d'hybridation ;
- c) éventuellement, au moins une amorce selon l'invention ainsi que les réactifs
15 nécessaires à une réaction d'amplification de l'ADN.

De même, la présente invention englobe également les kits ou nécessaires pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Photorhabdus luminescens* TT01, caractérisé en ce qu'il comprend les éléments suivants :

- a) une sonde nucléotidique, dite sonde de capture, selon l'invention ;
- 20 b) une sonde oligonucléotidique, dite sonde de révélation, selon l'invention ;
- c) éventuellement, au moins une amorce selon l'invention ainsi que les réactifs nécessaires à une réaction d'amplification de l'ADN.

Enfin, les kits ou nécessaires pour la détection et/ou l'identification de bactéries appartenant à l'espèce *Photorhabdus luminescens*, caractérisés en ce qu'ils comprennent
25 les éléments suivants :

- a) au moins une amorce ou une sonde selon l'invention ;
- b) éventuellement, les réactifs nécessaires pour effectuer une réaction d'amplification d'ADN ;
- c) éventuellement, un composant permettant de vérifier la séquence du fragment
30 amplifié, plus particulièrement une sonde oligonucléotidique selon l'invention, sont également objets de la présente invention.

De préférence, lesdites amorces et/ou sondes et/ou polypeptides et/ou anticorps selon la présente invention utilisés dans les procédés et/ou kits ou nécessaires selon la présente invention sont choisis parmi les amorces et/ou sondes et/ou polypeptides et/ou

anticorps spécifiques de l'espèce *Phototrhaddus luminescens*. De manière préférée, ces éléments sont choisis parmi les séquences nucléotidiques codant pour une protéine sécrétée, parmi les polypeptides sécrétés, ou parmi les anticorps dirigés contre des polypeptides sécrétés de *Phototrhaddus luminescens*.

5 La présente invention a également pour objet les souches de *Phototrhaddus luminescens* TT01 contenant une ou plusieurs mutation(s) dans une séquence nucléotidique selon l'invention, en particulier une séquence ORF, ou leurs éléments régulateurs (en particulier promoteurs).

10 On préfère, selon la présente invention, les souches de *Phototrhaddus luminescens* TT01 présentant une ou plusieurs mutation(s) dans les séquences nucléotidiques codant pour des polypeptides de préférence à activité de type toxine ou antibiotique, ou impliqués dans leur biosynthèse, ou encore sous un autre aspect impliqués dans la machinerie cellulaire, en particulier la sécrétion, le métabolisme intermédiaire central, le métabolisme énergétique, les processus de synthèse des acides
15 aminés, de transcription et de traduction, de synthèse des polypeptides.

Lesdites mutations peuvent mener à une inactivation du gène, ou en particulier lorsqu'elles sont situées dans les éléments régulateurs dudit gène, à une surexpression de celui-ci.

20 Selon la présente invention, les souches de *Phototrhaddus luminescens* TT01 présentant une ou plusieurs mutation(s) pourront être utilisées pour valider la fonction de gène sauvage de *Phototrhaddus luminescens*.

25 L'invention concerne en outre l'utilisation d'une séquence nucléotidique selon l'invention, d'un polypeptide selon l'invention, d'un anticorps selon l'invention, et/ou d'une cellule selon l'invention, pour la sélection de composé organique ou inorganique capable de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes d'une cellule végétale ou animale, ou d'un micro-organisme autre que *P. luminescens*, dont, par exemple, on veut modifier la résistance ou la sensibilité à au moins une toxine ou antibiotique produit par *P. luminescens*.

30 L'invention comprend également une méthode de sélection de composés capables de se lier à un polypeptide ou un de ses fragments selon l'invention, capables de se lier à une séquence nucléotidique selon l'invention, ou capables de reconnaître un anticorps selon l'invention, et/ou capables de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, et/ou de modifier la croissance ou la réplication cellulaire de cellules eucaryotes ou procaryotes, ou capables d'induire, d'inhiber ou d'accroître chez

un organisme animal ou végétal la résistance ou la sensibilité à au moins une toxine ou antibiotique produit par *P. luminescens*, ladite méthode comprenant les étapes suivantes :

- 5 a) mise en contact dudit composé avec ledit polypeptide, ladite séquence nucléotidique et/ou avec une cellule transformée selon l'invention ;
- b) détermination de la capacité dudit composé à se lier avec ledit polypeptide ou ladite séquence nucléotidique, ou de moduler, de réguler, d'induire ou d'inhiber l'expression de gènes, ou de moduler la croissance ou la réplication cellulaire, ou d'induire, d'inhiber ou d'accroître chez un organisme animal ou végétal la
10 résistance ou la sensibilité à au moins une toxine ou antibiotique produit par *P. luminescens*.

Les cellules transformées selon l'invention, pourront avantageusement servir de modèle et être utilisées dans des procédés pour étudier, identifier et/ou sélectionner des composés susceptibles d'être responsables de la résistance ou la sensibilité à au moins
15 une toxine ou antibiotique produit par *P. luminescens*. Les composés susceptibles d'être sélectionnés peuvent être des composés organiques tels que des polypeptides ou hydrates de carbone ou tous autres composés organiques ou inorganiques déjà connus, ou des composés organiques nouveaux élaborés à partir de techniques de modélisation moléculaire et obtenus par synthèse chimique ou biochimique, ces techniques étant
20 connues de l'homme de l'art.

L'invention concerne les composés susceptibles d'être sélectionnés par une méthode de sélection selon l'invention.

L'invention concerne également une composition, notamment pesticide ou pharmaceutique, comprenant un composé choisi parmi les composés suivants :

- 25 a) une séquence nucléotidique selon l'invention ;
- b) un polypeptide selon l'invention ;
- c) un vecteur selon l'invention ;
- d) un anticorps selon l'invention ; et
- e) un composé susceptible d'être sélectionné par une méthode de sélection selon
30 l'invention,

éventuellement en association avec un véhicule pharmaceutiquement acceptable.

L'invention concerne aussi une composition pharmaceutique selon l'invention pour la prévention ou le traitement d'une infection par un micro-organisme, tel qu'une

bactérie ou un champignon, sensible à au moins une toxine ou antibiotique produit par *P. luminescens*.

L'invention concerne aussi une composition pesticide, notamment contre les insectes, bactéries et/ou champignons, selon l'invention, pour la prévention ou le traitement de plantes infectées par des animaux, tels que des insectes, ou par un micro-organisme, tel qu'une bactérie ou un champignon, sensible à au moins une toxine ou antibiotique produit par *P. luminescens*.

L'invention comprend aussi l'utilisation d'une cellule transformée selon l'invention, pour la préparation d'une toxine ou d'un antibiotique produit par *P. luminescens*.

On entend désigner par véhicule pharmaceutiquement acceptable, un composé ou une combinaison de composés entrant dans une composition pharmaceutique ne provoquant pas de réactions secondaires et qui permet par exemple la facilitation de l'administration du composé actif, l'augmentation de sa durée de vie et/ou de son efficacité dans l'organisme, l'augmentation de sa solubilité en solution ou encore l'amélioration de sa conservation. Ces véhicules pharmaceutiquement acceptables sont bien connus et seront adaptés par l'homme de l'art en fonction de la nature et du mode d'administration du composé actif choisi.

De préférence, ces composés pharmaceutiques seront administrés par voie systémique, en particulier par voie intraveineuse, par voie intramusculaire, intradermique ou sous-cutanée, ou par voie orale.

Leurs modes d'administration, posologies et formes galéniques optimaux peuvent être déterminés selon les critères généralement pris en compte dans l'établissement d'un traitement adapté à un patient comme par exemple l'âge ou le poids corporel du patient, la gravité de son état général, la tolérance au traitement et les effets secondaires constatés.

Enfin, l'invention comprend l'utilisation d'une composition selon l'invention, pour la préparation d'un médicament destiné à la prévention ou le traitement d'une infection par un micro-organisme, tel qu'une bactérie ou un champignon, sensible à au moins une toxine ou antibiotique produit par *P. luminescens*.

Par ailleurs, la présente invention a également pour objet une banque d'ADN génomique d'une bactérie du genre *Phototrhabdus*, de manière préférée, *Phototrhabdus luminescens*, de manière préférée la souche TT01.

Les banques d'ADN génomique décrites dans la présente invention, en particulier la banque BAC déposée à la CNCM le 12 mai 2000 sous le n° I-2478 et qui recouvre le génome de *Photothabdus luminescens* TT01.

5 L'invention concerne également un procédé d'identification d'au moins une séquence nucléotidique de *P. luminescens* non présente dans le génome d'une autre espèce de bactérie, notamment pathogène, et/ou d'identification d'au moins une séquence nucléotidique d'un génome d'une bactérie, notamment pathogène, d'une autre espèce que *P. luminescens* et non présente dans le génome de *P. luminescens*, caractérisée en ce qu'elle comprend les étapes suivantes :

- 10 a) on aligne les séquences nucléotidiques de *P. luminescens* selon l'invention, ou contenues dans une banque génomique selon l'invention, avec la séquence génomique de l'autre espèce de bactérie, ou l'un de ses fragments ; et
- b) on traite les données obtenues par cet alignement pour isoler et identifier la ou lesdites séquences uniquement présentes dans l'un ou l'autre génome.

15 Une telle méthode, appelée encore « génomique soustractive » peut être utilisée ici pour identifier une séquence responsable de la pathogénicité d'une bactérie, telle qu'une bactérie gram négative, dont la bactérie *P. luminescens*, non pathogène, peut servir de modèle de comparaison.

20 La présente invention concerne ainsi les méthodes pour l'isolement d'un polynucléotide d'intérêt présent chez une souche de *Photothabdus* et absente chez une autre souche ou espèce, qui utilise au moins une banque d'ADN basée par exemple sur un plasmide pcDNA2.1 contenant le génome de *Photothabdus*. La méthode selon l'invention pour l'isolement d'un polynucléotide d'intérêt peut comprendre les étapes suivantes :

- 25 a) isoler au moins un polynucléotide contenu dans un clone de la banque d'ADN d'origine de *Photothabdus* ;
- b) isoler :
- 30 - au moins un polynucléotide génomique ou ADNc d'une bactérie, ladite bactérie appartenant à une souche ou espèce différente de la souche *Photothabdus* utilisée pour la construction de la banque d'ADN de l'étape a) ou, de façon alternative,
- au moins un polynucléotide contenu dans un clone d'une banque d'ADN préparé à partir du génome d'une bactérie appartenant à une souche ou espèce différente de la souche *Photothabdus* utilisée pour la construction de la banque d'ADN de

l'étape a) et hybrider le polynucléotide de l'étape a) au polynucléotide de l'étape b) ;

c) sélectionner les polynucléotides de l'étape a) qui n'ont pas formé de complexe d'hybridation avec les polynucléotides de l'étape b) ;

5 d) caractériser le polynucléotide sélectionné.

On peut préparer le polynucléotide de l'étape a) par la digestion d'au moins un clone recombinant avec une enzyme de restriction appropriée, et de façon optionnelle, l'amplification de l'insert polynucléotide qui en résulte.

10 Ainsi, la méthode de l'invention permet à l'homme du métier d'effectuer des études génomiques comparatives entre une bactérie du genre *Photorhabdus*, et entre par exemple une souche ou espèce pathogène.

En particulier, il est possible d'étudier et de déterminer les régions de polymorphisme entre lesdites souches.

15 La présente invention concerne également l'utilisation des séquences nucléiques ou des polypeptides selon la présente invention :

- pour la préparation de bio-pesticides, notamment d'entomotoxines, d'antibiotiques, d'antifongiques ou de cytotoxines,

20 - pour la sécrétion de protéines,

- comme facteurs de virulence,

- pour le contrôle par l'intermédiaire du quorum-sensing, pour l'identification de cibles pour les maladies humaines dont *Photorhabdus luminescens* est un modèle (en particulier la peste ou la coqueluche), et

25 - pour l'identification de cibles contre les bactéries Gram négatives pathogènes par la méthode de génomique soustractive (comme par exemple par comparaison avec *E. Coli* ou d'autres bactéries pathogènes gram négatives).

La présente invention concerne également l'utilisation des polypeptides selon la présente invention pour le criblage de composés capables de moduler l'activité de ces polypeptides, notamment les polypeptides à activité enzymatique.

30 D'autres caractéristiques et avantages de l'invention apparaissent dans les exemples suivants :

EXEMPLES

Exemple 1 : Matériels et Méthodes

La stratégie de séquençage du génome de *Photothabdus luminescens* souche TT01 repose sur un séquençage alléatoire (shot-gun). La première étape de ce travail a consisté à cloner l'ADN génomique de la bactérie *Photothabdus luminescens* dans différents vecteurs (plasmides et BAC).

5 Banques d'ADN génomique de *Photothabdus luminescens* utilisées.

Trois banques d'ADN génomique ont été réalisées :

I) - Une banque d'ADN génomique dans un vecteur bactérien à haut nombre de copies (pcDNA2.1, Invitrogen). Taille moyenne des inserts 1,5 kb.

10 II) - Une banque d'ADN génomique dans un vecteur bactérien à faible nombre de copies (pSYX34). Taille moyenne des inserts 10 kb.

III) - Une banque d'ADN génomique dans un vecteur BAC (pBeloBAC11, California Institute of Technology). Taille moyenne des inserts 50 à 100 kb.

15 Deux batchs d'ADN de la souche TT01 de la bactérie *Photothabdus luminescens* ont été extraits le 30/10/1998 et le 14/04/1999.

I) Etablissement d'une banque d'ADN génomique dans le vecteur bactérien pcDNA2.1 (Invitrogen)

A) Préparation du vecteur : pcDNA2.1

20 Nous avons préparé le plasmide pcDNA2.1, en réalisant en parallèle deux midipreps (KIT QIAGEN) selon les conditions préconisées par le fabricant. Le vecteur pcDNA2.1 a été digéré par l'enzyme de restriction BstX1.

B) Préparation de l'ADN chromosomique de *Photothabdus luminescens* souche TT01 et ligation dans le vecteur pcDNA2.1

25 1) Dissolution de l'ADN

Un culot sec d'ADN génomique de la souche TT01 préparé le 30/10/98 a été repris dans 200 µl de TE 10:1 puis dissout 30 min à 65°C. Sa concentration a été estimée à 0,15 µg/µl.

2) Nébulisation de l'ADN

30 50 µl d'ADN génomique de la souche TT01 dans 2 ml d'H₂O qsp ont été nébulisés durant 45 sec à une pression de 1 bar d'azote, centrifugés 2 min à 600 rpm afin de récupérer la totalité du volume.

3) Précipitation de l'ADN

Cet ADN a ensuite été précipité à l'acétate de sodium (2 ml d'ADN + 0,2 ml d'acétate de Na 3M pH 5,2 + 5 ml d'éthanol absolu ; 2 h à - 20°C ; centrifugé à 30 min à 14 000 rpm, 4°C puis redissous dans 100 µl d'eau.

4) Analyse de l'ADN

5 4 µl ont été déposés sur un gel d'agarose à 1 % en TBE.

Des fragments d'ADN de la taille attendue 500 pdb à 3 kb ont été visualisés.

5) Réparation de l'ADN

Afin de rendre les extrémités des fragments d'ADN franches (blunt end) une réparation à l'aide de la T4 DNA polymérase a été effectuée.

10 Dans 2 tubes séparés on mélange :

- 48 µl d'ADN de l'étape 3),

- 100 µl d'H₂O,

- 20 µl de tampon de ligation 5X,

- 2 µl de dNTP mix (10 mM),

15 - 5 µl de T4 DNA polymérase (Boehringer).

On incube 25 min à température ambiante puis on arrête la réaction par chauffage 15 min à 75°C.

6) Précipitation de l'ADN

20 Cet ADN a ensuite été précipité la nuit à - 20°C à l'acétate de sodium (1/10 du volume d'Acétate de Na et 2,5 volume d'éthanol absolu), centrifugé puis le culot d'ADN obtenu a été séché à l'air et redissout dans 30 µl d'eau.

7) Ligation de l'ADN

Cet ADN a été ligué une nuit à 16°C aux adaptateurs Bstx A + Bstx B (Invitrogen) en présence de 2 µl de ligase.

25 8) Préparation des inserts

Après migration de l'ADN ligué aux adaptateurs dans un gel d'agarose à 1 %, en TAE à 70 Volts, la région d'intérêt (comprise entre 1 et 3 Kb) a été découpée en quatre fragments.

9) Purification des inserts

30 Les fragments d'agarose contenant les régions d'intérêts ont été purifiés par GeneClean (BIO101) selon les conditions préconisées par le fabricant.

Un aliquot a été déposé sur un minigel d'agarose pour valider la qualité de la purification.

10) Ligation des inserts dans le vecteur pCDNA2.1 (Invitrogen)

- 4 µl d'ADN (insert après l'étape de purification GeneClean, étape 9),
- 2 µl de plasmide pCDNA2.1 (après l'étape de digestion BstX1 puis purification GeneClean),
- 2 µl de tampon de ligation (10X),
- ajouter 2 µl de ligase,
- 10 µl H₂O (volume total : 20 µl).

Incubation une nuit à 16°C.

11) Transformation de cellules ultracompétentes XL2 Blue (Stratagene)

La banque d'ADN génomique obtenue à l'étape 10 a été intégrée dans les
10 cellules ultracompétentes XL2 Blue (Stratagene) selon les conditions préconisées par le
fabricant.

L'analyse des inserts de 24 clones par digestion par l'enzyme de restriction PvuII et par séquençage des extrémités a été effectuée et a donné des résultats satisfaisants.

II) Etablissement d'une banque d'ADN génomique dans le vecteur bactérien

La technique de remplissage partiel (PARTIAL FILL-IN), développée dans le laboratoire, nous a permis de construire une banque d'ADN génomique de la souche 20 TT01 de la bactérie *Photorhabdus luminescens* clonée dans le plasmide pSYX34 (taille des inserts environ 10 Kb).

Note : dans ce cas, la digestion par l'enzyme de restriction Sal I, du vecteur pSYX34, libère les extrémités suivantes :

5' TCGAC-

G- 5'

Le PARTIAL FILL-IN a été réalisé, en présence des déoxynucléotides dCTP et dTTP.

5' TCGAC-

CTG- 5'

30 A) Préparation du vecteur : pSYX34

1) Obtention du vecteur

On a préparé du plasmide pSYX34, en réalisant en parallèle deux midipreps, KIT QIAGEN selon les conditions préconisées par le fabricant.

2) Digestion du plasmide pSYX34 par l'enzyme de restriction Sal I

Le volume final sera de 100 μ l :

- 20 μ l pSYX34,
- 10 μ l de tampon H,
- 66 μ l d' H_2O ,
- 4 μ l Sal I.

Incubation 2 h à 37°C.

Un aliquot ainsi qu'un marqueur de poids moléculaire ont été déposés sur un minigel d'agarose pour valider la qualité de la purification.

3) Extraction au chloroforme

- 10 L'extraction au chloroforme permet d'arrêter la digestion enzymatique, et d'éliminer toutes traces protéiques.

Après digestion, on récupère 95 μ l,
+ 105 μ l TE 10 mM,
+ 200 μ l chloroforme.

- 15 Vortexer, centrifuger 1 min à 1000 rpm.

Récupérer la phase aqueuse (phase supérieure).

4) Précipitation à l'acétate de sodium

- Ajouter 1/10 du volume d'acétate de sodium (3 M, pH : 5,2) soit 20 μ l,
- puis 2,5 volumes d'éthanol absolu propre, soit 500 μ l (flacon gardé à -
- 20 20°C).
- Laisser à - 20°C, au moins 1 heure (il est possible de laisser à - 20°C durant la nuit).
- Centrifuger à 4°C (chambre froide) durant 30 min, à 14.000 rpm.
- Eliminer le surnageant à l'aide de la pompe à vide.
- 25 - Ajouter 400 μ l d'éthanol à 70 %, centrifuger à 4°C, 5 min à 14.000 rpm.
- Eliminer le surnageant à l'aide de la pompe à vide, laisser sécher environ une heure sur la paillasse.

- Resuspendre le culot dans 20 μ l de TE 10 mM (1/10).

5) Partial fill-in

- 30 Volume final de la réaction : 50 μ l ; 20 μ l de pSYX34 digéré par Sal I
- 5 μ l de tampon synthesis,
 - 2,5 μ l de mix nucléotides (C-T) 1 mM,
 - 20,5 μ l d'eau,

- 2 μ l de Klenow (2 U/ μ l).

Laisser 30 min à température ambiante.

Vérification sur minigel d'agarose à 1 % puis congélation à - 20°C.

Mélange des nucléotides C-T :

5

mélanger :

- 2 μ l de nucléotides T (100 mM),

- 2 μ l de nucléotides C (100 mM),

- 16 μ l de TRIS 10 mM, pH = 7,5.

Les nucléotides sont ainsi dilués au 1/10, pour une concentration de 10 mM.

10

Une seconde dilution au 1/10 dans du tampon TRIS 10 mM, sera réalisée pour avoir une concentration de 1 mM.

D'autre part, au cours de la réaction, les nucléotides sont dilués au 1/20 (2,5 μ l dans 50 μ l), concentration finale ainsi obtenue de 50 μ M en nucléotides.

6) Purification du vecteur pSYX34 : gel préparatif

15

Préparer un gel d'agarose à 1 %, en TAE, des grands puits seront prévus pour nos échantillons.

Reprendre 30 μ l de pGB2 après le partial fill-in (il restera donc 20 μ l au congélateur), ajouter 6 μ l de solution de dépôt. En parallèle, déposer le marqueur de poids moléculaire dans les proportions suivantes :

20

- 5 μ l H₂O,

- 5 μ l du marqueur 1 Kb DNA,

- 2 μ l de la solution de dépôt.

Laisser migrer à 70 Volts.

25

Découper le gel côté marqueur à l'aide d'un scalpel, et repérer, en prenant une photo et à l'aide d'une règle, la région qui nous intéresse, dans notre cas on prendra la bande correspondant à 4 Kb. Chaque échantillon sera coupé en deux. Le poids de chaque échantillon nous indiquera son volume approximatif.

Nous aurons donc quatre échantillons à purifier par la technique GeneClean II.

7) Purification du vecteur pSYX34

30

- Reprendre dans 3 volumes de solution Iodure de Sodium (1 ml pour un échantillon de 0,2 g), mettre à 49°C, en agitant toutes les 2 min, jusqu'à complète dissolution de l'agarose.

- Ajouter 8 μ l de micro-billes : GLASSMILK R, laisser 5-10 min à température ambiante, l'ADN se fixe sur les micro-billes.

- Centrifuger 2 min à 14.000 rpm, éliminer le surnageant par aspiration.
 - Laver 3 fois avec la solution New Wash (600 µl/eppendorf, vortexer, centrifuger quelques secondes à 10.000 rpm), cette solution a été préparée et est gardée à - 20°C.
- 5 - Resuspendre le culot dans 10 µl d'H₂O, vortexer, laisser 5 min à 49°C. Ceci permet à l'ADN de se décrocher des micro-billes.
- Centrifuger 2 min à 14.000 tpm.
 - Récupérer les surnageants dans de nouveaux eppendorfs (N° 1 et N° 2, ...).
 - Ajouter à nouveau 10 µl d'H₂O sur les culots, pour être sûr de tout
- 10 récupérer, vortexer, laisser 2 min à 49°C.
- Centrifuger 2 min à 14.000 rpm.
 - Récupérer les surnageants dans les eppendorfs précédents (N° 1 et N° 2, ...).
 - Nous avons environ 20 µl de surnageant, centrifuger 2 min à 14.000 rpm.
 - Transférer les surnageants dans de nouveaux eppendorfs, de manière à être
- 15 sûr qu'il ne reste plus de micro-billes.
- Déposer sur un minigel d'agarose à 1 %, 1 µl de chaque préparation (+ 5 µl d'H₂O + 2 µl de solution de dépôt), laisser migrer à 80 volts, 2 heures.
- On gardera les échantillons les plus concentrés, ils seront alors congelés à - 20°C.
- 20 B) Préparation de l'ADN chromosomique de *Photorhabdus luminescens* souche TT01
- 1) Dissolution de l'ADN
- Un culot sec d'ADN génomique de la souche TT01 a été repris dans 200 µl de TE 10:1 puis dissous 30min à 65°C. Sa concentration a été estimée à 0,15 µg/µl.
- 25 2) Digestion partielle de l'ADN génomique par l'enzyme de restriction Sau3A
- 15 µl d'ADN ont été digérés par 2 ou 1 ou 0,5 ou 0,25 ou 0,125 ou 0,0625 ou 0,03125 unités d'enzyme de restriction Sau3A pendant 1 h à 37°C.
- 3) Extraction au chloroforme
- L'extraction au chloroforme nous permet d'arrêter la digestion enzymatique,
- 30 et d'éliminer toutes traces protéiques.
- Après digestion, on récupère 100 µl d'ADN chromosomique.
- + 100 µl TE 10 mM
 - + 200 µl chloroforme
- Vortexer, centrifuger 1 min à 1000 rpm.

Récupérer la phase aqueuse, phase supérieure, comportant l'ADN chromosomique.

4) Précipitation à l'acétate de sodium

Ajouter 1/10 du volume, d'acétate de sodium (3M, pH : 5,2) soit 20 µl.

5 Puis 2,5 volumes d'éthanol absolu propre, soit 500 µl (flacon gardé à - 20°C).
Laisser à - 20°C, au moins 1 heure (il est possible de laisser à - 20°C durant la nuit).

Centrifuger à 4°C (chambre froide) durant 30 min, à 14.000 rpm.

Éliminer le surnageant à l'aide de la pompe à vide.

10 Ajouter 400 µl d'éthanol à 70 %, centrifuger à 4°C, 5 min à 14.000 rpm.

Éliminer le surnageant à l'aide de la pompe à vide, laisser sécher environ une heure sur la paillasse.

Resuspendre le culot dans 20 µl H₂O.

15 5) Vérification des digestions partielles, après précipitation à l'acétate de sodium.

Préparer un gel d'agarose à 1 % en TBE. Déposer 1/10 du volume total des précipitations, soit 2 µl d'ADN + 8 µl d'H₂O + 2 µl de solution de dépôt.

En parallèle, déposer un marqueur de poids moléculaire : 1 µl + 9 µl d'H₂O + 2 µl de solution de dépôt.

20 6) Partial Fill-in

Volume final de la réaction : environ 50 µl

- 36 µl d'ADN partiellement digéré (ADN digéré par 0,25 ou 0,125 ou 0,0625 ou 0,03125 unités d'enzyme de restriction Sau3A)

- 5 µl de tampon synthesis

25 - 10 µl de mix nucléotides (A-G) 1mM ⇒ concentration finale : 200 µM

- 2 µl de Klenow (2 U/µl).

Laisser 30 min à température ambiante.

Mélange des nucléotides A-G

Mélanger :

30 - 2 µl de nucléotides A (100 mM)

- 2 µl de nucléotides G (100 mM)

- 16 µl de TRIS 10 mM, pH = 7,5.

Les nucléotides sont ainsi dilués au 1/10, on a une concentration de 10 mM.

Une seconde dilution au 1/10 dans H₂O sera réalisée, on a donc une concentration de 1 mM.

7) Extraction au chloroforme

L'extraction au chloroforme permet d'arrêter la digestion enzymatique, et d'éliminer toutes traces protéiques.

Après digestion, on récupère 53 µl d'ADN chromosomique.

+ 47 µl TE 10 mM

+ 100 µl chloroforme

Vortexer, centrifuger 1 min à 1000 tpm.

Récupérer la phase aqueuse, phase supérieure, comportant l'ADN chromosomique.

8) Précipitation à l'acétate de sodium

Ajouter 1/10 du volume, d'acétate de sodium (3M, pH : 5,2) soit 10 µl.

Puis 2,5 volumes d'éthanol absolu propre, soit 250 µl (flacon gardé à - 20°C).

Laisser à - 20°C, au moins 1 heure (il est possible de laisser à - 20°C durant la nuit).

Centrifuger à 4°C (chambre froide) durant 30 min, à 14.000 rpm.

Éliminer le surnageant à l'aide de la pompe à vide.

Ajouter 400 µl d'éthanol à 70 %, centrifuger à 4°C, 5 min à 14.000 rpm.

Éliminer le surnageant à l'aide de la pompe à vide, laisser sécher environ une heure sur la paillasse.

Resuspendre le culot dans 20 µl H₂O.

9) Purification de l'ADN chromosomique : Gel préparatif

Préparer un gel d'agarose à 1 %, en TAE, des grands puits seront prévus pour nos échantillons.

Reprendre la totalité d'ADN, soit 20 µl, ajouter 4 µl de solution de dépôt. En parallèle, déposer le marqueur de poids moléculaire dans les proportions suivantes :

- 5 µl H₂O

- 5 µl du marqueur 1 Kb DNA

- 2 µl de la solution de dépôt.

Laisser migrer à 70 Volts.

Découper le gel côté marqueur à l'aide d'un scalpel, et repérer, en prenant une photo et à l'aide d'une règle, la région intéressante. Les fragments d'ADN étant longs, on

utilisera pour purifier l'ADN, des colonnes SPIN X de chez COSTAR, ceci évitera de couper l'ADN chromosomique.

10) Purification : Colonne SPIN X

Après avoir récupéré les différents morceaux d'agarose, dans les colonnes
5 SPIN X, ajouter 200 µl de TE 10 mM, puis broyer à l'aide d'une spatule.

Ceci pourra être gardé à 4°C. Puis centrifuger 20 min à 5000 rpm. L'agarose sera retenue sur les filtres, alors que l'ADN chromosomique, sera retrouvé au fond du tube.

11) Extraction au chloroforme

10 L'extraction au chloroforme permet d'éliminer toutes traces protéiques.

On récupère 800 µl d'ADN chromosomique.

+ 800 µl chloroforme.

Vortexer, centrifuger 1 min à 1000 rpm.

Récupérer la phase aqueuse, phase supérieure, comportant l'ADN
15 chromosomique.

12) Précipitation à l'acétate de sodium

Ajouter 1/10 du volume, d'acétate de sodium (3 M, pH : 5,2) soit 80 µl.

Puis, 800 µl d'isopropanol.

Laisser à - 20°C, au moins 1 heure (il est possible de laisser à - 20°C durant
20 la nuit).

Centrifuger à 4°C (chambre froide) durant 30 min, à 14.000 rpm.

Éliminer le surnageant à l'aide de la pompe à vide.

Ajouter 400 µl d'éthanol à 70 %, centrifuger à 4°C, 5 min à 14.000 rpm.

Éliminer le surnageant à l'aide de la pompe à vide, laisser sécher environ
25 une demie heure sur la paillasse, et 2 min sous vide.

Resuspendre le culot dans 20 µl TE (0,1 X soit 1mM).

Incuber 10 min à 65°C.

Incuber environ 4 heures à 4°C, de manière à ce que l'ADN soit bien
resuspendu.

30 Vérification sur minigel d'agarose à 1 %, mettre en parallèle un marqueur de poids moléculaire.

C) Ligation de l'ADN chromosomique de *Photobacterium luminescens* souche TT01 dans le vecteur pSYX34

- Reprendre 6 µl d'ADN chromosomique.
Ajouter 2 µl de pSYX34.
Ajouter 2 µl de tampon de ligation (LB : ligation buffer).
Ajouter 2 µl de ligase.
- 5 Puis 8 µl H₂O (volume total : 20 µl).
En parallèle, faire un témoin de ligation, en remplaçant l'ADN chromosomique par du TE 0,1 X (1 mM).
Vortexer, laisser une nuit à 16°C.
- 10 Transformation de cellules ultracompetentes XL10-Gold Kanr (Stratagene)
La banque d'ADN génomique obtenue à l'étape précédente a été intégrée dans les cellules ultracompetentes XL10 Gold Kanr (Stratagene) selon les conditions préconisées par le fabricant.
L'analyse des inserts de 24 clones par digestion par l'enzyme de restriction Sall
- 15 et par séquençage des extrémités a été effectuée et a donné des résultats satisfaisants.

III) Etablissement d'une banque d'ADN génomique dans le vecteur bactérien (pBeloBAC11, California Institute of Technology)

Construction de la banque de BAC

- 20 Digestion partielle de l'ADN dans des morceaux d'agarose :
- les morceaux d'agarose sont lavés trois fois pendant 15 minutes à température ambiante dans une solution de TE (1x) sous agitation modérée ;
- on équilibre les morceaux d'agarose deux fois dans 300 µl d'un tampon de digestion Hind III (1x) (Boehringer ou Biolabs) pendant 30 minutes à température
- 25 ambiante ;
- on enlève le tampon de digestion et on ajoute un tampon de digestion Hind III glacé (1 ml par morceau d'agarose) contenant 20 U de Hind III (Boehringer ou Biolabs) ;
- on incube pendant deux heures dans de la glace ;
- 30 - on transfère les morceaux d'agarose dans un bain-marie à 37°C et on incube pendant 10 minutes à 30 minutes (en fonction de l'ADN contenu dans les morceaux d'agarose) ; et
- on arrête la digestion par addition de 100 µl d'une solution d'EDTA 250 mM (pH 8).

Sélection de la taille :

Séparation de l'ADN partiellement digéré réalisée par PFGE au moyen de l'appareillage CHEF DRII (Bio-Rad) :

- gel d'agarose à 1 % LMP dans un tampon Tris-acétate-EDTA (1 x) à 13°C,
- 5 - inverser le courant chaque 3 à 15 secondes à 6 V/cm pendant 16 heures,
- charger au moins deux morceaux d'agarose et le marqueur,
- colorer le marqueur et une ligne ou une partie de la ligne pour vérifier la digestion partielle,
- exciser les bandes (partie non colorée) de différentes tailles (i.e. de 50 à 100 kb
- 10 et de 150 à 250 kb),
- les bandes d'agarose peuvent être stockées à 4°C dans une solution de TE.

Préparation du vecteur :

- isolement de pBeloBACII par la méthode au chlorure de césium ;
- digestion par Hind II ;
- 15 - déphosphorylation avec CIP (éventuellement avec la phosphatase HK).

Ligation et transformation :

- les banques d'agarose contenant l'ADN sont fondues à 60°C pendant 10 minutes ;
- on équilibre la solution fondue d'agarose/ADN pendant 15 minutes à 45°C ;
- 20 - on ajoute de la gérase (Epicentre Technologies), à raison d'1 U pour 100 µl de bande de gel (ne pas ajouter de tampon de digestion qui provoque certains problèmes au moment de la ligation) ;
- on effectue la digestion pendant 1 heure à 45°C ;
- on effectue la ligation dans 50 µl d'une solution contenant pBeloBACII (2 µl),
- 25 de la ligase T4 (1 µl à 1:10), un tampon T4 10x (5µl), et la solution d'ADN/agarose (42 µl), incubation 20 heures à 16°C ;
- on chauffe le milieu de ligation pendant 15 minutes à 65°C ;
- on dialyse le milieu de ligation contre un tampon Tris-EDTA en utilisant des membranes Millipore de taille de pore VS 0,025 mM ;
- 30 - 1 ou 2 µl de la solution de ligation sont introduites par électroporation dans les cellules E. coli DH10B (Gibco BRL) en utilisant des cuvettes d'électroporation de largeur 2 mm avec les réglages suivants 2,5 kV, 25 µF et 200 Ω ;

- après électroporation on resuspend les cellules dans 600 µl de milieu SOC ou NYZ puis on incube pendant 45 minutes à 37°C sous agitation ;

- on étale 10 et 100 µl de chaque suspension cellulaire dans un milieu agar LB contenant du chloramphénicol (12,5 µg/ml), X-Gal (5-brom-4-chloro-3-indolyl-α-D-glucuronic acide ; 50 µg/ml) et de l'IPTG (isopropyl-α-D-thiogalactopyranoside ; 25 µg/ml) ; et

- on incube les boîtes ainsi obtenues pendant la nuit.

Extraction de l'ADN plasmidique et séquençage des inserts

L'extraction de l'ADN plasmidique a été effectuée par la technique de lyse alcaline en plaques 24 puits.

Le séquençage des inserts des clones a été effectué par le KIT PE Big Dye selon les conditions préconisées par le fabricant en utilisant les oligonucléotides spécifiques de chaque vecteur.

Les réactions sont ensuite introduites dans le thermocycleur afin de subir 35 cycles composés des trois étapes suivantes :

- dénaturation 10 secondes à 96°C,
- hybridation 10 secondes à 50°C,
- élongation 4 minutes à 56°C.

On réalise ensuite une précipitation à l'éthanol à 76 % durant 20 minutes à température ambiante.

Les plaques sont ensuite centrifugées 35 minutes à 2200 g puis égoutées sur papier absorbant puis centrifugées retournées sur du papier absorbant pendant 1 minute à 500 g afin de ne laisser aucune trace d'éthanol.

Les culots d'ADN sont ensuite :

- soit repris dans une solution de formamide-EDTA-bleu dextran, puis dénaturés pendant 2 minutes à 96°C. Les plaques sont ensuite immédiatement mises dans la glace, un aliquot étant alors déposé sur gel d'acrylamide d'un séquenceur automatique PE-377,
- soit repris dans une solution d'EDTA 0,3mM ; un aliquot étant alors automatiquement déposé dans un séquenceur automatique PE-3700.

Assemblage des séquences obtenues

Les séquences d'ADN génomique ont été assemblées en contig par le logiciel PHRED-PHRAP et visualisées par le logiciel CONSED.

Analyse et annotation

Les contigs ont tout d'abord été analysés et annotés automatiquement par le logiciel GMPTB.

Exemple 2 : Les gènes d'intérêt

- 5 Les différentes caractéristiques liées au mode de vie de *Phototrhaddus luminescens* et rapportées dans la littérature (Forst et al., 1997 ; Hu et al., 1998, etc.), ont conduit à rechercher dans le génome de cette bactérie la présence de gènes impliqués dans la biosynthèse d'antibiotiques et de toxines.

Les opérons de biosynthèse d'antibiotiques

- 10 La recherche de peptide-synthétases a été entreprise *in silico*. Pour ce faire nous avons utilisé dans un premier temps les différents motifs classiquement décrits dans la littérature (Stachelhaus & Marahiel, 1995, FEMS Microbiology Letters 125:3-14) comme sonde afin de repérer par homologie de séquence dans le génome de *Phototrhaddus luminescens*, des gènes susceptibles d'être impliqués dans la biosynthèse
- 15 d'antibiotique.

Modules d'adénylation

- 1 - LKAGGAYVPID
2 - YSGTTGxPKG V
3 - GELCIGGxGxARGYL
20 4 - YxTGD
5 - VKIRGxRIELGEIE

Module de thioester formation

- 6 - DNFYxLGGHSL

Module de N-méthylation

- 25 VLE/DxGxGxG

Module de peptide elongation

- His- HHILxDGW

Module de peptide racemisation (optionnel)

- His- HHILxDGW
30 A - AYxTExNDILLTAxG
B - EGHGRExIIE
C - RTVGWFTSMYPxxLD
D - FNYLGQFD

Parmi ces différents modules, certains nous ont permis d'identifier par recherche d'homologie en utilisant le programme BLASTP - Basic local alignment search tool. - (Altschul SF et al., 1990, J. Mol. Biol., 215:403-10) des gènes codant pour des protéines contenant certains de ces motifs.

- 5 Les gènes ainsi identifiés codant probablement pour des protéines impliquées dans la biosynthèse d'antibiotiques ont été catalogués, et apparaissent notamment dans le tableau I.

On a particulièrement mis l'accent sur les gènes homologues au gène syr E de *Pseudomonas syringae* ou au gène nosD.

10 Références

- Eric Guenzi, Giuliano Galli, Ingeborg Grgurina, Dennis C. Gross, and Guido Grandi, 1998. Characterization of the Syringomycin Synthetase Gene Cluster. A link between prokaryotic and eukaryotic peptide synthetases. J. Biol. Chem., 273:32857-32863.

- 15 - Bondi M, Messi P, Sabia C, Baccarani Contri M, Manicardi G., 1999. Antimicrobial properties and morphological characteristics of two *Photothabdus luminescens* strains. New Microbiol., 22:117-27.

Les opérons de biosynthèse de toxines

- 20 Comme pour les gènes de biosynthèse d'antibiotique, nous avons recherché, par homologie de séquence, dans le génome de *Photothabdus luminescens* des gènes codant potentiellement pour des protéines toxiques. Nous avons identifié de nombreux gènes codant pour des protéines retenant ces critères.

Les entomotoxines (Tc loci).

Des homologues au gène Tox A de *Clostridium difficile*.

- 25 Des Hémolysines.

Des gènes codant potentiellement pour des protéines homologues aux toxines RTX de *Vibrio cholerae*.

- 30 Des gènes codant potentiellement pour des protéines homologues aux gènes tphA et icmF de *Legionella pneumophila* (Purcell M, Shuman HA., 1998. The *Legionella pneumophila* icmGCDJBF genes are required for killing of human macrophages. Infect Immun., 66:2245-55).

Voir annotation de ces gènes au tableau I ci-après.

Références

- Ffrench-Constant R, Bowen D., 1999. *Photorhabdus* toxins: novel biological insecticides. *Curr Opin Microbiol.*, 2:284-8. Review.
- Blackburn M, Golubeva E, Bowen D, Ffrench-Constant RH, 1998. A novel insecticidal toxin from *Photorhabdus luminescens*, toxin complex a (Tca), and its
- 5 histopathological effects on the midgut of *manduca sexta*. *Appl Environ Microbiol.*, 64:3036-41.
- Bowen DJ, Ensign JC, 1998. Purification and characterization of a high-molecular-weight insecticidal protein complex produced by the entomopathogenic bacterium *Photorhabdus luminescens*. *Appl Environ Microbiol.*, 64:3029-35.
- 10 - Bowen D, Rocheleau TA, Blackburn M, Andreev O, Golubeva E, Bhartia R, Ffrench-Constant RH, 1998. Insecticidal toxins from the bacterium *Photorhabdus luminescens*. *Science.*, 280:2129-32.
- Guo L, Fatig RO 3rd, Orr GL, Schafer BW, Strickland JA, Sukhapinda K, Woodsworth AT, Petell JK, 1999. *Photorhabdus luminescens* W-14 insecticidal activity
- 15 consists of at least two similar but distinct proteins. Purification and characterization of toxin A and toxin B. *J Biol Chem.*, 274:9836-42.

Références générales

1. Altschul, S. F., T. L. Madden, A. A. Schaffer, J. Zhang, Z. Zhang, W. Miller, and D.
- 20 J. Lipman. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. [Review] [90 refs]. *Nucleic Acids Research.* 25:3389-402.
2. Birnboim, H. C. 1983. A rapid alkaline extraction method for the isolation of plasmid DNA. *Methods Enzymol.* 100:243-255.
3. Braun, L., F. Nato, B. Payrastre, J. C. Mazie, and P. Cossart. 1999. The 213-amino-
- 25 acid leucine-rich repeat region of the *Photorhabdus luminescens* InlB protein is sufficient for entry into mammalian cells, stimulation of PI 3-kinase and membrane ruffling. *Mol Microbiol.* 34:10-23.
4. Buchrieser, C., C. Rusniok, L. Frangeul, E. Couvé, A. Billault, F. Kunst, E. Carniel, and P. Glaser. 1999. The 102 kb locus of *Yersinia pestis* : sequence analysis and
- 30 comparison of selected regions among different *Yersinia pestis* and *Yersinia pseudotuberculosis* strains. *Infect. Immun.* 67:4851-4861.
5. Ewing, B., and P. Green. 1998. Base-calling of automated sequencer traces using phred. II. Error probabilities. *Genome Res.* 8:186-194.

6. Fitch, W. S. 1970. Distinguishing homologous from analogous proteins. *Syst. Zool.* 19:99-113.
7. Frangeul, L., K. E. Nelson, C. Buchrieser, A. Danchin, P. Glaser, and K. F. 1999. Cloning and assembly strategies in microbial genome projects. *Microbiology.* 145:2625-2634.
8. Gordon, D., C. Abajian, and P. Green. 1998. Consed: a graphical tool for sequence finishing. *Genome Res.* 8:195-202.
9. Jacquet, C., J. Bille, and J. Rocourt. 1992. Typing of *Photobacterium luminescens* by restriction polymorphism of the ribonucleic acid gene region. *Zentralbl. Bakteriol.* 276:356-365.
10. Li, P., K. C. Kupfer, C. J. Davies, D. Burbee, G. A. Evans, and H. R. Garner. 1997. PRIMO: A primer design program that applies base quality statistics for automated large-scale DNA sequencing. *Genomics.* 40:476-485.
11. Lukashin, A. V., and M. Borodovsky. 1998. GeneMark.hmm: new solutions for gene finding. *Nucleic Acids Res.* 15:1107-1115.

Description scientifique de la banque de BAC de *Photobacterium luminescens* souche TT01 déposée à la CNCM le 12 mai 2000 sous le numéro I-2478

- Collection de clones d'*Escherichia coli* DH 10B™ (Calvin et al., J. Bacteriol. 170, 2796, 1988) contenant des fragments d'ADN génomique de la bactérie *Photobacterium luminescens* souche TT01, clonés dans le vecteur pBelo BACII (Kim et al., Genomics, 34, 213, 1996) au site Hind III. La taille moyenne des inserts est de 60 kb.

Banques de données

On a utilisé des refontes locales de principales banques publiques. La banque de protéines utilisée est constituée par la fusion non redondante de ces banques, telle que la banque Genpept (traduction automatique de GenBank et NCBI).

- On a utilisé l'ensemble de logiciel BLAST (domaine public, Altschul et al., 1990) de recherche d'homologies entre une séquence et des banques de données protéiques ou nucléiques. Les seuils de signification utilisés dépendent de la longueur et de la complexité de la région testée ainsi que de la taille de la banque de référence. Ils ont été ajustés et adaptés à chaque analyse.

Les résultats de recherche d'homologies entre une séquence selon l'invention et des banques de données protéiques ou nucléiques sont présentés et résumés dans le tableau I et II ci-après.

5 **Tableau I**

Liste des fonctions putatives (colonne «homology with non-redundant protein data base- description », et colonne « annotations » pour les séquences sélectionnées comme impliquées dans une activité ou à activité de type toxine ou antibiotique) des protéines de séquences SEQ ID N° 42 à SEQ ID N° 3855 codées par leur séquence nucléotidique respective du génome de *Photorehabdus luminescens* souche TT01 (génome représenté par les séquences des 41 contigs (SEQ ID N° 1 à SEQ ID N° 41).

Les séquences nucléiques des protéines de séquence SEQ ID N° 42 à SEQ ID N° 3855 peuvent être aisément identifiées par leur position de début (colonne « start ») et de fin (colonne « end ») sur chacune des séquences de contig (colonne « contig »).

15 **Légende du tableau I :**

L'ensemble des fonctions putatives associées aux protéines de séquence SEQ ID N° 42 à SEQ ID N° 3855 a été obtenu par une recherche d'homologie utilisant notamment logiciel BLASTP (Altschul et al., 1990). Ont été prises en compte notamment les identités significatives, ou la présence de différents motifs (cf. exemples) représentatifs de ces fonctions. La description de la ou les fonctions les plus probables sont données dans la colonne « homology with » et « Annotation ».

Tableau II

Liste des fonctions putatives (colonne « fonction obtenue par comparaison sur banque de données ») des protéines codées par les séquences SEQ ID N° 5835 à SEQ ID N°10784 du génome de *Photorehabdus luminescens* souche TT01 (génome ici représenté par les séquences des 9 contigs (SEQ ID N° 5826 à SEQ ID N° 5834).

Les séquences nucléiques de séquence séquences SEQ ID N° 5835 à SEQ ID N°10784 peuvent être aisément identifiées par leur position de début (colonne « CONTIG », « from ») et de fin (colonne « CONTIG » « to ») sur chacune des séquences de contig

30 **Légende du tableau II :**

L'ensemble des fonctions putatives associées aux protéines codées par les séquences SEQ ID N° 5835 à SEQ ID N°10784 a été obtenu par une recherche d'homologie utilisant notamment logiciel BLASTP (Altschul et al., 1990). Ont été prises

en compte notamment les identités significatives, ou la présence de différents motifs (cf. exemples) représentatifs de ces fonctions. La description de la ou les fonctions les plus probables sont données dans la colonne « homology with » et « Annotation ».

- 5 Dans la dernière colonne « HOMOLOGUE A LA SEQUENCE SEQ ID », le terme « #N/A » signifie qu'aucune homologie pour la séquence concernée n'avait été identifiée avec l'une des séquences SEQ ID Nos. 42 à 3855. Lorsque qu'une séquence homologue a été trouvée parmi les séquences SEQ ID Nos. 42 à 3855 pour la séquence concernée, celle-ci est mentionnée par son numéro de SEQ ID dans cette colonne.

TABLEAU I

SEQ ID	Prot n°	Contig	start	end	%	Homology with non-redundant protein data base / descriptions	/	Annotations
SEQ ID n°42	Prot n°PL-1.2	Contig41	1	600	47%	pdj1F3l A Chain A, Crystal Structure Of Tn5 Transposase Complexed With Transposon End Dna Length = 481		
SEQ ID n°43	Prot n°PL-10.1	Contig41	19115	19816	41%	Identities = 54/214 (25%), Positives = 98/214 (45%), Gaps = 9/214 (4%) gb AAG04736.1 AE004564.5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230		
SEQ ID n°44	Prot n°PL-100.1	Contig41	171451	173322	67%	Identities = 309/620 (49%), Positives = 430/620 (68%), Gaps = 3/620 (0%) sp P77241 PPIID_ECOLI PEPTIDYL-PROLYL CIS-TRANS ISOMERASE D (PIPIASE D) (ROTAMASE D) pir A64774 ybaU protein - Escherichia coli dbj BAA11845.1 (D82943) YbaU [Escherichia coli] gb AAB40197.1 (U82864) similar to H. influenzae HI1004 [Escherichia coli] gb AAC73544.1 (AE000150) putative protease maturation protein [Escherichia coli] Length = 623 Identities = 254/291 (87%), Positives = 271/291 (92%)		
SEQ ID n°45	Prot n°PL-1000.1	Contig40	602348	603223	91%	sp P76143 YNEB_ECOLI PUTATIVE ALDOLASE YNEB pir H64905 conserved hypothetical protein b1517 - Escherichia coli gb AAC74590.1 (AE000249) orf. hypothetical protein [Escherichia coli] Length = 291 Identities = 278/334 (83%), Positives = 298/334 (88%), Gaps = 1/334 (0%)		
SEQ ID n°46	Prot n°PL-1001.1	Contig40	603292	604311	79%	pir G64905 sugar-binding protein homolog b1516 precursor - Escherichia coli gb AAC74589.1 (AE000249) putative LACI-type transcriptional regulator [Escherichia coli] Length = 340 Identities = 251/326 (76%), Positives = 296/326 (89%)		
SEQ ID n°47	Prot n°PL-1002.1	Contig40	604374	605375	87%	sp P77651 YDEZ_ECOLI HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN YDEZ pir F64905 probable sugar transport permease protein b1515 - Escherichia coli dbj BAA15202.1 (D90794) Ribose transport system permease protein RbsC. [Escherichia coli] gb AAC74588.1 (AE000249) putative transport system permease protein [Escherichia coli] Identities = 253/324 (78%), Positives = 294/324 (90%)		
SEQ ID n°48	Prot n°PL-1003.1	Contig40	605375	606376	86%	sp P77672 YDEY_ECOLI HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN YDEY pir E64905 probable sugar transport permease protein b1514 - Escherichia coli dbj BAA15201.1 (D90794) L-arabinose transport system permease protein AraH. [Escherichia coli] gb AAC74587.1 (AE000249) putative transport system permease protein [Escherichia coli] Identities = 324/510 (63%), Positives = 398/510 (77%), Gaps = 1/510 (0%)		
SEQ ID n°49	Prot n°PL-1004.1	Contig40	606370	607905	77%	sp P77575 EGO_ECOLI PUTATIVE ABC TRANSPORTER ATP-BINDING PROTEIN EGO (EGO10A) pir D64905 probable sugar transport ATP-binding protein b1513 - Escherichia coli dbj BAA15200.1 (D90794) Ribose transport ATP-binding protein RbsA. [Escherichia coli] gb AAC74586.1 (AE000249) putative ATP-binding component of a transport system [Escherichia coli] gb AAC61747.1 (AF089855) aerobic growth essential protein [Escherichia coli] Length = 511		

TABLEAU I

SEQ ID n°50	Prot n°PL-1005.1	Contig40	608137	609138	76%	<p>Identities = 214/312 (68%), Positives = 257/312 (81%)</p> <p>sp P76141 YDEW_ECOLI HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN HIPB-UXAB INTERGENIC REGION P C64905 probable transcription regulator ydeW - Escherichia coli gb AAC74585.1 (AE000249) putative transcriptional regulator, sorC family [Escherichia coli] P C64905</p> <p>Identities = 399/518 (77%), Positives = 455/518 (87%)</p> <p>sp P77432 YDEV_ECOLI HYPOTHETICAL SUGAR KINASE IN HIPB-UXAB INTERGENIC REGION P J1884905 sugar kinase homolog ydev - Escherichia coli dbj BAA15191.1 (D90793) Xylulose kinase (EC 2.7.1.17) (Xylulokinase) [Escherichia coli] dbj BAA15198.1 (D90794) Xylulose kinase (EC 2.7.1.17) (Xylulokinase) [Escherichia coli] gb AAC74584.1 (AE000248) putative kinase [Escherichia coli] Length = 530</p> <p>Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%)</p> <p>dbj BAB08239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188</p>
SEQ ID n°51	Prot n°PL-1006.1	Contig40	609339	610946	84%	
SEQ ID n°52	Prot n°PL-1007.1	Contig40	611688	612755	21%	
SEQ ID n°53	Prot n°PL-1008.1	Contig40	612722	613891	No Hits found	
SEQ ID n°54	Prot n°PL-1009.1	Contig40	614050	615284	46%	<p>Identities = 118/378 (31%), Positives = 190/378 (50%), Gaps = 20/378 (5%)</p> <p>sp P14165 CISY_PSEAE CITRATE SYNTHASE gb AAA25769.1 (M29728) citrate synthase [Pseudomonas aeruginosa] Length = 428</p> <p>Identities = 71/9794 (90%), Positives = 758/794 (94%) gb AB40195.1 (U82664) ATP-dependent protease LA [Escherichia coli] Length = 799</p>
SEQ ID n°55	Prot n°PL-101.1	Contig41	174120	176474	95%	
SEQ ID n°56	Prot n°PL-1010.1	Contig40	615228	616625	No Hits found	
SEQ ID n°57	Prot n°PL-1011.1	Contig40	616635	617816	30%	<p>Identities = 67/302 (22%), Positives = 119/302 (39%), Gaps = 28/302 (9%)</p> <p>pir E69804 multidrug resistance protein homolog yfIS - Bacillus subtilis emb CAB12667.1 (Z99108) similar to multidrug resistance protein [Bacillus subtilis] dbj BAA24459.1 (D85082) YfIS [Bacillus subtilis] Length = 417</p> <p>Identities = 216/524 (41%), Positives = 307/524 (58%), Gaps = 10/524 (1%)</p> <p>gb AAG07585.1 AE004836_4 (AE004836) probable AMP-binding enzyme [Pseudomonas aeruginosa] Length = 540</p>
SEQ ID n°58	Prot n°PL-1012.1	Contig40	617809	619419	55%	<p>Identities = 207/430 (48%), Positives = 290/430 (67%), Gaps = 2/430 (0%)</p> <p>sp Q51955 PCAK_PSEPU 4-HYDROXYBENZOATE TRANSPORTER gb AA85137.1 (U10895) PcaK [Pseudomonas putida] Length = 448</p> <p>Identities = 165/325 (50%), Positives = 233/325 (70%), Gaps = 16/325 (4%)</p> <p>gb AAF81206.1 AF247502_1 (AF247502) YW2 [Salmonella dublin] Length = 316</p>
SEQ ID n°59	Prot n°PL-1013.1	Contig40	619729	621051	65%	
SEQ ID n°60	Prot n°PL-1014.1	Contig40	622612	623566	69%	
SEQ ID n°61	Prot n°PL-1015.1	Contig40	625512	635447	53%	<p>Identities = 1364/2831 (48%), Positives = 1771/2831 (62%), Gaps = 97/2831 (3%) pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] Length = 9376</p> <p>Unknown, similar to proteins involved in antibiotic biosynthesis</p>

TABLEAU I

SEQ ID n°62	Prot n°PL-1017.1	Contig40	636548	643777	10%	Identities = 132/574 (22%), Positives = 249/574 (42%), Gaps = 75/574 (13%) pir A37052 toxin A - Clostridium difficile gb AA23283.1 (M30307) toxin A [Clostridium difficile] Length = 2710	Unknown, similar to toxins
SEQ ID n°63	Prot n°PL-1018.1	Contig40	643822	645960	71%	Identities = 407/693 (58%), Positives = 528/693 (75%) gb AAF94603.1 (AE004223) toxin secretion transporter, putative [Vibrio cholerae] Length = 721	
SEQ ID n°64	Prot n°PL-1019.1	Contig40	645981	647408	58%	Identities = 222/474 (46%), Positives = 316/474 (65%), Gaps = 9/474 (1%) gb AAD21060.1 (AF119150) Rbd protein [Vibrio cholerae] gb AAF94604.1 (AE004223) RTX toxin transporter [Vibrio cholerae] Length = 467	
SEQ ID n°65	Prot n°PL-102.1	Contig41	176683	177957	95%	Identities = 395/423 (93%), Positives = 411/423 (96%) sp O33873 CLPX_YEREN ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX gb AAC45783.1 (U66330) ClpX [Yersinia enterocolitica] Length = 423	
SEQ ID n°66	Prot n°PL-1020.1	Contig40	647369	649501	71%	Identities = 387/691 (56%), Positives = 505/691 (73%), Gaps = 5/691 (0%) gb AAF94605.1 (AE004223) RTX toxin transporter [Vibrio cholerae] Length = 720	
SEQ ID n°67	Prot n°PL-1021.1	Contig40	651483	667856	55%	Identities = 2280/5157 (44%), Positives = 3048/5157 (58%), Gaps = 245/5157 (4%) pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] Length = 9376	Unknown, similar to proteins involved in antibiotic biosynthesis

TABLEAU I

SEQ ID n°68	Prot n°PL-1022.1	Contig40	671025	671948	No Hits found	
SEQ ID n°69	Prot n°PL-1023.1	Contig40	673074	674021	No Hits found	
SEQ ID n°70	Prot n°PL-1024.1	Contig40	669993	674504	25%	Identities = 272/938 (28%), Positives = 388/938 (40%), Gaps = 108/938 (11%) emb CAB82067.1 (AL161803) putative Rhs protein [Streptomyces coelicolor A3(2)] Length = 927
SEQ ID n°71	Prot n°PL-1025.1	Contig40	676288	677793	53%	Identities = 201/511 (39%), Positives = 274/511 (53%), Gaps = 38/511 (7%) dbj BA84886.1 (AB024946) orf51 [Escherichia coli] Length = 523
SEQ ID n°72	Prot n°PL-1026.1	Contig40	681255	682463	78%	Identities = 246/401 (61%), Positives = 316/401 (78%) gb AA851148.1 (U90416) N-(alpha)-acetylornithine-(delta)-aminotransferase [Escherichia coli] Length = 408
SEQ ID n°73	Prot n°PL-1027.1	Contig40	682485	683516	69%	Identities = 178/342 (52%), Positives = 243/342 (71%), Gaps = 1/342 (0%) sp P76218 ASTA_ECOLI ARGININE N-SUCCINYLTRANSFERASE (AOST) p I C64934 hypothetical protein b1747 - Escherichia coli (strain K-12) gb AAC74817.1 (AE000269) orf, hypothetical protein [Escherichia coli] Length = 344
SEQ ID n°74	Prot n°PL-1028.1	Contig40	683519	684994	75%	Identities = 314/488 (64%), Positives = 375/488 (76%) emb CAA21339.1 (AL031866) ORF16, len:505 aa, aruD, probable succinylglutamate 5-semialdehyde dehydrogenase, belongs to Pseudomonas aeruginosa aru gene cluster, highly similar to many, eg: AruD Pseudomonas aeruginosa, Fasta scores: opt: 2117, E(0.0, 63.5% identity in > identities = 292/447 (65%), Positives = 346/447 (77%), Gaps = 1/447 (0%) emb CAA21338.1 (AL031866) ORF15, len: 447 aa, aruB, probable succinylarginine dihydrolyase, belongs to Pseudomonas aeruginosa aru gene cluster similar to many eg. Pseudomonas aeruginosa O50175, Fasta scores opt: 1764, E(0.0, 60.8% identity in 446 aa overlap and E. coli) Length = 447
SEQ ID n°75	Prot n°PL-1029.1	Contig40	685045	686388	74%	Identities = 189/207 (91%), Positives = 200/207 (96%) sp Q60107 CLPP_YEREN ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (ENDOPEPTIDASE CLP) gb AAC45782.1 (U55059) ClpP [Yersinia enterocolitica] Length = 207
SEQ ID n°76	Prot n°PL-103.1	Contig41	178091	178714	94%	Identities = 152/322 (47%), Positives = 210/322 (65%), Gaps = 6/322 (1%) emb CAA21337.1 (AL031866) ORF14, len:330 aa, aruE, probable succinylglutamate desuccinylase, belongs to Pseudomonas aeruginosa aru gene cluster similar to many, eg. AF011922_8 Pseudomonas aeruginosa aruB gene, Fasta scores: opt: 697, E(0.0, 38.0% identity in 324 aa) Length = 330
SEQ ID n°77	Prot n°PL-1030.1	Contig40	686401	687378	63%	

TABLEAU I

SEQ ID n°78	Prot n°PL-1031.1	Contig40	687468	688937	68%	Identities = 243/452 (53%), Positives = 336/452 (73%), Gaps = 2/452 (0%) sp P39312 CYCA_ECOLI D-SERINED-ALANINE/GLYCINE TRANSPORTER pir J568433 D-serine/D-alanine/glycine transporter - Escherichia coli gb AA97104.1 (U14003) ORF_0470 [Escherichia coli] gb AAC77165.1 (AE000492) transport of D-alanine, D-serine, and glycine [Escherichia coli] Length = 470
SEQ ID n°79	Prot n°PL-1032.1	Contig40	689828	690718	No Hits found	Identities = 149/384 (38%), Positives = 222/384 (57%), Gaps = 6/384 (1%) pir J71682 iron-sulfur cofactor synthesis protein RP486 - Rickettsia prowazekii emb CAA14839.1 (AJ235272) NIFS PROTEIN HOMOLOG (spi1) [Rickettsia prowazekii] Length = 410
SEQ ID n°80	Prot n°PL-1033.1	Contig40	690718	691884	56%	Identities = 76/257 (29%), Positives = 122/257 (48%), Gaps = 28/257 (10%) gb AAD28459.1 AF127374_14 (AF127374) MitM [Streptomyces lavendulae] Length = 283
SEQ ID n°81	Prot n°PL-1034.1	Contig40	691851	692720	42%	Identities = 94/169 (55%), Positives = 128/169 (73%), Gaps = 4/169 (2%) gi 9632491 repressor protein C1 gb AAD25430.1 AF125520_25 (AF125520) repressor protein C1 [Bacteriophage 933W] Length = 235
SEQ ID n°82	Prot n°PL-1035.2	Contig40	693369	694013		Identities = 109/419 (26%), Positives = 197/419 (47%), Gaps = 44/419 (10%) emb CAC04160.1 (AJ292531) putative helicase [Lactococcus bacteriophage phi31] Length = 448
SEQ ID n°83	Prot n°PL-1036.1	Contig36	72	722	58%	Identities = 84/314 (26%), Positives = 116/314 (36%), Gaps = 41/314 (13%) gi 9627512 alpha gene product (AA 1-777) sp P10277 PRIM_BPP4 PUTATIVE P4-SPECIFIC DNA PRIMASE pir RPBPP4 DNA primase - satellite phage P4 emb CAA2911.1 (X05623) alpha gene (pot P4-specific DNA primase) (AA 1-777) [Bacteriophage P4] emb CAA35898.1 (X51522) alpha gene product (AA 1-777) [Bacteriophage P4] Length = 777
SEQ ID n°84	Prot n°PL-1037.1	Contig36	2553	4178	36%	Identities = 107/269 (39%), Positives = 152/269 (55%), Gaps = 23/269 (8%) pir B84911 hypothetical protein b1559 - Escherichia coli gb AAC74632.1 (AE000253) orf, hypothetical protein [Escherichia coli] Length = 260
SEQ ID n°85	Prot n°PL-1038.1	Contig36	4063	5097	33%	Identities = 357/430 (83%), Positives = 394/430 (91%) sp P22257 TIG_ECOLI TRIGGER FACTOR (TF) pir D64773 trigger factor - Escherichia coli gb AAB40192.1 (U82664) trigger factor [Escherichia coli] gb AAC73539.1 (AE000150) trigger factor, a molecular chaperone involved in cell division [Escherichia coli] Length = 432 "
SEQ ID n°86	Prot n°PL-1039.1	Contig36	7047	7862	53%	Identities = 65/187 (34%), Positives = 100/187 (52%), Gaps = 20/187 (10%) ref NP_060879.1 P18 gb AA03961.1 AF157835_18 (AF157835) P18 [Bacteriophage APSE-1] Length = 469
SEQ ID n°87	Prot n°PL-104.1	Contig41	178988	180292	89%	
SEQ ID n°88	Prot n°PL-1040.1	Contig36	11591	12274	No Hits found	
SEQ ID n°89	Prot n°PL-1041.1	Contig36	12660	13946	23%	

TABLEAU I

SEQ ID n°90	Prot n°PL-1042.1	Contig36	13871	15319	46%	Identities = 128/420 (30%), Positives = 225/420 (53%), Gaps = 10/420 (2%) sp P44183 YE09_HAEIN HYPOTHETICAL PROTEIN H11409 pir J64028 hypothetical protein H11409 - Haemophilus influenzae (strain Rd KW20) gb AAC23057.1 (U32820) H. influenzae predicted coding region H11409 [Haemophilus influenzae Rd] Length = 436
SEQ ID n°91	Prot n°PL-1043.1	Contig36	15246	16091	48%	Identities = 94/291 (32%), Positives = 146/291 (49%), Gaps = 36/291 (12%) gb AAF84383.1 AE003986_13 (AE003986) plasmid-related protein [Xylella fastidiosae] gb AAF84488.1 AE003993_7 (AE003993) plasmid-related protein [Xylella fastidiosae] Length = 281
SEQ ID n°92	Prot n°PL-1044.1	Contig36	16092	17252	48%	Identities = 109/374 (29%), Positives = 188/374 (50%), Gaps = 48/374 (12%) sp P44180 YE05_HAEIN HYPOTHETICAL PROTEIN H11405 pir J64028 hypothetical protein H11405 - Haemophilus influenzae (strain Rd KW20) gb AAC23055.1 (U32820) H. influenzae predicted coding region H11405 [Haemophilus influenzae Rd] Length = 366
SEQ ID n°93	Prot n°PL-1045.1	Contig36	17733	18704	No Hits found	Identities = 60/184 (32%), Positives = 89/184 (47%), Gaps = 44/184 (23%) gb AAF84389.1 AE003986_19 (AE003986) hypothetical protein [Xylella fastidiosae] gb AAF84494.1 AE003993_13 (AE003993) hypothetical protein [Xylella fastidiosae] Length = 157
SEQ ID n°94	Prot n°PL-1046.1	Contig36	19048	19671	42%	Identities = 201/510 (39%), Positives = 288/510 (56%), Gaps = 19/510 (3%) gb AAF84392.1 AE003986_22 (AE003986) hypothetical protein [Xylella fastidiosae] gb AAF84497.1 AE003993_16 (AE003993) hypothetical protein [Xylella fastidiosae] Length = 498
SEQ ID n°95	Prot n°PL-1047.1	Contig36	20423	21934	56%	Identities = 123/498 (24%), Positives = 209/498 (41%), Gaps = 59/498 (11%) gb AAF84501.1 AE003993_20 (AE003993) hypothetical protein [Xylella fastidiosae] Length = 597
SEQ ID n°96	Prot n°PL-1048.1	Contig36	22882	24903	31%	Identities = 41/100 (41%), Positives = 59/100 (59%), Gaps = 7/100 (7%) gi 9633007 hypothetical protein emb CAB52485.1 (AJ131519) hypothetical protein [Lactobacillus bacteriophage phi adh] Length = 159
SEQ ID n°97	Prot n°PL-1049.1	Contig36	25784	26767	17%	

TABLEAU I

SEQ ID n°98	Prot n°PL-105.1	Contig41	179414	180316	No Hits found	
SEQ ID n°99	Prot n°PL-1050.1	Contig36	27271	28020	56%	Identities = 86/250 (34%), Positives = 140/250 (56%), Gaps = 24/250 (9%) gb AAF84400.1 AE003987_4 (AE003987) hypothetical protein [Xylella fastidiosa] Length = 256
SEQ ID n°100	Prot n°PL-1051.1	Contig36	28330	29175	65%	Identities = 141/273 (51%), Positives = 180/273 (66%), Gaps = 2/273 (0%) gb AAF84402.1 AE003987_6 (AE003987) hypothetical protein [Xylella fastidiosa] Length = 276
SEQ ID n°101	Prot n°PL-1052.1	Contig36	29147	29821	49%	Identities = 85/223 (38%), Positives = 112/223 (50%), Gaps = 20/223 (8%) gb AAF84403.1 AE003987_7 (AE003987) hypothetical protein [Xylella fastidiosa] Length = 213
SEQ ID n°102	Prot n°PL-1053.1	Contig36	30149	31297	50%	Identities = 134/356 (37%), Positives = 199/356 (55%), Gaps = 2/356 (0%) gb AAF84513.1 AE003994_12 (AE003994) hypothetical protein [Xylella fastidiosa] Length = 387
SEQ ID n°103	Prot n°PL-1054.1	Contig36	31290	31946	46%	Identities = 66/205 (32%), Positives = 101/205 (49%), Gaps = 31/205 (15%) gb AAF84514.1 AE003994_13 (AE003994) hypothetical protein [Xylella fastidiosa] Length = 186
SEQ ID n°104	Prot n°PL-1055.1	Contig36	31933	33255	19%	Identities = 67/160 (41%), Positives = 88/160 (54%), Gaps = 16/160 (10%) pir S18687 Sc/SvN protein - Escherichia coli plasmid p15B emb CAA44050.1 (X62121) DNA inversion product [Escherichia coli] Length = 762
SEQ ID n°105	Prot n°PL-1056.1	Contig36	33186	33881	44%	Identities = 71/181 (39%), Positives = 104/181 (57%), Gaps = 1/181 (0%) ref NP_040605.1 orf-194 sp P03740 TFA_LAMBD TAIL FIBER ASSEMBLY PROTEIN pir QXBP3L hypothetical protein A-194 - phage lambda gb AAAG6558.1 J02459 orf-194 [bacteriophage lambda] Length = 194
SEQ ID n°106	Prot n°PL-1057.1	Contig36	34197	35936	73%	Identities = 342/590 (57%), Positives = 433/590 (72%), Gaps = 15/590 (2%) sp P33922 YEJM_EC01 HYPOTHETICAL 67.3 KD PROTEIN IN RPLY-PROL INTERGENIC REGION pir C64988 hypothetical 67.3 kD protein in rply-prol intergenic region - Escherichia coli (strain K-12) gb AAA16384.1 (U00008) yejM [Escherichia coli] gb AAC75249.1 (AE000308) putative sulfatase [Escherichia coli] Length = 586
SEQ ID n°107	Prot n°PL-1058.1	Contig36	36468	37472	86%	Identities = 263/333 (78%), Positives = 297/333 (88%) sp P33920 INA37_EC01 37 KD NUCLEOID-ASSOCIATED PROTEIN pir A64988 hypothetical 37.8 kD protein in rply-proL intergenic region - Escherichia coli (strain K-12) gb AAA16382.1 (U00008) yejK [Escherichia coli] gb AAC75247.1 (AE000308) orf, hypothetical protein [Escherichia coli] Length = 434/584 (74%), Positives = 487/584 (83%)
SEQ ID n°108	Prot n°PL-1059.1	Contig36	37988	39745	79%	sp P33919 YEJH_EC01 HYPOTHETICAL 66.4 KD PROTEIN IN RSUA-RPLY INTERGENIC REGION pir G64987 yejH protein - Escherichia coli (strain K-12) gb AAC75245.1 (AE000308) putative ATP-dependent helicase [Escherichia coli] Length = 586

TABLEAU I

SEQ ID n°109	Prot n°PL-108.1	Contig41	181229	181807	73%	<p>Identities = 119/200 (59%), Positives = 152/200 (75%) pir B64773 lipoprotein yel G precursor - Escherichia coli gb AAB40190.1 (U82664) hypothetical 20.9 kd lipoprotein [Escherichia coli] gb AAC73537.1 (AE000149) putative polymerase/proteinase [Escherichia coli] Length = 226</p> <p>Identities = 167/230 (72%), Positives = 191/230 (82%)</p>
SEQ ID n°110	Prot n°PL-1060.1	Contig36	40035	40736	79%	<p>sp P33918 RSUA_ECOLI_RIBOSOMAL_SMALL_SUBUNIT_PSEUDOURIDINE SYNTHASE A (16S PSEUDOURIDYLATE 516 SYNTHASE) (16S PSEUDOURIDINE 516 SYNTHASE) (URACIL HYDROLYASE) pir F64987 hypothetical 25.9 kd protein in bor-ply intergenic region - Escherichia coli (strain K-12) gb AAA16377.1 (U00008) yelD [Escherichia coli] gb AAB34905.1 16S RNA pseudouridine 516 synthase, 16S RNA psi 516 synthase=rsua gene product [Escherichia coli, Peptide, 231 aa] gb AAC75244.1 (AE000308) 16S pseudouridylate 516 synthase [Escherichia coli] Length = 237/393 (60%), Positives = 309/393 (78%), Gaps = 1/393 (0%)</p> <p>Identities = 123/191 (64%), Positives = 151/191 (78%), Gaps = 3/191 (1%)</p>
SEQ ID n°111	Prot n°PL-1061.1	Contig36	40780	41984	77%	<p>pir E64987 bicyclomycin resistance protein - Escherichia coli gb AAC75243.1 (AE000308) bicyclomycin resistance protein; transmembrane protein [Escherichia coli] Length = 398</p> <p>Identities = 135/232 (58%), Positives = 174/232 (74%), Gaps = 2/232 (0%)</p>
SEQ ID n°112	Prot n°PL-1062.1	Contig36	43620	44210	74%	<p>sp P77885 SPR_ECOLI_LIPOPROTEIN_SPR_PRECURSOR pir F64986 hypothetical protein b2175 - Escherichia coli (strain K-12) dbj BAA13140.1 (D86610) Spr [Escherichia coli] dbj BAA15983.1 (D90849) Probable lipoprotein NlpC homolog precursor. [Escherichia coli] gb AAC75236.1 (AE000307) putative lipoprotein [Escherichia coli] Length = 188</p> <p>Identities = 149/207 (71%), Positives = 179/207 (85%)</p>
SEQ ID n°113	Prot n°PL-1063.1	Contig36	44559	45263	70%	<p>pir E64986 hypothetical protein b2174 - Escherichia coli (strain K-12) gb AAC75235.1 (AE000307) ori, hypothetical protein [Escherichia coli] Length = 249</p> <p>Identities = 149/207 (71%), Positives = 179/207 (85%)</p>
SEQ ID n°114	Prot n°PL-1064.1	Contig36	46384	46936	85%	<p>sp P33028 YEIP_ECOLI_30.9_KDA_PROTEIN_IN_FRUB-SPR_INTERGENIC_REGION pir B64986 hypothetical 30.9 kd protein in fruB 5'region - Escherichia coli (strain K-12) gb AAA60519.1 (U00007) yelP [Escherichia coli] dbj BAA15980.1 (D90849) Elongation factor P (EF-P). [Escherichia coli] gb AAC75232.1 (AE000308) putative elongation factor [Escherichia coli] prf 2014253BR yelP gene [Escherichia coli] Length = 238/417 (57%), Positives = 306/417 (73%), Gaps = 9/417 (2%)</p> <p>Identities = 238/417 (57%), Positives = 306/417 (73%), Gaps = 9/417 (2%)</p>
SEQ ID n°115	Prot n°PL-1065.1	Contig36	47069	48328	64%	<p>gb AAG08819.1 AE004956_3 (AE004956) tryptophan permease [Pseudomonas aeruginosa] Length = 417</p>

TABLEAU I

SEQ ID n°116	Prot n°PL-1066.1	Contig36	49068	50006	85%	<p>Identities = 245/310 (79%), Positives = 273/310 (88%)</p> <p>sp P23539 K1PF_ECOLI_1-PHOSPHOFRUCTOKINASE (FRUCTOSE 1-PHOSPHATE KINASE) pir J37245_1-phosphofructokinase (EC 2.7.1.56) - [Escherichia coli emb CAA37896.1 (X53948) 1-phosphofructokinase [Escherichia coli] gb AAA60525.1 (U00007) 1-phosphofructokinase (EC [Escherichia coli] db JBA15977.1 (D90849) 1-phosphofructokinase (EC 2.7.1.56) (Fructose 1-phosphate kinase). [Escherichia coli] gb AAC75229.1 (AE000306) fructose-1-phosphate kinase [Escherichia coli] prf J2014253BP fruK gene [Escherichia coli] Length = 312</p>
SEQ ID n°117	Prot n°PL-1067.1	Contig36	50026	50868	82%	<p>Identities = 217/281 (77%), Positives = 238/281 (84%)</p> <p>sp P12638 END4_ECOLI_ENDONUCLEASE IV (ENDONUCLEASE IV) (phage-T4-Induced) (EC 3.1.21.2) - [Escherichia coli pdb 1QUM A Chain A, Crystal Structure Of Escherichia Coli Endonuclease IV In Complex With Damaged Dna gb AAC75220.1 (AE000305) endonuclease IV [Escherichia Identities = 205/336 (61%), Positives = 259/336 (77%), Gaps = 7/336 (2%)</p>
SEQ ID n°118	Prot n°PL-1068.1	Contig36	50991	52022	71%	<p>sp P33010 YEIH_ECOLI_HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION pir J64984_hypothetical 36.9 kD protein in lysP-nfo Intergenic region - [Escherichia coli (strain K-12) gb AAA60511.1 (U00007) yeiH [Escherichia coli] gb AAC75219.1 (AE000305) orf, hypothetical protein [Escherichia coli] prf J2014253BD yeiH gene [Escherichia coli] Length = 349</p>
SEQ ID n°119	Prot n°PL-1069.1	Contig36	52251	53126	81%	<p>Identities = 198/286 (69%), Positives = 241/286 (84%)</p> <p>sp P32484 YEIE_ECOLI_HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN LYSP-NFO INTERGENIC REGION pir J64984_hypothetical transcription regulator lysP-nfo Intergenic region - [Escherichia coli (strain K-12) gb AAA60508.1 (U00007) probable transcriptional regulator yeiE [Escherichia coli] gb AAA17052.1 (M89774) ORF 1 function unknown [Escherichia coli] gb AAC75218.1 (AE000305) putative transcriptional regulator LYSR-type [Escherichia coli] prf J2014253BC yeiE gene</p>
SEQ ID n°120	Prot n°PL-107.1	Contig41	181861	183339	77%	<p>Identities = 338/491 (68%), Positives = 400/491 (81%), Gaps = 1/491 (0%)</p> <p>sp P36670 AMPG_ECOLI_AMPG PROTEIN pir J37391 signal transducer ampG - [Escherichia coli gb AAB28884.1 (S87816) AmpG [Escherichia coli] gb AAB40189.1 (U82664) beta-lactamase induction signal transducer AmpG [Escherichia coli] gb AAC73536.1 (AE000149) regulates beta-lactamase synthesis [Escherichia coli] Length = 491</p>
SEQ ID n°121	Prot n°PL-1070.1	Contig36	53203	54762	85%	<p>Identities = 408/472 (86%), Positives = 446/472 (94%)</p> <p>pir J64984 lysine-specific permease - [Escherichia coli gb AAA17053.1 (M89774) lysine specific permease [Escherichia coli] gb AAC75217.1 (AE000305) lysine-specific permease [Escherichia coli] Length = 489</p>

TABLEAU I

SEQ ID n°122	Prot n°PL-1071.1	Contig36	55198	56349	40%	Identities = 84/343 (27%), Positives = 156/343 (45%), Gaps = 49/343 (14%) pir E72406 hypothetical protein TM0189 - Thermotoga maritima (strain MSB6) gb AAD35281.1 AE001704_2 (AE001704) iron(III) ABC transporter, periplasmic iron-binding protein, putative [Thermotoga maritima]
SEQ ID n°123	Prot n°PL-1072.1	Contig36	56470	57459	54%	Identities = 120/339 (35%), Positives = 202/339 (59%), Gaps = 8/339 (2%) pir F71087 probable ferrichrome transport permease protein - Pyrococcus horikoshii dbj BAA30336.1 (AP000005) 343aa long hypothetical ferrichrome transport permease protein [Pyrococcus horikoshii] Length = 343
SEQ ID n°124	Prot n°PL-1073.1	Contig36	57456	58256	57%	Identities = 85/255 (33%), Positives = 154/255 (60%), Gaps = 10/255 (3%) sp Q57554 Y089_METJA HYPOTHETICAL ABC TRANSPORTER ATP- BINDING PROTEIN MJ0089 pir JA64311 ferric enterobactin transport ATP- binding protein homolog - Methanococcus jannaschii gb AAB98070.1 (U67466) ferric enterobactin transport ATP-binding protein [Methanococcus jannaschii] Length = 254
SEQ ID n°125	Prot n°PL-1074.1	Contig36	58387	60366	64%	Identities = 297/670 (44%), Positives = 433/670 (64%), Gaps = 29/670 (4%) gb AAAF93848.1 (AE004134) iron-regulated outer membrane virulence protein, TonB receptor family [Vibrio cholerae] Length = 652
SEQ ID n°126	Prot n°PL-1075.1	Contig36	61181	62467	80%	Identities = 321/453 (70%), Positives = 380/453 (83%) sp P33016 YEELF_EC01 HYPOTHETICAL 49.8 KD TRANSPORT PROTEIN IN SBCB-HISL INTERGENIC REGION pir E64966 probable amino acid permease yeeF - Escherichia coli gb AAA16420.1 (U00009) yeeF [Escherichia coli] dbj BAA15842.1 (D90839) Proline transport protein [Escherichia coli] dbj BAA15847.1 (D90840) Proline transport protein [Escherichia coli] gb AAC75075.1 (AE000293) putative amino acid/amine
SEQ ID n°127	Prot n°PL-1076.1	Contig36	62662	64377	81%	Identities = 403/569 (70%), Positives = 469/569 (81%) sp P06149 DLD_EC01 D-LACTATE DEHYDROGENASE pir DDEECDL D-lactate dehydrogenase (EC 1.1.1.28) - Escherichia coli pdb 1FOX A Chain A, Crystal Structure Of D- Lactate Dehydrogenase, A Peripheral Membrane Respiratory Enzyme. pdb 1FOX B Chain B, Crystal Structure Of D-Lactate Dehydrogenase, A Peripheral Membrane Respiratory Enzyme. emb CAA25531.1 (X01067) D-lactate dehydrogenase [Escherichia coli] gb AAA23688.1 (M10038) D-lactate dehydrogenase [Escherichia coli] gb AAC75194.1 (AE000302) D-lactate dehydrogenase, FAD protein, NADH independent [Escherichia coli] Length = 571

TABLEAU I

SEQ ID n°128	Prot n°PL-1077.1	Contig36	64505	65935	80%	<p>Identities = 323/474 (68%), Positives = 385/474 (81%), Gaps = 1/474 (0%) spiP04995 EX1_ECOLI EXODEOXYRIBONUCLEASE I (EXONUCLEASE I) (DNA DEOXYRIBOPHODIESTERASE) (DRPase) pir INCECX1 exodeoxyribonuclease I (EC 3.1.11.1) - Escherichia coli gb AA18417.1 (U00009) exonuclease I [Escherichia coli] dbj BAA15839.1 (D90839) Exodeoxyribonuclease I (EC 3.1.11.1) (Exonuclease I) (DNA deoxyribophosphodiesterase) (DRPase), [Escherichia coli] dbj BAA15844.1 (D90840) Exodeoxyribonuclease I (EC 3.1.11.1) (Exonuclease I) (DNA deoxyribophosphodiesterase) (DRPase), [Escherichia coli] gb AAC75072.1 (AE000292) exonuclease I, 3' -> 5' specific; deoxyribophosphodiesterase [Escherichia coli] Length = 475 "</p>
SEQ ID n°129	Prot n°PL-1078.1	Contig36	66038	66769	No Hits found	
SEQ ID n°130	Prot n°PL-1079.1	Contig36	69539	70171	66%	<p>Identities = 107/209 (51%), Positives = 142/209 (67%), Gaps = 6/209 (2%) pir TT12087 hypothetical protein Y - Yersinia pestis gb AAC64864.1 (U60647) unknown [Yersinia pestis] Length = 216</p>
SEQ ID n°131	Prot n°PL-108.1	Contig41	183590	184351	71%	<p>Identities = 155/257 (60%), Positives = 181/257 (74%), Gaps = 7/257 (2%) spiP45564 YFEN_ECOLI HYPOTHETICAL 29.2 KD PROTEIN IN XAPA-LIG INTERGENIC REGION (ORF254) pir G65014 hypothetical 29.2 kd protein in xapa-lig intergenic region - Escherichia coli (strain K-12) emb CAA52046.1 (X73828) orf254 [Escherichia coli] gb AAC75461.1 (AE000328) putative sugar hydrolase [Escherichia coli] dbj BAA16279.1 (D90870) similar to [SwissProt Accession Number P45564] [Escherichia coli] Length = 254</p>
SEQ ID n°132	Prot n°PL-1080.1	Contig36	70356	73460	76%	<p>Identities = 680/1074 (63%), Positives = 792/1074 (73%), Gaps = 59/1074 (5%) pir S27311 ribonuclease E (EC 3.1.4.-) - Escherichia coli dbj BAA35893.1 (D90744) Ribonuclease e (EC 3.1.4.-) (RNase E). [Escherichia coli] gb AAC74188.1 (AE000209) RNase E, membrane attachment, mRNA turnover, maturation 5S RNA [Escherichia coli]</p>
SEQ ID n°133	Prot n°PL-1081.1	Contig36	73999	74979	83%	<p>Identities = 250/316 (79%), Positives = 274/316 (86%), Gaps = 2/316 (0%) spiP23851 RLUC_ECOLI RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) pir C64852 probable pseudouridyate synthase yceC - Escherichia coli gb AAC74170.1 (AE000209) orf, hypothetical protein [Escherichia coli] dbj BAA35894.1 (D90744) Hypothetical 36.0 kd protein in me-rpmF intergenic region (orf), [Escherichia coli] Length = 319</p>
SEQ ID n°134	Prot n°PL-1082.1	Contig36	74976	75584	73%	<p>Identities = 124/194 (63%), Positives = 155/194 (78%) spiP27244 YCEF_ECOLI HYPOTHETICAL 23.2 KDA PROTEIN IN RNE- RPMF INTERGENIC REGION (ORF7) pir D64852 yceF protein - Escherichia coli gb AA23829.1 (M96791) orfY [Escherichia coli] gb AAC74171.1 (AE000209) orf, hypothetical protein [Escherichia coli] dbj BAA35895.1 (D90744) Hypothetical 23.2 kd protein in rne-rpmF intergenic region</p>

TABLEAU I

SEQ ID n°135	Prot n°PL-1084.1	Contig36	76445	77482	84%	<p>Identities = 248/342 (72%), Positives = 295/342 (86%), Gaps = 1/342 (0%) sp O85138 PLSX_SALTY_FATTY_ACID/PHOSPHOLIPID SYNTHESIS PROTEIN PLSX Length = 359</p>	
SEQ ID n°136	Prot n°PL-1085.1	Contig36	77489	78442	85%	<p>Identities = 235/317 (74%), Positives = 273/317 (85%) sp O85139 FABH_SALTY_3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS II) gb AAC38848.1 (AF044668) 3-oxoacyl-acyl carrier protein synthase III</p>	
SEQ ID n°137	Prot n°PL-1086.1	Contig36	78461	79399	84%	<p>Identities = 231/308 (75%), Positives = 269/308 (87%) sp P25715 FABD_ECOLI_MALONYL_COA-ACYL_CARRIER_PROTEIN TRANSACYLASE (MCT) pir B41856 [acyl-carrier-protein] S- malonyltransferase (EC 2.3.1.39) - Escherichia coli pdb 1MLA Mol_id: 1; Molecule: Malonyl-Coenzyme A Acyl Carrier Protein Transacylase; Chain: Null; Synonym: Malonyl-CoA Acp Transacylase; Engineered: Yes emb CAA77658.1 (Z11565) malonyl CoA-acyl carrier protein transacylase [Escherichia coli] gb AA23742.1 (M87040) malonyl coenzyme A-acyl carrier protein transacylase [Escherichia coli] dbj BAA35900.1 (D90745) [Acyl- carrier-protein] s-malonyltransferase (EC 2.3.1.39). [Escherichia coli] gb AAC74176.1 (AE000210) malonyl-CoA-[acyl-carrier-protein] transacylase</p>	
SEQ ID n°138	Prot n°PL-1087.1	Contig36	79407	80141	80%	<p>Identities = 177/243 (72%), Positives = 204/243 (83%) sp P25716 FABG_ECOLI_3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE) pir B42147 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Escherichia coli dbj BAA35901.1 (D90745) 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100). [Escherichia coli] gb AAC74177.1 (AE000210) 3-oxoacyl-[acyl-carrier-protein] reductase [Escherichia coli]</p>	
SEQ ID n°139	Prot n°PL-1088.1	Contig36	80806	81856	86%	<p>Identities = 347/414 (83%), Positives = 379/414 (90%), Gaps = 2/414 (0%) sp P39435 FABF_ECOLI_3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II (BETA-KETOACYL-ACP SYNTHASE II) (KAS II) pir J41060 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Escherichia coli emb CAA84431.1 (Z34979) beta ketoacyl-acyl carrier protein synthase [Escherichia coli] gb AA83255.1 (U20767) beta-ketoacyl- acyl carrier protein synthase II [Escherichia coli] gb AAC74179.1 (AE000210) 3-oxoacyl-[acyl-carrier-protein] synthase II [Escherichia coli] dbj BAA35903.1 (D90745) 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II [Escherichia coli] Length = 413</p>	

TABLEAU I

SEQ ID n°140	Prot n°PL-1089.1	Contig36	82211	83035	65%	<p>Identities = 134/271 (49%), Positives = 183/271 (67%), Gaps = 6/271 (2%) sp P28305 PABC_ECOLI_4-AMINO-4-DEOXYCHORISMATE LYASE (ADC LYASE) (ADCL) pir A42954 4-amino-4-deoxychorismate lyase (EC 4.-.-) - Escherichia coli pdb 1ETOJA Chain A, Crystal Structure Of Aminodeoxychorismate Lyase From Escherichia coli gb AA24287.1 (M93135) 4-amino-4-deoxychorismate lyase [Escherichia coli] db BAA35904.1 (D90745) 4-amino-4-deoxychorismate lyase. [Escherichia coli] gb AAC74180.1 (AE000210) 4-amino-4-deoxychorismate lyase [Escherichia coli] Length = 269</p>
SEQ ID n°141	Prot n°PL-109.1	Contig41	184701	185636	78%	<p>Identities = 199/315 (63%), Positives = 246/315 (77%), Gaps = 9/315 (2%) sp P18400 CYOA_ECOLI_UBIQUINOL OXIDASE POLYPEPTIDE II PRECURSOR (CYTOCHROME O SUBUNIT 2) (OXIDASE BO(3) SUBUNIT 2) (CYTOCHROME O UBIQUINOL OXIDASE SUBUNIT 2) pir A42228 bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Escherichia coli gb AA23631.1 (J05492) cytochrome o ubiquinol oxidase subunit II [Escherichia coli] gb AAB40188.1 (U82684) cytochrome o ubiquinol oxidase subunit II [Escherichia coli] gb AAC73535.1 (AE000149) cytochrome o ubiquinol oxidase subunit II [Escherichia coli] Length = 315</p>
SEQ ID n°142	Prot n°PL-1090.1	Contig36	83087	84116	70%	<p>Identities = 183/335 (54%), Positives = 239/335 (70%) sp P28308 YCEG_ECOLI_HYPOTHETICAL 38.2 KD PROTEIN IN PABC-HOLB INTERGENIC REGION pir F64853 yceG protein precursor - Escherichia coli gb AAC74181.1 (AE000210) putative thymidylate kinase (EC 2.7.4.9) [Escherichia coli] Length = 340</p>
SEQ ID n°143	Prot n°PL-1091.1	Contig36	84122	84760	80%	<p>Identities = 184/210 (78%), Positives = 183/210 (87%) sp O69169 KTHY_YERPE_THYMIDYLATE KINASE (DTMP KINASE) gb AAC18855.1 (AF065312) thymidylate kinase [Yersinia pestis] Length = 212</p>
SEQ ID n°144	Prot n°PL-1092.1	Contig36	84760	85749	62%	<p>Identities = 159/323 (49%), Positives = 211/323 (65%), Gaps = 4/323 (1%) sp P28631 HOLB_ECOLI_DNA POLYMERASE III, DELTA' SUBUNIT pir S35523 DNA-directed DNA polymerase (EC 2.7.7.7) III delta' chain - Escherichia coli pdb 1A5T Crystal Structure Of The Delta Prime Subunit Of The Clamp-Loader Complex Of Escherichia coli Dna Polymerase III gb AA23696.1 (L01483) DNA polymerase III delta prime subunit [Escherichia coli] db BAA35906.1 (D90745) DNA-directed dna polymerase (EC 2.7.7.7) III delta' chain [Escherichia coli] gb AAC74183.1 (AE000210) DNA polymerase III, delta prime subunit [Escherichia coli] Length =</p>

TABLEAU I

SEQ ID n°145	Prot n°PL-1093.1	Contig36	85775	86560	78%	<p>Identities = 188/262 (71%), Positives = 225/262 (85%)</p> <p>sp P37346 YCFH_ECOLI_HYPOTHETICAL 29.8 KDA PROTEIN IN HOLB-PTSG INTERGENIC REGION pir J64854 probable metal-dependent hydrolase (EC 3.---) ycfH - Escherichia coli gb AAC74184.1 (AE000210) orf, hypothetical protein [Escherichia coli] dbj BAA35907.1 (D90745) Hypothetical protein in holB 3'region. [Escherichia coli] Length = 89/210 (42%), Positives = 120/210 (56%), Gaps = 21/210 (10%)</p> <p>dbj BAA35912.1 (D90745) Fibronectin-binding protein B [Escherichia coli]</p> <p>dbj BAA35920.1 (D90746) Fibronectin-binding protein B [Escherichia coli] Length = 214</p>
SEQ ID n°146	Prot n°PL-1094.1	Contig36	87292	87864	56%	<p>Identities = 92/216 (42%), Positives = 128/216 (59%), Gaps = 15/216 (6%)</p> <p>sp P75948 YCFN_ECOLI_HYPOTHETICAL 32.4 KDA PROTEIN IN FHUE-NDH INTERGENIC REGION pir J64854 ycfN protein - Escherichia coli gb AAC74190.1 (AE000211) putative beta-glucosidase (EC 3.2.1.21) [Escherichia coli] dbj BAA35913.1 (D90745) ORF_ID:0237#5 [Escherichia coli] dbj BAA35921.1 (D90746) ORF_ID:0237#5 [Escherichia coli] Length = 274</p>
SEQ ID n°147	Prot n°PL-1095.1	Contig36	87821	88714	42%	<p>Identities = 243/337 (72%), Positives = 276/337 (81%), Gaps = 1/337 (0%)</p> <p>sp P75949 YCFQ_ECOLI_HYPOTHETICAL 37.6 KDA PROTEIN IN FHUE-NDH INTERGENIC REGION pir J64854 probable glucosidase (EC 3.2.1.-) ycfQ - Escherichia coli gb AAC74191.1 (AE000211) orf, hypothetical protein [Escherichia coli] dbj BAA35914.1 (D90745) Hypothetical protein HI0959 [Escherichia coli] dbj BAA35922.1 (D90746) Hypothetical protein HI0959 [Escherichia coli] Length = 341</p>
SEQ ID n°148	Prot n°PL-1096.1	Contig36	88837	89859	80%	<p>Identities = 355/434 (81%), Positives = 389/434 (88%)</p> <p>sp P00393 DHNA_ECOLI_NADH_DEHYDROGENASE pir JDEECR NADH dehydrogenase (EC 1.6.99.3) - Escherichia coli emb CAA23588.1 (V00306) NADH dehydrogenase [Escherichia coli] dbj BAA35924.1 (D90746) NADH dehydrogenase (EC 1.6.99.3) [Escherichia coli] gb AAC74193.1 (AE000211) respiratory NADH dehydrogenase [Escherichia coli] Length = 434</p> <p>emb CAB69803.1 (AJ243711) putative subtilase family serine protease [Bacillus cereus] Length = 613</p>
SEQ ID n°149	Prot n°PL-1097.1	Contig36	90285	91569	87%	<p>Identities = 116/276 (42%), Positives = 176/276 (63%), Gaps = 3/276 (1%)</p> <p>gb AAEF95092.1 (AE004270) PvcB protein [Vibrio cholerae] Length = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%)</p> <p>dbj BAB08239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188</p>
SEQ ID n°150	Prot n°PL-1098.1	Contig36	91656	93350	24%	
SEQ ID n°151	Prot n°PL-1099.1	Contig36	95795	96640	53%	
SEQ ID n°152	Prot n°PL-11.1	Contig41	20349	21416	21%	

TABLEAU I

SEQ ID n°153	Prot n°PL-110.1	Contig41	185641	187632	90%	<p>Identities = 546/663 (82%), Positives = 612/663 (91%)</p> <p>sp P18401 CYOB_ECOLI_UBIQUINOL_OXIDASE_POLYPEPTIDE_I (CYTOCHROME O SUBUNIT 1) (OXIDASE BO(3) SUBUNIT 1) 1) pir B42226 bo-type ubiquinol oxidase (EC 1.10.3.-) chain I - Escherichia coli gb AAA23632.1 (J05492) cytochrome o ubiquinol oxidase B subunit I [Escherichia coli] gb AAB40187.1 (U82664) cytochrome o ubiquinol oxidase [Escherichia coli] gb AAC73534.1 (AE000149) cytochrome o ubiquinol oxidase subunit I</p> <p>Identities = 178/312 (57%), Positives = 229/312 (73%), Gaps = 2/312 (0%)</p> <p>gb AAG08642.1 AE004651_4 (AE004651) pyoverdine biosynthesis protein PvcA [Pseudomonas aeruginosa] Length = 328</p>
SEQ ID n°154	Prot n°PL-1100.1	Contig36	96652	97662	67%	<p>Identities = 908/1147 (79%), Positives = 1011/1147 (87%), Gaps = 1/1147 (0%)</p> <p>sp P30958 MFD_ECOLI_TRANSCRIPTION-REPAIR_COUPLING_FACTOR (TRCF) pir G84855 transcription/repair-coupling protein - Escherichia coli dbj BAA35929.1 (D90746) Transcription-repair coupling protein mfd [Escherichia coli] dbj BAA35934.1 (D90747) Transcription-repair coupling protein mfd [Escherichia coli] gb AAC74198.1 (AE000211) transcription-repair coupling factor; mutation frequency decline [Escherichia coli] Length = 1148 "</p>
SEQ ID n°155	Prot n°PL-1101.1	Contig36	98348	101803	87%	<p>Identities = 300/411 (72%), Positives = 347/411 (83%), Gaps = 3/411 (0%)</p> <p>dbj BAA35936.1 (D90747) Hypothetical protein H11555 [Escherichia coli] Length = 416</p>
SEQ ID n°156	Prot n°PL-1102.1	Contig36	101992	103194	82%	<p>Identities = 187/259 (72%), Positives = 213/259 (82%), Gaps = 1/259 (0%)</p> <p>dbj BAA35937.1 (D90747) Heterocyst maturation protein (devA) homolog [Escherichia coli] Length = 263</p>
SEQ ID n°157	Prot n°PL-1103.1	Contig36	103088	103891	75%	<p>Identities = 288/412 (69%), Positives = 349/412 (83%)</p> <p>sp P75958 LOLE_ECOLI_LIPOPROTEIN_RELEASEING_SYSTEM_TRANSMEMBRANE_PROTEIN_LOLE Length = 413</p>
SEQ ID n°158	Prot n°PL-1104.1	Contig36	103891	105138	82%	<p>Identities = 193/271 (71%), Positives = 226/271 (83%)</p> <p>pir E64856 hypothetical protein b1120 - Escherichia coli gb AAC74204.1 (AE000212) putative nicotinic acid mononucleotide:5,6-dimethylbenzimidazole (DMB) phosphoribosyltransferase [Escherichia coli] dbj BAA35940.1 (D90747) ORF_ID:0238#9 [Escherichia coli] Length = 279</p>
SEQ ID n°159	Prot n°PL-1105.1	Contig36	105230	106081	77%	<p>Identities = 279/405 (68%), Positives = 344/405 (84%)</p> <p>sp P28745 PEPT_ECOLI_PEPTIDASE_T (AMINOTRIPEPTIDASE) (TRIPETIDASE) pir D64857 aminotripeptidase (EC 3.4.11.-) - Escherichia coli dbj BAA35949.1 (D90748) Peptidase T (EC 3.4.11.-) (aminotripeptidase) (tripeptidase) . [Escherichia coli] gb AAC74211.1 (AE000213) putative peptidase T [Escherichia coli] Length = 408</p>
SEQ ID n°160	Prot n°PL-1106.1	Contig36	106137	107402	80%	

TABLEAU I

SEQ ID n°161	Prot n°PL-1107.1	Contig36	107581	108702	80%	Identities = 261/373 (69%), Positives = 308/373 (81%) - Escherichia coli gblAAC74212.1 (AE000213) orf, hypothetical protein [Escherichia coli] Length = 376
SEQ ID n°162	Prot n°PL-1108.1	Contig36	108786	110249	82%	Identities = 345/488 (70%), Positives = 415/488 (84%), Gaps = 4/488 (0%) gblAAC38776.1 (AF041833) putative sensor kinase [Providencia stuartii] Length = 485
SEQ ID n°163	Prot n°PL-1109.1	Contig36	110269	110937	79%	Identities = 165/222 (74%), Positives = 189/222 (84%) (X86587) phoP [Yersinia pseudotuberculosis] Length = 223
SEQ ID n°164	Prot n°PL-111.1	Contig41	186880	187650	No Hits found	Identities = 394/456 (86%), Positives = 425/456 (92%) sp P25739 PUR8_ECOLI ADENYLOSUCCINATE LYASE (ADENYLOSUCCINASE) (ASL) pir S19212 adenylosuccinate lyase (EC 4.3.2.2) - Escherichia coli emb CAA41996.1 (X59307) adenylosuccinate lyase (EC 4.3.2.2) [Escherichia coli] dbj BAA35953.1 (D90748) Adenylosuccinate lyase (EC 4.3.2.2) [Escherichia coli] dbj BAA35962.1 (D90749) Adenylosuccinate lyase (EC 4.3.2.2) [Escherichia coli] gblAAC74215.1 (AE000213) adenylosuccinate lyase [Escherichia coli] Length = 456
SEQ ID n°165	Prot n°PL-1110.1	Contig36	111175	112545	81%	Identities = 132/208 (63%), Positives = 164/208 (78%), Gaps = 1/208 (0%) sp P25746 YCF_C_ECOLI HYPOTHETICAL 22.9 KDA PROTEIN IN PURB-ICDA INTERGENIC REGION (ORF-23) pir S19211 ycfC protein - Escherichia coli emb CAA41995.1 (X59307) ORF-23 [Escherichia coli] gblAAC74216.1 (AE000213) orf, hypothetical protein [Escherichia coli] dbj BAA35954.1 (D90748) Hypothetical protein 23. [Escherichia coli] dbj BAA35963.1 (D90749) Hypothetical protein 23. [Escherichia coli] Length = 383
SEQ ID n°166	Prot n°PL-1111.1	Contig36	112569	113195	72%	Identities = 312/375 (83%), Positives = 343/375 (91%), Gaps = 1/375 (0%) pir B64858 probable ATPase ycfB - Escherichia coli gblAAC74217.1 (AE000213) orf, hypothetical protein [Escherichia coli] Length = 383
SEQ ID n°167	Prot n°PL-1112.1	Contig36	113198	114301	90%	Identities = 378/417 (90%), Positives = 401/417 (95%), Gaps = 1/417 (0%) sp P08200 IDH_ECOLI ISOCITRATE DEHYDROGENASE [NADP] (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDC) (IDP) pir DCECIS isocitrate dehydrogenase (NADP+) (EC 1.1.1.42) - Escherichia coli pdb 1A12 Isocitrate Dehydrogenase Complexed With Isocitrate, NADP+, And Calcium (Flash-Cooled) pdb 1A13 Orbital Steering In The Catalytic Power Of Enzymes: Small Structural Changes With Large Catalytic Consequences pdb 11KA Isocitrate Dehydrogenase (E.C.1.1.1.42) Complexed With Alpha-Ketoglutarate pdb 1SJS Access To Phosphorylation In Isocitrate Dehydrogenase May Occur By Domain Shifting pdb 5ICD Isocitrate Dehydrogenase (E.C.1.1.1.42) Complex With Mg2+ And Isocitrate pdb 9ICD Isocitrate Dehydrogenase (E.C.1.1.1.42) Complex With NADP+ pdb 3ICD Isocitrate Dehydrogenase (E.C.1.1.1.42) gblAAA24006.1 (J02799) Isocitrate
SEQ ID n°168	Prot n°PL-1113.1	Contig36	115598	116851	85%	

TABLEAU I

SEQ ID n°169	Prot n°PL-1114.1	Contig36	118208	118972	59%	Identities = 110/242 (45%), Positives = 153/242 (62%), Gaps = 3/242 (1%) gb AAF84266.1 AE003975_9 (AE003975) pteridine reductase 1 [Xylella fastidiosa] Length = 245	
SEQ ID n°170	Prot n°PL-1115.1	Contig36	119017	120384	No Hits found		Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°171	Prot n°PL-1116.1	Contig36	120385	123213	29%	Identities = 165/566 (29%), Positives = 280/566 (49%), Gaps = 23/566 (4%) emb CAC01604.1 (AJ269505) peptide synthetase [Anabaena sp. 90] Length = 5060	
SEQ ID n°172	Prot n°PL-1117.1	Contig36	123234	125198	47%	Identities = 186/664 (28%), Positives = 311/664 (46%), Gaps = 38/664 (5%) gb AAF39449.1 (AE002330) 2-oxoisovalerate dehydrogenase, E1 component, alpha and beta subunit [Chlamydia muridarum] Length = 678	
SEQ ID n°173	Prot n°PL-1118.1	Contig36	125802	126593	37%	Identities = 70/178 (39%), Positives = 100/178 (55%), Gaps = 7/178 (3%) dbj BAA93678.1 (AB029431) GTP cyclohydrolase I [Tetrahymena pyriformis] Length = 223	
SEQ ID n°174	Prot n°PL-1119.1	Contig36	127190	128083	70%	Identities = 159/289 (55%), Positives = 212/289 (73%), Gaps = 1/289 (0%) emb CAB72138.1 (AJ011922) BphR protein [Ralstonia eutropha] Length = 313	
SEQ ID n°175	Prot n°PL-112.1	Contig41	187622	188236	84%	Identities = 149/205 (72%), Positives = 175/205 (84%), Gaps = 2/205 (0%) sp P18402 CYOC_ECOLI CYTOCHROME O UBIQUINOL OXIDASE SUBUNIT III pir C42226 bo-type ubiquinol oxidase (EC 1.10.3.-) chain III - Escherichia coli gb AAA23633.1 (J05492) cytochrome o ubiquinol oxidase C subunit [Escherichia coli] gb AAB40186.1 (U82664) cytochrome o ubiquinol oxidase [Escherichia coli] gb AAC73533.1 (AE000149) cytochrome o ubiquinol oxidase subunit III [Escherichia coli] Length = 204	
SEQ ID n°176	Prot n°PL-1120.1	Contig36	130481	131953	81%	Identities = 338/472 (71%), Positives = 403/472 (84%), Gaps = 1/472 (0%) gb AAF95499.1 (AE004306) sodium/alanine symporter [Vibrio cholerae] Length = 476	
SEQ ID n°177	Prot n°PL-1121.1	Contig36	132254	133075	57%	Identities = 131/268 (48%), Positives = 173/268 (63%), Gaps = 4/268 (1%) sp P75820 YBJR_ECOLI PROBABLE N-ACETYLMURAMOYL-L-ALANINE AMIDASE YBJR pir C64825 hypothetical protein b0867 precursor - Escherichia coli gb AAC73954.1 (AE000188) putative regulator [Escherichia coli] dbj BAA35561.1 (D90724) AmpD protein. [Escherichia coli] Length = 268	
SEQ ID n°178	Prot n°PL-1122.1	Contig36	136029	137408	77%	Identities = 304/454 (66%), Positives = 364/454 (79%) pir QRECAA aromatic amino acid transport protein arnP - Escherichia coli gb AAC73223.1 (AE000120) aromatic amino acid transport protein [Escherichia coli] Length = 457	

TABLEAU I

SEQ ID n°179	Prot n°PL-1123.1	Contig36	137727	138353	55%	<p>Identities = 91/161 (56%), Positives = 115/161 (70%), Gaps = 1/161 (0%) sp P37001 CRCA_ECOLI_CRCA PROTEIN pir D64796 crca protein - Escherichia coli gb AA067555.1 (L29054) putative [Escherichia coli] gb AAB40822.1 (U82598) hypothetical protein [Escherichia coli] gb AAC73723.1 (AE000167) orf, hypothetical protein [Escherichia coli] Length = 188</p>
SEQ ID n°180	Prot n°PL-1124.1	Contig36	139460	140257	78%	<p>Identities = 186/266 (69%), Positives = 221/266 (82%) sp P55882 THID_SALTY PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE) gb AAB68492.1 (U87940) HMP-P Kinase [Salmonella typhimurium] Length = 266</p>
SEQ ID n°181	Prot n°PL-1125.1	Contig36	140552	141801	92%	<p>Identities = 301/350 (86%), Positives = 326/350 (93%), Gaps = 1/350 (0%) sp P71285 ALF1_ECOLI FRUCTOSE-BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE) Length = 350</p>
SEQ ID n°182	Prot n°PL-1126.1	Contig36	143788	145164	87%	<p>Identities = 378/450 (84%), Positives = 411/450 (91%) sp P78403 YEGQ_ECOLI PUTATIVE PROTEASE YEGQ pir H64974 hypothetical protein b2081 - Escherichia coli (strain K-12) dbj BAA15936.1 (D90846) Collagenase precursor (EC 3.4.-.-) [Escherichia coli] dbj BAA15947.1 (D90847) Collagenase precursor (EC 3.4.-.-) [Escherichia coli] gb AAC75142.1 (AE000298) orf, hypothetical protein [Escherichia coli] Identities = 182/229 (79%), Positives = 196/229 (84%), Gaps = 5/229 (2%)</p>
SEQ ID n°183	Prot n°PL-1127.1	Contig36	145805	146509	80%	<p>sp P30846 BAER_ECOLI TRANSCRIPTIONAL REGULATORY PROTEIN BAER pir JX0283 response-regulator BaeR protein - Escherichia coli dbj BAA03141.1 (D14054) BaeR [Escherichia coli] dbj BAA15935.1 (D90846) Response-regulator BaeR protein [Escherichia coli] dbj BAA15948.1 (D90847) Response-regulator BaeR protein [Escherichia coli] gb AAC75140.1 (AE000297) transcriptional response regulatory protein (sensor BaeS) [Escherichia coli] Length = 240</p>
SEQ ID n°184	Prot n°PL-1128.1	Contig36	146506	147894	71%	<p>Identities = 281/460 (61%), Positives = 351/460 (76%), Gaps = 3/460 (0%) sp P30847 BAES_ECOLI SENSOR PROTEIN BAES pir E64974 sensory kinase BaeS (EC 2.7.3.-) - Escherichia coli dbj BAA15934.1 (D90846) Sensor protein BaeS (EC 2.7.3.-) [Escherichia coli] dbj BAA15945.1 (D90847) Sensor protein BaeS (EC 2.7.3.-) [Escherichia coli] gb AAC75139.1 (AE000297) sensor protein (for BaeR) [Escherichia coli] Length = 467</p>
SEQ ID n°185	Prot n°PL-1129.1	Contig36	148015	151125	86%	<p>Identities = 774/1018 (76%), Positives = 898/1018 (88%) sp P76399 YEGO_ECOLI HYPOTHETICAL 111.0 KD PROTEIN IN ALKA-BAES INTERGENIC REGION pir C64974 hypothetical protein b2076 - Escherichia coli (strain K-12) dbj BAA15932.1 (D90846) Acriflavin resistance protein F (EnvD protein). [Escherichia coli] gb AAC75137.1 (AE000297) orf, hypothetical protein [Escherichia coli] Length = 1025</p>

TABLEAU I

SEQ ID n°186	Prot n°PL-113.1	Contig41	188581	189465	87%	<p>Identities = 241/288 (83%), Positives = 261/288 (89%) gb AAB40184.1 (U82664) cytochrome o ubiquinol oxidase C subunit [Escherichia coli] Length = 311</p> <p>Identities = 803/1032 (77%), Positives = 916/1032 (87%) sp P76398 YEGN_ECOLI_HYPOTHETICAL_112.1_KD_PROTEIN_IN_ALKA-BAES_INTERGENIC_REGION_pir B64974_hypothetical_protein_b2075_Escherichia_coli_(strain_K-12)_dbj BAA15929.1 (D90845) Acriflavin resistance protein D. [Escherichia coli] gb AAC75136.1 (AE000297)orf, hypothetical protein [Escherichia coli] Length = 1040</p>
SEQ ID n°187	Prot n°PL-1130.1	Contig36	151122	154268	86%	<p>Identities = 243/378 (64%), Positives = 303/378 (79%), Gaps = 10/378 (2%) sp P76397 YEGM_ECOLI_HYPOTHETICAL_44.5_KDA_PROTEIN_IN_ALKA-BAES_INTERGENIC_REGION_PRECURSOR Length = 415</p>
SEQ ID n°188	Prot n°PL-1131.1	Contig36	154268	155488	74%	<p>Identities = 105/306 (34%), Positives = 160/306 (51%), Gaps = 5/306 (1%) emb CAB91168.1 (AL356920) putative inosine-uridine preferring nucleoside hydrolase [Schizosaccharomyces pombe] Length = 310</p>
SEQ ID n°189	Prot n°PL-1132.1	Contig36	155964	156893	51%	<p>Identities = 102/346 (29%), Positives = 158/346 (45%), Gaps = 29/346 (8%) pir T35340_probable_adenosine_deaminase - Streptomyces coelicolor emb CAB42949.1 (AL049863) putative adenosine deaminase [Streptomyces coelicolor A3(2)] Length = 359</p>
SEQ ID n°190	Prot n°PL-1133.1	Contig36	156916	157926	46%	<p>Identities = 53/197 (26%), Positives = 87/197 (43%), Gaps = 10/197 (5%) pir F7285_transcription_regulator_crp_family - Thermotoga maritima (strain MSB8) gb AAD36246.1 AE001774_3 (AE001774) transcriptional regulator, crp family [Thermotoga maritima] Length = 201</p>
SEQ ID n°191	Prot n°PL-1134.1	Contig36	158234	158908	38%	<p>Identities = 157/475 (33%), Positives = 245/475 (51%), Gaps = 30/475 (6%) sp P22106 ASNB_ECOLI ASPARAGINE SYNTHETASE B [GLUTAMINE-HYDROLYZING] pir AJECN asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - Escherichia coli gb AA23498.1 (J05554) asparagine synthetase B [Escherichia coli] dbj BAA35317.1 (D90706) Asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) [Escherichia coli] gb AAC73768.1 (AE000171) asparagine synthetase B [Escherichia coli] Length = 150/426 (35%), Positives = 225/426 (52%), Gaps = 11/426 (2%)</p>
SEQ ID n°192	Prot n°PL-1135.1	Contig36	159097	160644	47%	<p>sp Q9RVD3 AROA_DEIRA_3-PHOSPHOSHIMKIMATE_1-CARBOXYVINYLTRANSFERASE (6-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS) Length = 439</p>
SEQ ID n°193	Prot n°PL-1136.1	Contig36	160665	162035	49%	<p>Identities = 100/437 (22%), Positives = 191/437 (42%), Gaps = 37/437 (8%) sp Q57925 AROA_METJA_PROBABLE_3-PHOSPHOSHIMKIMATE_1-CARBOXYVINYLTRANSFERASE (6-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS) Length = 429</p>
SEQ ID n°194	Prot n°PL-1137.1	Contig36	162048	163370	43%	<p>gb AAB98493.1 (U67500) 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) [Methanococcus jannaschii] Length = 429</p>

TABLEAU I

SEQ ID n°195	Prot n°PL-1138.1	Contig36	164350	165612	33%	Identities = 82/313 (26%), Positives = 141/313 (44%), Gaps = 24/313 (7%) sp P55641 Y4RH_RHISN HYPOTHETICAL 52.5 KD PROTEIN Y4RH gb AAB91833.1 (AE000094) Y4RH [Rhizobium sp. NGR234] Length = 313 Identities = 71/279 (25%), Positives = 116/279 (41%), Gaps = 12/279 (4%) pir C75275 hypothetical protein - Deinococcus radiodurans (strain R1) gb AAF11982.1 AE002073_12 (AE002073) hypothetical protein [Deinococcus radiodurans] Length = 278
SEQ ID n°196	Prot n°PL-1139.1	Contig36	165616	166473	40%	Identities = 299/453 (66%), Positives = 377/453 (83%) sp P77726 YAJR_EC0LJ HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION pir C64772 probable transport protein yajR - Escherichia coli gb AAB40183.1 (U82684) hypothetical protein [Escherichia coli] gb AAC73530.1 (AE000149) putative transport protein [Escherichia coli] Identities = 367/509 (72%), Positives = 432/509 (84%), Gaps = 2/509 (0%) gb AAC34891.1 (AF085682) exopolyphosphatase [Salmonella typhimurium] Length = 513
SEQ ID n°197	Prot n°PL-114.1	Contig41	189620	190999	79%	Identities = 550/688 (79%), Positives = 623/688 (89%), Gaps = 2/688 (0%) sp P28688 PPK_EC0LI POLYPHOSPHATE KINASE pir A44306 polyphosphate kinase (EC 2.7.4.1) - Escherichia coli gb AAC75554.1 (AE000336) polyphosphate kinase [Escherichia coli] db BAA16389.1 (D90878) polyphosphate kinase (EC 2.7.4.1) [Escherichia coli] Length = 688 Identities = 145/211 (68%), Positives = 173/211 (81%) pdb 3GAR A Ph-Dependent Stabilization Of An Active Site Loop Observed From Low And High Ph Crystal Structures Of Ribonucleotide Transformylase pdb 2GAR A Ph-Dependent Stabilization Of An Active Site Loop Observed From Low And High Ph Crystal Structures Of Mutant Monomeric Transformylase Length = 212
SEQ ID n°198	Prot n°PL-1140.1	Contig36	168808	168340	84%	Identities = 289/346 (83%), Positives = 314/346 (90%), Gaps = 1/346 (0%) gb AAG14577.1 AF293164_1 (AF293164) phosphoribosylaminimidazole synthetase [Escherichia coli] Length = 350
SEQ ID n°199	Prot n°PL-1141.1	Contig36	168344	170413	87%	Identities = 190/210 (90%), Positives = 201/210 (95%) pir A65026 uracil phosphoribosyltransferase (EC 2.4.2.9) upp - Escherichia coli gb AAC75551.1 (AE000336) uracil phosphoribosyltransferase [Escherichia coli] Length = 217
SEQ ID n°200	Prot n°PL-1142.1	Contig36	171165	171803	78%	Identities = 247/432 (57%), Positives = 319/432 (73%), Gaps = 1/432 (0%) gb AAF94443.1 (AE004207) 8-phospho-beta-glucosidase [Vibrio cholerae] Length = 440
SEQ ID n°201	Prot n°PL-1143.1	Contig36	171800	172840	86%	Identities = 238/424 (56%), Positives = 319/424 (75%) gb AAF94441.1 (AE004207) PTS system, cellobiose-specific IIC component [Vibrio cholerae] Length = 446
SEQ ID n°202	Prot n°PL-1144.1	Contig36	173067	173693	94%	
SEQ ID n°203	Prot n°PL-1145.1	Contig36	174742	176049	71%	
SEQ ID n°204	Prot n°PL-1146.1	Contig36	176424	177752	69%	
SEQ ID n°205	Prot n°PL-1147.1	Contig36	178344	178973	No Hits found	

TABLEAU I

SEQ ID n°206	Prot n°PL-1148.1	Contig36	179256	179957	87%	<p>Identities = 193/243 (79%), Positives = 216/243 (88%)</p> <p>sp P76570 YFGE_ECOLI HYPOTHETICAL 28.4 KD PROTEIN IN FOCC-URAA INTERGENIC REGION pir J665025 hypothetical protein b2496 - Escherichia coli (strain K-12) gb AAC75549.1 (AE000336) putative DNA replication factor [Escherichia coli] Length = 248</p>
SEQ ID n°207	Prot n°PL-1149.1	Contig36	180478	181941	74%	<p>Identities = 297/481 (61%), Positives = 369/481 (75%), Gaps = 1/481 (0%)</p> <p>pir J665025 hypothetical protein b2494 - Escherichia coli (strain K-12) gb AAC75547.1 (AE000336) orf, hypothetical protein [Escherichia coli] Length = 487</p>
SEQ ID n°208	Prot n°PL-115.1	Contig41	191750	192622	63%	<p>Identities = 157/291 (53%), Positives = 209/291 (70%)</p> <p>sp P77728 APBA_ECOLI 2-DEHYDROPANTOATE 2-REDUCTASE (KETOPANTOATE REDUCTASE) (KPA REDUCTASE) pir J64772 ketopantoate reductase - Escherichia coli gb AAB40181.1 (U82664) similar to S. typhimurium apbA [Escherichia coli] gb AAC73528.1 (AE000149) involved in thiamin biosynthesis, alternative pyrimidine biosynthesis [Escherichia coli] Identities = 245/347 (70%), Positives = 294/347 (84%)</p>
SEQ ID n°209	Prot n°PL-1150.1	Contig36	182078	183157	79%	<p>sp P77406 PERM_ECOLI PUTATIVE PERMEASE PERM pir J65025 hypothetical protein b2493 - Escherichia coli (strain K-12) gb AAC75546.1 (AE000336) putative permease [Escherichia coli] db JBA16382.1 (D90878) similar to [SwissProt Accession Number P43970] [Escherichia coli]</p>
SEQ ID n°210	Prot n°PL-1151.1	Contig36	184709	185608	82%	<p>Identities = 230/292 (78%), Positives = 262/292 (88%), Gaps = 1/292 (0%)</p> <p>sp P05640 DAPA_ECOLI DIHYDRODIPICOLINATE SYNTHASE (DHDP) pir SYECDP dihydrodipicolinate synthase (EC 4.2.1.52) - Escherichia coli pdb 1DHP A Chain A, Dihydrodipicolinate Synthase pdb 1DHP B Chain B, Dihydrodipicolinate Synthase gb AAC75531.1 (AE000335) dihydrodipicolinate synthase [Escherichia coli] db JBA16355.1 (D90876) dihydrodipicolinate synthase (EC 4.2.1.52) [Escherichia coli] db JBA16365.1 (D90877) dihydrodipicolinate synthase (EC 4.2.1.52) [Escherichia coli] Length = 292</p>
SEQ ID n°211	Prot n°PL-1152.1	Contig36	185625	186674	68%	<p>Identities = 179/346 (51%), Positives = 243/346 (69%), Gaps = 1/346 (0%)</p> <p>pir J65023 lipoprotein-34 precursor - Escherichia coli gb AAC75530.1 (AE000335) lipoprotein-34 [Escherichia coli] Length = 345</p>

TABLEAU I

SEQ ID n°212	Prot n°PL-1153.1	Contig36	186954	187667	91%	<p>Identities = 212/237 (89%), Positives = 227/237 (95%)</p> <p>spiP21165 PUR7_ECOLI PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (SAICAR SYNTHETASE) pir C36146 phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6) - Escherichia coli gb AA24448.1 (M33928) 5'-phosphoribosyl-5-aminimidazole-4- N-succinocarboxamide synthetase (EC 6.3.2.6) [Escherichia coli] gb AAC75529.1 (AE000334) phosphoribosylaminoimidazole succinocarboxamide synthetase = SAICAR synthetase [Escherichia coli] db BAA16353.1 (D90876)</p> <p>phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6) [Escherichia coli] db BAA16363.1 (D90877)</p> <p>phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6) [Escherichia coli] gb AAC75529.1 (AE000334) phosphoribosylaminoimidazole succinocarboxamide synthetase = SAICAR synthetase [Escherichia coli] db BAA16353.1 (D90876)</p>
SEQ ID n°213	Prot n°PL-1154.1	Contig36	188002	189069	21%	<p>Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db BAB09239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188</p>
SEQ ID n°214	Prot n°PL-1155.1	Contig36	189354	191102	48%	<p>Identities = 156/567 (27%), Positives = 284/567 (49%), Gaps = 25/567 (4%) pir S74455 ABC-type transport protein slr1488 - Synechocystis sp. (strain PCC 6803) db BAA16607.1 (D90899) ABC transporter [Synechocystis sp.] Length = 605</p>
SEQ ID n°215	Prot n°PL-1156.1	Contig36	191084	192754	48%	<p>Identities = 143/589 (24%), Positives = 271/589 (45%), Gaps = 80/589 (10%) pir J574461 ABC transporter slr1494 - Synechocystis sp. (strain PCC 6803) db BAA16613.1 (D90899) ABC transporter [Synechocystis sp.] Length = 613</p>
SEQ ID n°216	Prot n°PL-1157.1	Contig36	193463	194680	34%	<p>Identities = 81/307 (26%), Positives = 141/307 (45%), Gaps = 38/307 (12%) pir J72391 conserved hypothetical protein - Thermotoga maritima (strain MSB8) gb AAD35423.1 (AE001714_14 (AE001714) conserved hypothetical protein [Thermotoga maritima] Length = 412</p>
SEQ ID n°217	Prot n°PL-1158.1	Contig36	194957	196249	48%	<p>Identities = 126/385 (32%), Positives = 208/385 (53%), Gaps = 10/385 (2%) gb AAG05778.1 (AE004665_5 (AE004665) probable ATP-binding/permease fusion ABC transporter [Pseudomonas aeruginosa] Length = 663</p>
SEQ ID n°218	Prot n°PL-1159.1	Contig36	196183	196848	57%	<p>Identities = 95/222 (42%), Positives = 146/222 (64%) emb CAA11724.1 (AJ223978) putative ABC transporter, YvrO [Bacillus subtilis] Length = 127/365 (33%), Positives = 204/365 (55%), Gaps = 10/365 (2%) spiP755913 THI1_SALTY</p>
SEQ ID n°219	Prot n°PL-116.1	Contig41	192839	194287	90%	<p>Identities = 392/482 (81%), Positives = 438/482 (90%) spiP755913 THI1_SALTY THIAMINE BIOSYNTHESIS PROTEIN THI1 gb AAB63031.1 (U94901) ThiI [Salmonella typhimurium] Length = 482</p>
SEQ ID n°220	Prot n°PL-1160.1	Contig36	196832	197898	51%	<p>Identities = 121/365 (33%), Positives = 204/365 (55%), Gaps = 10/365 (2%) spiP75830 YBJY_ECOLI HYPOTHETICAL 41.7 KDA PROTEIN IN AQPZ-CSPD INTERGENIC REGION db BAA35597.1 (D90725) MtrC protein [Escherichia coli] Length = 371</p>

TABLEAU I

SEQ ID n°221	Prot n°PL-1161.1	Contig36	198014	202429	42%	Identities = 343/1547 (22%), Positives = 631/1547 (40%), Gaps = 152/1547 (9%) emb[CAC01604.1] (AJ269505) peptide synthetase [Anabaena sp. 90] Length = 5060	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°222	Prot n°PL-1162.1	Contig36	202914	203942	No Hits found	Identities = 56/237 (23%), Positives = 104/237 (43%), Gaps = 27/237 (11%) pir[E70091] hypothetical protein yydG - Bacillus subtilis dbj[BAA11275.1] (D78193) yydG [Bacillus subtilis] emb[CAB16054.1] (Z99124) yydG [Bacillus subtilis] Length = 319	
SEQ ID n°223	Prot n°PL-1163.1	Contig36	204667	205734	29%	Identities = 305/534 (57%), Positives = 398/534 (74%), Gaps = 2/534 (0%) emb[CAA70629.1] (Y09356) ATP-dependent activating enzyme [Pseudomonas fluorescens] Length = 611	
SEQ ID n°224	Prot n°PL-1164.1	Contig36	206110	207729	70%	Identities = 127/207 (61%), Positives = 159/207 (76%) spiP15048]ENTB_ECOLI ISOCHORISMATASE (2,3 DIHYDRO-2,3 DIHYDROXYBENZOATE SYNTHASE) pir[YXECIC isochorismatase (EC 3.3.2.1) - Escherichia coli gb AAA16102.1] (M24148) isochorismatase [Escherichia coli] gb AA76835.1] (M24143) 2,3-dihydro-2,3-dihydroxybenzoate synthase [Escherichia coli] gb AAB40795.1] (U82598) isochorismatase [Escherichia coli] gb AAC73696.1] (AE000165) 2,3-dihydro-2,3-dihydroxybenzoate synthetase, isochorismatase Length = 258	
SEQ ID n°226	Prot n°PL-1166.1	Contig36	208449	209219	68%	Identities = 139/246 (56%), Positives = 178/246 (71%) gb AAB40796.1] (U82598) 2,3-dihydro-2,3-dihydroxybenzoate [Escherichia coli] Length = 258	
SEQ ID n°227	Prot n°PL-1167.1	Contig36	210015	212063	60%	Identities = 320/657 (48%), Positives = 420/657 (63%), Gaps = 9/657 (1%) spiP76562]YPFL_ECOLI HYPOTHETICAL 74.9 KD PROTEIN IN DAPE-PURC INTERGENIC REGION pir A65023 hypothetical protein b2474 - Escherichia coli (strain K-12) gb AAC75527.1] (AE000334) orf, hypothetical protein [Escherichia coli] Length = 671	
SEQ ID n°228	Prot n°PL-1168.1	Contig36	212202	212915	57%	Identities = 97/220 (44%), Positives = 136/220 (61%), Gaps = 5/220 (2%) gb AA59298.1] (AE004287) D,D-carboxypeptidase-related protein [Vibrio cholerae] Length = 249	

TABLEAU I

SEQ ID n°229	Prot n°PL-1169.1	Contig36	212876	214003	82%	<p>sp P241176 DAPE_ECOLI_SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (SDAP) pir J42959 succinyl-diaminopimelate desuccinylase (EC 3.5.1.18) - Escherichia coli emb CAA40665.1 (X57403) succinyl-diaminopimelate desuccinylase [Escherichia coli] gb AAB22798.1 (S41760) N-succinyl-L-diaminopimelic acid desuccinylase, DapE, MspB [EC 3.5.1.18] [Escherichia coli, Peptide, 375 aa] gb AAC75525.1 (AE000334) N-succinyl-diaminopimelate deacylase [Escherichia coli] db JBA16346.1 (D90875) succinyl-diaminopimelate desuccinylase (EC 3.5.1.18) [Escherichia coli] db BAA16350.1 (D90876) succinyl-diaminopimelate desuccinylase (EC 3.5.1.18) [Escherichia coli] Length = 375</p>
SEQ ID n°230	Prot n°PL-117.1	Contig41	194758	195687	77%	<p>sp P22939 SPA_ECOLI_GERANYLTRANSTRANSFERASE (FARNESYL-DIPHOSPHATE SYNTHASE) (FPP SYNTHASE) pir JQ0665 geranyltransferase (EC 2.5.1.10) - Escherichia coli db JBA00599.1 (D00694) ORF2 for farnesyl diphosphate synthase [Escherichia coli] gb AAB40177.1 (U82864) geranyltransferase [Escherichia coli] gb AAC73524.1 (AE000148) geranyltransferase (farnesyl diphosphate) Identities = 117/204 (57%), Positives = 160/204 (78%), Gaps = 3/204 (1%) gb AAA18411.1 (U00008) narP [Escherichia coli] Length = 225</p>
SEQ ID n°231	Prot n°PL-1170.1	Contig36	214618	215253	74%	<p>sp P76558 MAO2_ECOLI_NADP-DEPENDENT MALIC ENZYME (NADP-ME) pir JF65021 hypothetical protein b2463 - Escherichia coli (strain K-12) gb AAC75516.1 (AE000333) putative multimodular enzyme [Escherichia coli] Identities = 115/250 (46%), Positives = 163/250 (65%), Gaps = 2/250 (0%) gb AAG08091.1 (AE004884_9 (AE004884) hypothetical protein [Pseudomonas aeruginosa] Length = 295</p>
SEQ ID n°232	Prot n°PL-1171.1	Contig36	215940	218219	89%	<p>sp Q05613 TONB_PSEPU_TONB PROTEIN pir J528444 tonB protein - Pseudomonas putida emb CAA49716.1 (X70139) inner-membrane protein TonB [Pseudomonas putida] Length = 243</p>
SEQ ID n°233	Prot n°PL-1172.1	Contig36	218198	219196	48%	<p>Identities = 77/255 (30%), Positives = 120/255 (46%), Gaps = 44/255 (17%) sp Q05613 TONB_PSEPU_TONB PROTEIN pir J528444 tonB protein - Pseudomonas putida emb CAA49716.1 (X70139) inner-membrane protein TonB [Pseudomonas putida] Length = 243</p>
SEQ ID n°234	Prot n°PL-1173.1	Contig36	218332	220150	43%	<p>Identities = 360/690 (52%), Positives = 486/690 (70%), Gaps = 10/690 (1%) pir JQ1151 proteinase II (EC 3.4.21.-) - Escherichia coli db JBA001750.1 (D10976) protease II [Escherichia coli] Length = 707</p>
SEQ ID n°235	Prot n°PL-1174.1	Contig36	220282	222339	66%	<p>Identities = 285/769 (37%), Positives = 418/769 (54%), Gaps = 81/769 (10%) emb CAB72681.1 (AL139074) putative outer membrane siderophore receptor [Campylobacter jejuni] Length = 755</p>
SEQ ID n°236	Prot n°PL-1175.1	Contig36	222433	224745	54%	

TABLEAU I

SEQ ID n°237	Prot n°PL-1176.1	Contig36	224833	226206	79%	<p>Identities = 307/446 (68%), Positives = 371/446 (82%), Gaps = 3/446 (0%) sp P04994 EX7L_ECOLI EXODEOXYRIBONUCLEASE LARGE SUBUNIT (EXONUCLEASE VII LARGE SUBUNIT) pir NCEC7 exodeoxyribonuclease VII (EC 3.1.11.6) large chain - Escherichia coli (strain K-12) gb AAC75562.1 (AE000337) exonuclease VII, large subunit [Escherichia coli] dbj BAA16396.1 (D90880) exodeoxyribonuclease VII (EC 3.1.11.6) large chain [Escherichia coli] Length = 456</p>
SEQ ID n°238	Prot n°PL-1177.1	Contig36	226373	227845	88%	<p>Identities = 443/493 (89%), Positives = 463/493 (93%) dbj BAA16395.1 (D90880) IMP dehydrogenase (EC 1.1.1.205) [Escherichia coli] Length = 511</p>
SEQ ID n°239	Prot n°PL-1178.1	Contig36	227919	229496	89%	<p>Identities = 454/525 (86%), Positives = 485/525 (91%) sp P04079 GUAA_ECOLI GMP SYNTHASE [GLUTAMINE-HYDROLYZING] (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE) pir SYECGU GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) - Escherichia coli pdb 1GPM A Chain A, Escherichia coli Gmp Synthetase Complexed With Amp And Pyrophosphate pdb 1GPM C Chain C, Escherichia coli Gmp Synthetase Complexed With Amp And Pyrophosphate pdb 1GPM B Chain B, Escherichia coli Gmp Synthetase Complexed With Amp And Pyrophosphate pdb 1GPM D Chain D, Escherichia coli Gmp Synthetase Complexed With Amp And Pyrophosphate gb AAB18619.1 (M10101) GMP synthetase [Escherichia coli] gb AAC75560.1 (AE000337) GMP synthetase (glutamine-hydrolyzing) [Escherichia coli] dbj BAA16394.1 (D90880) GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) [Escherichia coli] Length = 525</p>
SEQ ID n°240	Prot n°PL-1179.1	Contig36	229949	231598	84%	<p>Identities = 456/551 (82%), Positives = 497/551 (89%), Gaps = 4/551 (0%) sp P05103 MTPT7_PSEAE MODIFICATION METHYLASE PAER71 (ADENINE-SPECIFIC METHYLTRANSFERASE PAER71) (M.PAER71) Length = 549</p>
SEQ ID n°241	Prot n°PL-118.1	Contig41	195750	197615	89%	<p>Identities = 500/615 (81%), Positives = 567/615 (90%) sp P77488 DXS_ECOLI 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) pir D64771 dxs protein - Escherichia coli gb AAB40176.1 (U82664) similar to H. influenzae HI1439 [Escherichia coli] gb AAC73523.1 (AE000148) 1-deoxyxylulose-5-phosphate synthase; flavoprotein [Escherichia coli] gb AAC46162.1 (AF035440) D-1-deoxyxylulose 5-phosphate synthase [Escherichia coli] Length = 620</p>
SEQ ID n°242	Prot n°PL-1180.1	Contig36	231599	232339	96%	<p>Identities = 228/246 (92%), Positives = 239/246 (96%) sp P05104 T2P7_PSEAE TYPE II RESTRICTION ENZYME PAER71 (ENDONUCLEASE PAER71) (R.PAER71) pir NDPS7A type II site-specific deoxyribonuclease (EC 3.1.21.4) PaeR71 - Pseudomonas aeruginosa plasmid pMG7 emb CAA27026.1 (X03274) put. endonuclease (aa 1-246) [Pseudomonas aeruginosa] Length = 246</p>

TABLEAU I

SEQ ID n°243	Prot n°PL-1181.1	Contig36	232302	233165	No Hits found	
SEQ ID n°244	Prot n°PL-1182.1	Contig36	234544	238449	11%	Identities = 91/332 (27%), Positives = 161/332 (48%), Gaps = 42/332 (12%) sp P55383 Y4CA_RHISN HYPOTHETICAL 133.7 KD PROTEIN Y4CA pir J28628 Y4cA protein - Rhizobium sp. plasmid pNGR234a gb AAB91631.1 (AE000087) Y4cA [Rhizobium sp. NGR234] Length = Identities = 159/270 (58%), Positives = 197/270 (72%), Gaps = 3/270 (1%) sp P36999 RRMA_EC01 RIBOSOMAL RNA LARGE SUBUNIT METHYLTRANSFERASE A (RRNA (GUANINE-N1)- METHYLTRANSFERASE) (23S RRNA M1G745 METHYLTRANSFERASE) pir J549049 probable S-adenosylmethionine- dependent methyltransferase yebH - Escherichia coli db JBA05856.1 (D28496) ORF30 [Escherichia coli] db JBA015633.1 (D90826) Mycinamicin- resistance protein MyrA. [Escherichia coli] gb AAC74892.1 (AE000276) putative enzyme [Escherichia coli] Length = 269
SEQ ID n°245	Prot n°PL-1183.1	Contig36	239123	239941	70%	Identities = 113/192 (58%), Positives = 151/192 (77%) sp P76264 YEBN_EC01 HYPOTHETICAL 22.1 KD PROTEIN IN MANZ- CSPC INTERGENIC REGION pir J64943 probable membrane protein b1821 Escherichia coli db JBA015632.1 (D90826) ORF_ID:0335#4; similar to [SwissProt Accession Number P39164] [Escherichia coli] gb AAC74891.1 (AE000276) orf, hypothetical protein [Escherichia coli] Identities = 234/291 (80%), Positives = 258/291 (88%), Gaps = 5/291 (1%) sp P08188 PTND_EC01 PTS SYSTEM, MANNOSE-SPECIFIC IID COMPONENT (EIID-MAN) (MANNOSE-PERMEASE IID COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, D COMPONENT) (EII-M- MAN) pir JWQECMM phosphotransferase system enzyme II (EC 2.7.1.69), mannose-specific, factor IID - Escherichia coli gb AAA24445.1 (J02699) mannose permease subunit II-M-Man [Escherichia coli] db JBA015631.1 (D90826) PTS system, Mannose-specific IID component (EIID-MAN) (Mannose-permease IID component) (Phosphotransferase enzyme II, D component) (EII-M-MAN). [Escherichia coli] gb AAC74889.1 (AE000276) PTS enzyme IID, mannose-specific [Escherichia coli] Length = 286
SEQ ID n°246	Prot n°PL-1184.1	Contig36	240008	240569	65%	
SEQ ID n°247	Prot n°PL-1185.1	Contig36	241594	242469	87%	

TABLEAU I

SEQ ID n°248	Prot n°PL-1188.1	Contig36	242474	243274	89%	<p>Identities = 222/266 (83%), Positives = 244/266 (91%)</p> <p>spiP08187 PTNC_ECOLI PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EIIC-MAN) (MANNOSE-PERMEASE IIC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, C COMPONENT) (EIIC-P-MAN) piI WQECMP phosphotransferase system enzyme II (EC 2.7.1.69), mannose-specific, factor IIC - Escherichia coli gb AAA2444.1 (J02699) mannose permease subunit II-P-Man [Escherichia coli] dbj BAA15625.1 (D90825) Phosphotransferase system enzyme II (EC 2.7.1.69), mannose-specific, factor II-P [Escherichia coli] dbj BAA15630.1 (D90826) Phosphotransferase system enzyme II (EC 2.7.1.69), mannose-specific, factor II-P [Escherichia coli] gb AAC74888.1 (AE000276) PTS enzyme IIC, factor II-P [Escherichia coli]</p> <p>Identities = 239/324 (73%), Positives = 273/324 (83%), Gaps = 9/324 (2%)</p> <p>spiP08186 PTNA_ECOLI PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) (MANNOSE-PERMEASE IIAB COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, AB COMPONENT) (EIIAB-MAN) piI WQECM3 phosphotransferase system enzyme II (EC 2.7.1.69), mannose-specific, factor IIAB - Escherichia coli gb AAA24443.1 (J02699) mannose permease subunit III-Man [Escherichia coli] dbj BAA15624.1 (D90825) Phosphotransferase system enzyme II (EC 2.7.1.69), Mannose-specific, factor III [Escherichia coli] dbj BAA15629.1 (D90826) Phosphotransferase system enzyme II (EC 2.7.1.69), Mannose-specific, factor III [Escherichia coli] gb AAC74887.1 (AE000276) PTS enzyme IIAB, mannose-specific</p>
SEQ ID n°249	Prot n°PL-1187.1	Contig36	243333	244316	82%	<p>Identities = 382/454 (84%), Positives = 415/454 (91%)</p> <p>spiP16095 SDHL_ECOLI L-SERINE DEHYDRATASE 1 (L-SERINE DEAMINASE 1) (SDH 1) (L-SD1) piI DWECL L-serine dehydratase (EC 4.2.1.13) 1 - Escherichia coli gb AAA63580.1 (M28695) L-serine deaminase [Escherichia coli] dbj BAA15621.1 (D90825) L-serine dehydratase 1 (EC 4.2.1.13) (L-serine deaminase 1) (SDH 1) (L-SD1), [Escherichia coli] gb AAC74884.1 (AE000275) L-serine deaminase [Escherichia coli]</p>
SEQ ID n°250	Prot n°PL-1188.1	Contig36	244939	246303	85%	<p>Identities = 286/441 (64%), Positives = 344/441 (77%)</p> <p>spiP12680 PABB_SALTY PARA-AMINOBENZOATE SYNTHASE COMPONENT I (ADC SYNTHASE) piI A31132 p-aminobenzoate synthase (EC 4.1.3.-) component I - Salmonella typhimurium gb AAA8618.1 (M22079) p-aminobenzoate synthase component I [Salmonella typhimurium]</p>
SEQ ID n°251	Prot n°PL-1189.1	Contig36	247038	248408	74%	<p>Identities = 231/324 (71%), Positives = 272/324 (83%)</p> <p>spiP77785 THIL_ECOLI THIAMINE-MONOPHOSPHATE KINASE (THIAMINE-PHOSPHATE KINASE) piI A64771 thiamin-phosphate kinase (EC 2.7.4.16) - Escherichia coli gb AAB40173.1 (U82664) similar to H. influenzae HI1305 [Escherichia coli] gb AAC73520.1 (AE000148) thiamin-monophosphate kinase [Escherichia coli]</p>
SEQ ID n°252	Prot n°PL-119.1	Contig41	201472	202461	80%	

Length = 325

TABLEAU I

SEQ ID n°253	Prot n°PL-1190.1	Contig36	249283	250236	83%	<p>Identities = 236/317 (74%), Positives = 278/317 (87%) pir JC6696 prolyl aminopeptidase (EC 3.4.11.5) - Serratia marcescens pdb 1QTR A Chain A, Crystal Structure Analysis Of The Prolyl Aminopeptidase From Serratia Marcescens dbj BAA23336.1 (D87897) prolyl aminopeptidase [Serratia marcescens] Length = 317</p>
SEQ ID n°254	Prot n°PL-1191.1	Contig36	252045	252938	56%	<p>Identities = 99/296 (33%), Positives = 173/296 (58%), Gaps = 10/296 (3%) pir H64945 probable membrane protein b1840 - Escherichia coli gb AAC74910.1 (AE000278) putative resistance protein [Escherichia coli] Length = 290</p>
SEQ ID n°255	Prot n°PL-1192.1	Contig36	255344	256063	75%	<p>Identities = 162/239 (63%), Positives = 184/239 (76%), Gaps = 7/239 (2%) sp P45577 PROQ_EC01 PROPEPTIDASE gb AAD41527.1 L48409_1 (L48409) ProQ [Escherichia coli] Length = 232</p>
SEQ ID n°256	Prot n°PL-1193.1	Contig36	256083	258134	83%	<p>Identities = 502/682 (73%), Positives = 581/682 (84%), Gaps = 10/682 (1%) sp P23865 PRC_EC01 TAIL-SPECIFIC PROTEASE PRECURSOR (PROTEASE RE) (PRC PROTEIN) pir A41798 carboxy-terminal proteinase (EC 3.4.21.-) precursor - Escherichia coli gb AAA24699.1 (M75634) tail-specific protease [Escherichia coli] dbj BAA15638.1 (D90826) Tail-specific protease precursor (EC 3.4.21.-) (Protease RE) (PRC protein). [Escherichia coli] gb AAC74900.1 (AE000277) carboxy-terminal protease for penicillin-binding protein 3 [Escherichia coli] Length = 682</p>
SEQ ID n°257	Prot n°PL-1194.1	Contig36	258464	259351	86%	<p>Identities = 236/293 (81%), Positives = 261/293 (88%), Gaps = 1/293 (0%) sp P23884 HTPX_EC01 PROBABLE PROTEASE HTPX (HEAT SHOCK PROTEIN HTPX) pir A43659 heat shock protein htpX - Escherichia coli gb AAA62779.1 (M58470) htpX [Escherichia coli] dbj BAA15637.1 (D90826) Heat shock protein HtpX [Escherichia coli] gb AAC74899.1 (AE000277) heat shock protein, integral membrane protein [Escherichia coli] Length = 293</p>
SEQ ID n°258	Prot n°PL-1195.1	Contig36	259419	260810	88%	<p>Identities = 352/461 (76%), Positives = 415/461 (89%) sp P77529 YDJN_EC01 HYPOTHETICAL SYMPORTER YDJN pir A64932 hypothetical protein b1729 - Escherichia coli (strain K-12) dbj BAA15509.1 (D90816) Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein). [Escherichia coli] dbj BAA15512.1 (D90816) Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein). [Escherichia coli] gb AAC74799.1 (AE000268) part of a kinase [Escherichia coli] Length = 463</p>

TABLEAU I

SEQ ID n°259	Prot n°PL-1198.1	Contig36	261884	262549	73%	<p>Identities = 132/220 (60%), Positives = 163/220 (74%)</p> <p>sp P77247 YNIC_ECOLI HYPOTHETICAL 24.3 KD PROTEIN IN PFKB-CEDA INTERGENIC REGION pir G64931 yniC protein - Escherichia coli dbj BAA15508.1 (D90815) Phosphoglycolate phosphatase (EC 3.1.3.18). [Escherichia coli] dbj BAA15511.1 (D90816) Phosphoglycolate phosphatase (EC 3.1.3.18). [Escherichia coli] gb AAC74797.1 (AE000267) putative phosphatase [Escherichia coli] Length = 222</p>
SEQ ID n°260	Prot n°PL-1197.1	Contig36	263334	264203	74%	<p>Identities = 169/284 (59%), Positives = 217/284 (75%) pir E84931 hypothetical protein b1725 - Escherichia coli dbj BAA15501.1 (D90814) ORF_ID:0324#5; similar to [SwissProt Accession Number P46381] [Escherichia coli] dbj BAA15507.1 (D90815) ORF_ID:0324#5; similar to [SwissProt Accession Number P46381] [Escherichia coli] dbj BAA15510.1 (D90816) ORF_ID:0324#5; similar to [SwissProt Accession Number P46381] [Escherichia coli] gb AAC74795.1 (AE000267) orf, hypothetical protein [Escherichia coli] Length = 286 "</p>
SEQ ID n°261	Prot n°PL-1198.1	Contig36	264322	265209	72%	<p>Identities = 220/275 (80%), Positives = 248/275 (90%)</p> <p>sp Q56954 YFED_YERPE CHELATED IRON TRANSPORT SYSTEM MEMBRANE PROTEIN YFED gb AAC46150.1 (U50597) YfeD [Yersinia pestis] Length = 297</p>
SEQ ID n°262	Prot n°PL-1199.1	Contig36	265206	266084	88%	<p>Identities = 244/279 (87%), Positives = 263/279 (93%)</p> <p>sp Q56954 YFEC_YERPE CHELATED IRON TRANSPORT SYSTEM MEMBRANE PROTEIN YFEC gb AAC46149.1 (U50597) YfeC [Yersinia pestis] Length = 294</p>
SEQ ID n°263	Prot n°PL-12.1	Contig41	22119	23645	82%	<p>Identities = 358/507 (70%), Positives = 436/507 (85%)</p> <p>sp P46133 YDAH_ECOLI HYPOTHETICAL 55.1 KDA PROTEIN IN OGT-DBPA INTERGENIC REGION pir C64883 membrane protein ydah - Escherichia coli gb AAC74418.1 (AE000231) putative pump protein (transport) [Escherichia coli] Length = 510</p>
SEQ ID n°264	Prot n°PL-120.1	Contig41	203602	204711	76%	<p>Identities = 255/362 (70%), Positives = 308/362 (84%)</p> <p>sp P25539 RIBD_ECOLI RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBD [INCLUDES: DIAMINOHYDROXYPHOSPHORIBOSYLAMINOPYRIMIDINE DEAMINASE (RIBOFLAVIN-SPECIFIC DEAMINASE); 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL REDUCTASE (HTP REDUCTASE)] pir S26201 riboflavin-specific deaminase (EC 3.5.4.-) - Escherichia coli emb CAA45735.1 (X64395) orf2, homologue to B.subtilis ribG [Escherichia coli] gb AAB40170.1 (U82664) riboflavin biosynthesis protein RibG [Escherichia coli] gb AAC73517.1 (AE000148) bifunctional protein Identities = 236/293 (80%), Positives = 262/293 (88%) gb AAC46148.1 (U50597) YfeB [Yersinia pestis] Length = 296</p>
SEQ ID n°265	Prot n°PL-1200.1	Contig36	266081	266977	87%	

TABLEAU I

SEQ ID n°266	Prot n°PL-1201.1	Contig36	266974	267894	82%	Identities = 227/288 (78%), Positives = 257/288 (88%) gb AAC46147.1 (U50597) YfeA [Yersinia pestis] Length = 322	
SEQ ID n°267	Prot n°PL-1202.1	Contig36	268037	268763	63%	Identities = 114/243 (46%), Positives = 157/243 (63%), Gaps = 22/243 (9%) spiP7609 MLTE_ECOLI MEMBRANE-BOUND LYTC MUREIN TRANSGLYCOSYLASE E (MUREIN HYDROLASE E) pir F94865 murein hydrolase E (EC 3.2.1.-) - Escherichia coli gb AAC74277.1 (AE000217) murein transglycosylase E [Escherichia coli] dbj BAA36051.1 (D90754)	
SEQ ID n°268	Prot n°PL-1203.1	Contig36	269739	318842	32%	Hypothetical protein H10761 [Escherichia coli] Length = 241 Identities = 3918/8999 (43%), Positives = 5308/8999 (58%), Gaps = 431/8999 (4%) pir T14693 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] Length = 9376	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°269	Prot n°PL-1204.1	Contig36	319220	321148	92%	Identities = 545/642 (85%), Positives = 566/642 (92%) spiP00955 SYT_ECOLI THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRS) pir SYECTT threonine-TRNA ligase (EC 6.1.1.3) - Escherichia coli pdb 1QF6 A Chain A, Structure Of E. Coli Threonyl-Trna Synthetase Complexed With Its Cognate Trna dbj BAA15498.1 (D90814) Threonine-TRNA ligase (EC 6.1.1.3) [Escherichia coli] dbj BAA15504.1 (D90815) Threonine-TRNA ligase (EC 6.1.1.3) [Escherichia coli] gb AAC74789.1 (AE000267) threonine tRNA synthetase [Escherichia coli] Identities = 279/330 (84%), Positives = 308/330 (92%) dbj BAA15482.1 (D90813) Phenylalanine-TRNA ligase (EC 6.1.1.20) a chain [Escherichia coli] dbj BAA15494.1 (D90814) Phenylalanine-TRNA ligase (EC 6.1.1.20) a chain [Escherichia coli] Length = 331	
SEQ ID n°270	Prot n°PL-1205.1	Contig36	322656	323639	87%	Identities = 617/795 (77%), Positives = 704/795 (87%) spiP07395 SYFB_ECOLI PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE-TRNA LIGASE BETA CHAIN) (PHERS) pir J41284 phenylalanine-TRNA ligase (EC 6.1.1.20) beta-subunit - Escherichia coli pir SYECFB phenylalanine-TRNA ligase (EC 6.1.1.20) beta chain - Escherichia coli gb AAA51470.1 (K02844) phenylalanyl-TRNA synthetase beta-subunit [Escherichia coli] dbj BAA15481.1 (D90813) Phenylalanine-TRNA ligase (EC 6.1.1.20) b chain [Escherichia coli] dbj BAA15493.1 (D90814) Phenylalanine-TRNA ligase (EC 6.1.1.20) b chain [Escherichia coli] gb AAC74783.1 (AE000266) phenylalanine tRNA synthetase, beta-subunit [Escherichia coli]	
SEQ ID n°272	Prot n°PL-1207.1	Contig36	326409	327416	74%	Identities = 199/321 (61%), Positives = 252/321 (77%), Gaps = 1/321 (0%) gb AAA23526.1 (M14031) cytoplasmic membrane protein [Escherichia coli] Length = 328	

TABLEAU I

SEQ ID n°273	Prot n°PL-1208.1	Contig36	327420	328196	54%	<p>Identities = 99/234 (42%), Positives = 141/234 (59%), Gaps = 2/234 (0%)</p> <p>sp P08611 BTUD_ECOLI_VITAMIN B12 TRANSPORT ATP-BINDING PROTEIN BTUD pir I QRECB vitamin b12 transport ATP-binding protein btud - Escherichia coli gb AAA23528.1 (M14031) peripheral membrane component [Escherichia coli] dbj BAA15477.1 (D90813) Vitamin B12 transport protein btud [Escherichia coli] dbj BAA15489.1 (D90814) Vitamin B12 transport protein btud [Escherichia coli] gb AAC74779.1 (AE000266) ATP-binding component of vitamin B12 transport system [Escherichia coli]</p>
SEQ ID n°274	Prot n°PL-1209.1	Contig36	328348	329502	77%	<p>Identities = 249/379 (65%), Positives = 299/379 (78%)</p> <p>sp P77690 YFBE_ECOLI_HYPOTHETICAL 42.9 KD PROTEIN IN AIS-PMRD INTERGENIC REGION pir I C64996 probable hydro-lyase (EC 4.2.1.-) b2263 - Escherichia coli (strain K-12) gb AAC76313.1 (AE000315) putative enzyme [Escherichia coli] dbj BAA16076.1 (D90856) SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSC. [Escherichia coli]</p>
SEQ ID n°275	Prot n°PL-121.1	Contig41	205281	206249	85%	<p>Identities = 257/337 (76%), Positives = 295/337 (87%), Gaps = 1/337 (0%)</p> <p>gb AAB40165.1 (U82664) protein-export membrane protein secF [Escherichia coli] Length = 338</p>
SEQ ID n°276	Prot n°PL-1210.1	Contig36	329503	330480	83%	<p>Identities = 229/308 (74%), Positives = 272/308 (87%)</p> <p>sp P7757 YFBE_ECOLI_HYPOTHETICAL 36.3 KD PROTEIN IN AIS-PMRD INTERGENIC REGION pir I D64996 hypothetical protein b2254 - Escherichia coli (strain K-12) gb AAC75314.1 (AE000315) putative sugar transferase [Escherichia coli] dbj BAA16077.1 (D90856) DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) (DOLICHOL- PHOSPHATE MANNOSE SYNTHASE) (DOLICHYL-PHOSPHATE BETA-D-MANNOSYLTRANSFERASE) [Escherichia coli] Length = 322</p>
SEQ ID n°277	Prot n°PL-1211.1	Contig36	330481	332463	81%	<p>Identities = 451/651 (69%), Positives = 539/651 (82%)</p> <p>sp P77398 YFBG_ECOLI_HYPOTHETICAL 74.3 KD PROTEIN IN AIS-PMRD INTERGENIC REGION pir I E64996 hypothetical protein b2255 - Escherichia coli (strain K-12) gb AAC75315.1 (AE000315) putative transformylase [Escherichia coli] dbj BAA16078.1 (D90856) METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9) [Escherichia coli] dbj BAA16082.1 (D90857) METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9) [Escherichia coli] Length = 660</p>
SEQ ID n°278	Prot n°PL-1212.1	Contig36	332463	333356	68%	<p>Identities = 178/297 (59%), Positives = 217/297 (72%), Gaps = 4/297 (1%)</p> <p>pir I F64996 hypothetical protein b2256 - Escherichia coli (strain K-12) gb AAC75316.1 (AE000315) orf, hypothetical protein [Escherichia coli] Length = 296</p>
SEQ ID n°279	Prot n°PL-1213.1	Contig36	333367	335025	65%	<p>Identities = 261/545 (47%), Positives = 369/545 (66%), Gaps = 10/545 (1%)</p> <p>pir I G64996 hypothetical protein b2257 - Escherichia coli (strain K-12) gb AAC75317.1 (AE000315) orf, hypothetical protein [Escherichia coli] Length = 550</p>

TABLEAU I

SEQ ID n°280	Prot n°PL-1214.1	Contig36	337320	338270	No Hits found	
SEQ ID n°281	Prot n°PL-1215.1	Contig36	340210	340902	67%	Identities = 128/202 (63%), Positives = 157/202 (77%) gb AAG07982.1 AE004873_4 (AE004873) probable ATP-binding component of ABC transporter [Pseudomonas aeruginosa] Length = 228
SEQ ID n°282	Prot n°PL-1216.1	Contig36	340904	342109	63%	Identities = 208/390 (53%), Positives = 274/390 (69%), Gaps = 1/390 (0%) gb AAG07981.1 AE004873_3 (AE004873) probable permease of ABC transporter [Pseudomonas aeruginosa] Length = 397
SEQ ID n°283	Prot n°PL-1217.1	Contig36	342090	343580	77%	Identities = 312/484 (64%), Positives = 385/484 (79%), Gaps = 5/484 (1%) gb AAG07980.1 AE004873_2 (AE004873) hypothetical protein [Pseudomonas aeruginosa] Length = 493
SEQ ID n°284	Prot n°PL-1218.1	Contig36	343552	344850	61%	Identities = 181/418 (43%), Positives = 266/418 (63%), Gaps = 4/418 (0%) gb AAG07979.1 AE004873_1 (AE004873) hypothetical protein [Pseudomonas aeruginosa] Length = 425
SEQ ID n°285	Prot n°PL-1219.1	Contig36	344935	346734	40%	Identities = 152/486 (31%), Positives = 253/486 (51%), Gaps = 29/486 (5%) emb CAC01603.1 AJ269505) peptide synthetase [Anabaena sp. 90] Length = 2258
SEQ ID n°286	Prot n°PL-122.1	Contig41	208260	208107	88%	Identities = 502/615 (81%), Positives = 556/615 (89%) (AF163861) SecD protein [Enterobacter aerogenes] Length = 615
SEQ ID n°287	Prot n°PL-1220.1	Contig36	348844	348064	70%	Identities = 215/385 (55%), Positives = 287/385 (73%) gb AAG05702.1 AE004657_9 (AE004657) probable MFS transporter [Pseudomonas aeruginosa] Length = 417
SEQ ID n°288	Prot n°PL-1221.1	Contig36	348089	350845	32%	Identities = 223/445 (50%), Positives = 296/445 (66%), Gaps = 1/445 (0%) emb CAB87990.1 AJ277403) indigoidine synthase [Erwinia chrysanthemi] Length = 1488
SEQ ID n°289	Prot n°PL-1222.1	Contig36	351267	352154	66%	Identities = 154/293 (52%), Positives = 206/293 (69%) gb AAG05704.1 AE004657_11 (AE004657) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 297
SEQ ID n°290	Prot n°PL-1223.1	Contig36	355455	356129	No Hits found	
SEQ ID n°291	Prot n°PL-1224.1	Contig36	356179	356973	63%	Identities = 177/262 (67%), Positives = 206/262 (78%) protein - Yersinia enterocolitica emb CAA54884.1 (X77867) ATPase component [Yersinia enterocolitica] Length = 266
SEQ ID n°292	Prot n°PL-1225.1	Contig36	356973	357974	79%	Identities = 238/333 (71%), Positives = 284/333 (84%) splQ56992 HMMU_YERPE HEMIN TRANSPORT SYSTEM PERMEASE PROTEIN HMMU pir T12072 ABC-type permease - Yersinia pestis gb AAC64869.1 U60647) ABC-type permease [Yersinia pestis] Length = 334
SEQ ID n°293	Prot n°PL-1226.1	Contig36	357971	358799	72%	Identities = 165/276 (59%), Positives = 211/276 (75%) (X77867) hemin binding protein [Yersinia enterocolitica] Length = 279

Unknown, similar to proteins involved in antibiotic biosynthesis

TABLEAU I

SEQ ID n°294	Prot n°PL-1227.1	Contig36	358786	359859	74%	<p>Identities = 217/347 (62%), Positives = 268/347 (76%), Gaps = 11/347 (3%) sp P31517 HEMS_YEREN HEMIN TRANSPORT PROTEIN HEMS pir IS54436 hemS protein - Yersinia enterocolitica emb CAA54865.1 (X77867) hemS [Yersinia enterocolitica] Length = 345</p>
SEQ ID n°295	Prot n°PL-1228.1	Contig36	359890	361811	75%	<p>Identities = 412/684 (60%), Positives = 513/684 (74%), Gaps = 19/684 (2%) sp Q56989 HMR_YERPE HEMIN RECEPTOR PRECURSOR pir T12069 hemin receptor - Yersinia pestis gb AAC64866.1 (U60647) TonB-dependent outer membrane receptor [Yersinia pestis] Length = 676</p>
SEQ ID n°296	Prot n°PL-1229.1	Contig36	362371	363429	79%	<p>Identities = 252/348 (72%), Positives = 293/348 (83%), pir ADECH 2-dehydro- 3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) Escherichia coli dbj BAA15473.1 (D90813) Phospho-2-dehydro-3- deoxyheptonate aldolase, TRP-sensitive (EC 4.1.2.15) (Phospho-2-keto- 3-deoxyheptonate aldolase) (DAHP synthetase) (3-DEOXY-D-ARABINO HEPTULOSONATE 7-PHOSPHATE SYNTHASE), [Escherichia coli] gb AAC74774.1 (AE000265) 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tryptophan repressible) [Escherichia coli] Length = 348</p>
SEQ ID n°297	Prot n°PL-123.1	Contig41	208556	209680	93%	<p>Identities = 330/375 (88%), Positives = 350/375 (93%), sp Q54177 TGT_SHIFL QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) (VIRULENCE-ASSOCIATED PROTEIN VACC) dbj BAA05482.1 (D26469) VacC [Shigella flexneri] Length = 375</p>
SEQ ID n°298	Prot n°PL-1230.1	Contig36	363559	364458	79%	<p>Identities = 207/273 (75%), Positives = 239/273 (86%) sp P03822 YDIA_ECOLI HYPOTHELICAL 31.2 KDA PROTEIN IN PPSA- AROH INTERGENIC REGION pir QQECAD probable membrane protein ydia Escherichia coli gb AAC74773.1 (AE000265) orf, hypothetical protein [Escherichia coli] Length = 277</p>
SEQ ID n°299	Prot n°PL-1231.1	Contig36	364653	367031	90%	<p>Identities = 662/783 (82%), Positives = 726/783 (91%), Gaps = 1/793 (0%) sp P23538 PPSA_ECOLI PHOSPHOENOLPYRUVATE SYNTHASE (PYRUVATE, WATER DOKINASE) (PEP SYNTHASE) pir S20554 pyruvate, water dikinase (EC 2.7.9.2) ppsA - Escherichia coli emb CAA42024.1 (X59381) pyruvate, water dikinase [Escherichia coli] dbj BAA15471.1 (D90813) Pyruvate, water dikinase (EC 2.7.9.2) [Escherichia coli] gb AAC74772.1 (AE000265) phosphoenolpyruvate synthase [Escherichia coli] Length = 782</p>

TABLEAU I

SEQ ID n°300	Prot n°PL-1232.1	Contig36	367476	368585	77%	<p>Identities = 215/357 (60%), Positives = 287/357 (80%), Gaps = 4/357 (1%) sp P77175 YDIK_ECOLI_HYPOTHETICAL_39.8_KDA_PROTEIN_IN_LPP-AROD_INTERGENIC_REGION pir JH64926 probable membrane protein b1688 - Escherichia coli dbj BAA15450.1 (D90811) ORF_ID:0320#8; similar to [SwissProt Accession Number Q04454] [Escherichia coli] gb AAC74758.1 (AE000264) orf, hypothetical protein [Escherichia coli] Length = 370 "</p>
SEQ ID n°301	Prot n°PL-1233.1	Contig36	368942	372001	85%	<p>Identities = 765/1018 (75%), Positives = 887/1018 (86%), Gaps = 1/1018 (0%) sp P7748 YDIJ_ECOLI_HYPOTHETICAL_113.2_KDA_PROTEIN_IN_LPP-AROD_INTERGENIC_REGION pir JG64926 probable iron-sulfur protein ydiJ - Escherichia coli dbj BAA15451.1 (D90811) Glycolate oxidase subunit GicD. [Escherichia coli] gb AAC74757.1 (AE000263) putative oxidase [Escherichia coli] Length = 1018</p>
SEQ ID n°302	Prot n°PL-1235.1	Contig36	373188	374282	26%	<p>Identities = 51/221 (23%), Positives = 98/221 (44%), Gaps = 24/221 (10%) gb AAF96112.1 (AE0004360) hypothetical protein [Vibrio cholerae] Length = 638</p>
SEQ ID n°303	Prot n°PL-1236.1	Contig36	377055	378563	89%	<p>Identities = 412/495 (83%), Positives = 452/495 (91%), Gaps = 4/495 (0%) sp P77522 YNHE_ECOLI_HYPOTHETICAL_54.7_KDA_PROTEIN_IN_LPP-AROD_INTERGENIC_REGION Length = 495 Identities = 201/248 (81%), Positives = 222/248 (89%)</p>
SEQ ID n°304	Prot n°PL-1237.1	Contig36	378821	379367	82%	<p>sp P77499 YNHD_ECOLI_PROBABLE_ATP-DEPENDENT_TRANSPORTER_YNHD pir JB64926 probable ABC-type transport protein ynhD - Escherichia coli dbj BAA15455.1 (D90811) Multidrug resistance protein 1 (P-glycoprotein 1). [Escherichia coli] dbj BAA15461.1 (D90812) Multidrug resistance protein 1 (P-glycoprotein 1). [Escherichia coli] gb AAC74752.1 (AE000263) putative ATP-binding component of a transport system Length = 423 "</p>
SEQ ID n°305	Prot n°PL-1238.1	Contig36	379381	380658	64%	<p>Identities = 224/414 (54%), Positives = 294/414 (70%), Gaps = 3/414 (0%) sp P77689 YNHC_ECOLI_HYPOTHETICAL_48.8_KD_PROTEIN_IN_LPP-AROD_INTERGENIC_REGION pir JA64926 ynhC protein - Escherichia coli dbj BAA15456.1 (D90811) ORF_ID:0320#15; similar to [SwissProt Accession Number P48260] [Escherichia coli] dbj BAA15462.1 (D90812) ORF_ID:0320#15; similar to [SwissProt Accession Number P48260] [Escherichia coli] gb AAC74751.1 (AE000263) orf, hypothetical protein [Escherichia coli] Length = 423 "</p>
SEQ ID n°306	Prot n°PL-1239.1	Contig36	380655	381893	77%	<p>Identities = 261/412 (63%), Positives = 326/412 (78%), Gaps = 6/412 (1%) pir JH64925 aminotransferase nifs homolog b1680, pyridoxal phosphate-dependent - Escherichia coli dbj BAA15457.1 (D90811) Nifs protein. [Escherichia coli] dbj BAA15463.1 (D90812) Nifs protein. [Escherichia coli] gb AAC74750.1 (AE000263) orf, hypothetical protein [Escherichia coli] emb CAC07717.1 (AX018966) unnamed protein product [Escherichia coli] Length = 406</p>

TABLEAU I

SEQ ID n°307	Prot n°PL-124.1	Contig41	209831	210898	90%	<p>Identities = 288/356 (80%), Positives = 326/356 (90%)</p> <p>sp P21516 QUEA_ECOLI S-ADENOSYLMETHIONINE:TRNA RIBOSYLTRANSFERASE-ISOMERASE (QUEUOSINE BIOSYNTHESIS PROTEIN QUEA) pir B38530 S-adenosylmethionine:trna ribosyltransferase-isomerase (EC 5.-.-) - Escherichia coli gb AAA16114.1 (M37702) queuosine biosynthesis [Escherichia coli] gb AAB40161.1 (U82664) S-adenosylmethionine:trna ribosyltransferase-isomerase [Escherichia coli] gb AAC73508.1 (AE000147) synthesis of queuine in tRNA; probably S-adenosylmethionine:trna ribosyltransferase-isomerase [Escherichia coli] Length = 356 "</p>
SEQ ID n°308	Prot n°PL-1240.1	Contig36	382469	383551	58%	<p>Identities = 184/311 (59%), Positives = 221/311 (70%), Gaps = 3/311 (0%)</p> <p>sp P75954 YCF5_ECOLI HYPOTHETICAL 34.8 KDA PROTEIN IN NDH-MFD INTERGENIC REGION PRECURSOR pir F64855 ycf5 protein precursor - Escherichia coli gb AAC74197.1 (AE000211) orf, hypothetical protein [Escherichia coli] dbj BAA35928.1 (D90746) Protein ErfK/Srk precursor. [Escherichia coli] dbj BAA35933.1 (D90747) Protein ErfK/Srk precursor. [Escherichia coli] Length = 320</p>
SEQ ID n°309	Prot n°PL-1241.1	Contig36	384340	385191	52%	<p>Identities = 89/262 (33%), Positives = 150/262 (56%), Gaps = 1/262 (0%)</p> <p>gb AAG05210.1 AE004608_9 (AE004606) probable enoyl-CoA hydratase/isomerase [Pseudomonas aeruginosa] Length = 270</p>
SEQ ID n°310	Prot n°PL-1242.1	Contig36	385813	386436	No Hits found	
SEQ ID n°311	Prot n°PL-1243.1	Contig36	385444	386853	93%	<p>Identities = 399/470 (84%), Positives = 439/470 (92%), Gaps = 1/470 (0%)</p> <p>sp P77983 KPY1_SALTY PYRUVATE KINASE I (PK-1) emb CAA68205.1 (X99945) pyruvate kinase like protein [Salmonella typhimurium] Length = 470</p>
SEQ ID n°312	Prot n°PL-1244.1	Contig36	387802	389175	83%	<p>Identities = 308/456 (67%), Positives = 384/456 (83%)</p> <p>sp P37340 YDHE_ECOLI HYPOTHETICAL 49.4 KDA PROTEIN IN RIB-PYKF INTERGENIC REGION dbj BAA15430.1 (D90809) ORF_ID:0319#7; similar to [SwissProt Accession Number P37340] [Escherichia coli] dbj BAA15439.1 (D90810) ORF_ID:0319#7; similar to [SwissProt Accession Number P37340] [Escherichia coli] Length = 457 "</p>
SEQ ID n°313	Prot n°PL-1245.1	Contig36	389402	390079	77%	<p>Identities = 163/214 (76%), Positives = 186/214 (86%), Gaps = 3/214 (1%)</p> <p>sp P29015 RISA_ECOLI RIBOFLAVIN SYNTHASE ALPHA CHAIN pir S28528 riboflavin synthase (EC 2.5.1.9) alpha chain - Escherichia coli emb CAA48861.1 (X69109) riboflavin synthase [Escherichia coli] gb AAB47940.1 (U68703) riboflavin synthase, alpha chain [Escherichia coli] dbj BAA15429.1 (D90809) Riboflavin synthase a chain (EC 2.5.1.9). [Escherichia coli] dbj BAA15438.1 (D90810) Riboflavin synthase a chain (EC 2.5.1.9). [Escherichia coli] gb AAC74734.1 (AE000261) riboflavin synthase, alpha chain [Escherichia coli] Length = 213</p>
SEQ ID n°314	Prot n°PL-1248.1	Contig36	390441	391463	No Hits found	

TABLEAU I

SEQ ID n°315	Prot n°PL-1247.1	Contig36	391767	392918	78%	<p>Identities = 267/383 (69%), Positives = 319/383 (82%), Gaps = 1/383 (0%)</p> <p>sp P30010 CFA_ECOLI_CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (CYCLOPROPANE FATTY ACID SYNTHASE) (CFA SYNTHASE) pir J44292 cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.78) - Escherichia coli gb AA23562.1 (M98330) cyclopropane fatty acid synthase [Escherichia coli] dbj BAA15428.1 (D90809) Cyclopropane fatty acid synthase [Escherichia coli] dbj BAA15437.1 (D90810) Cyclopropane fatty acid synthase [Escherichia coli] gb AAC74733.1 (AE000261) cyclopropane fatty acyl phospholipid synthase [Escherichia coli] Identities = 219/384 (57%), Positives = 288/384 (74%), Gaps = 4/384 (1%) dbj BAA15426.1 (D90809) Bicyclomycin resistance protein (Sulfonamide resistance protein). [Escherichia coli] dbj BAA15435.1 (D90810) Bicyclomycin resistance protein (Sulfonamide resistance protein). [Escherichia coli] Length = 403</p>
SEQ ID n°316	Prot n°PL-1248.1	Contig36	393339	394559	61%	<p>Identities = 210/303 (69%), Positives = 245/303 (80%)</p> <p>sp P37598 YDHB_ECOLI_HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PURR-CFA INTERGENIC REGION pir J64923 probable transcription regulator ydhh - Escherichia coli gb AAC74731.1 (AE000261) putative transcriptional regulator LYSR-type [Escherichia coli] Identities = 108/191 (57%), Positives = 135/191 (70%)</p>
SEQ ID n°317	Prot n°PL-1249.1	Contig36	394807	395715	79%	<p>sp P21515 YAJB_ECOLI_HYPOTHETICAL 23.0 KD PROTEIN IN MALZ-QUEA INTERGENIC REGION (ORF 14) pir D64769 yajB protein - Escherichia coli gb AAB40160.1 (U62664) hypothetical 14.0 kd protein [Escherichia coli] gb AAC73507.1 (AE000147) putative glycoprotein Identities = 270/341 (79%), Positives = 312/341 (91%)</p>
SEQ ID n°318	Prot n°PL-125.1	Contig41	211003	211599	63%	<p>sp O68446 PURR_SALTY PURINE NUCLEOTIDE SYNTHESIS REPRESSOR gb AAC05741.1 (AF040636) purine nucleotide synthesis repressor [Salmonella typhimurium] Length = 341</p>
SEQ ID n°319	Prot n°PL-1250.1	Contig36	395722	396747	88%	<p>Identities = 160/214 (74%), Positives = 180/214 (83%) sp P30014 RNT_ECOLI_RIBONUCLEASE T (EXORIBONUCLEASE T) (RNASE T) pir J45065 ribonuclease T (EC 3.1.13.-) mt - Escherichia coli gb AAC37008.1 (L01622) RNaseT [Escherichia coli] gb AAC74724.1 (AE000260) RNase T, degrades tRNA [Escherichia coli] Length = 215</p>
SEQ ID n°320	Prot n°PL-1251.1	Contig36	397907	398560	81%	<p>Identities = 88/288 (30%), Positives = 151/288 (51%), Gaps = 10/288 (3%) gb AAG07125.1 AE004793_2 (AE004793) integrase/recombinase XerD [Pseudomonas aeruginosa] Length = 298</p>
SEQ ID n°321	Prot n°PL-1252.1	Contig40	92071	93264	37%	<p>Identities = 117/390 (30%), Positives = 177/390 (45%), Gaps = 59/390 (15%) dbj BAB05094.1 (AP001511) DNA primase [Bacillus halodurans] Length = 599</p>
SEQ ID n°322	Prot n°PL-1253.1	Contig40	88830	92147	16%	
SEQ ID n°323	Prot n°PL-1254.1	Contig40	88881	87849	No Hits found	

TABLEAU I

SEQ ID n°324	Prot n°PL-1255.1	Contig40	80341	86769	40%	<p>Identities = 522/2187 (23%), Positives = 861/2187 (38%), Gaps = 357/2187 (16%) gb AA03431.1 AE004443_9 (AE004443) probable hemagglutinin [Pseudomonas aeruginosa] Length = 3535</p> <p>Identities = 773/959 (80%), Positives = 859/959 (88%), Gaps = 3/959 (0%) sp P33195 GCSP_ECOLI GLYCINE DEHYDROGENASE [DECARBOXYLATING] (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) pir S36834 glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) - Escherichia coli gb AA23867.1 (L20872) gcvHP [Escherichia coli] emb CAA52146.1 (X73958) glycine dehydrogenase (decarboxylating) [Escherichia coli] gb AAC7594.1 (AE000373) glycine decarboxylase, P. protein of glycine cleavage (Identities = 221/281 (78%), Positives = 249/281 (87%))</p>
SEQ ID n°325	Prot n°PL-1255.1	Contig40	76553	79429	89%	<p>sp P27248 GCST_ECOLI AMINOMETHYLTRANSFERASE (GLYCINE CLEAVAGE SYSTEM T PROTEIN) pir J56889 aminomethyltransferase (EC 2.1.2.10) - Escherichia coli gb AAC36843.1 (M97263) T-protein [Escherichia coli] emb CAA52144.1 (X73958) aminomethyltransferase [Escherichia coli] gb AAA69073.1 (U28377) ORF_f364 [Escherichia coli] gb AAC75943.1 (AE000374) aminomethyltransferase (T protein; tetrathiodifolate-dependent) of glycine cleavage system [Escherichia coli] Length = 285/400 (71%), Positives = 320/400 (79%), Gaps = 1/400 (0%)</p>
SEQ ID n°326	Prot n°PL-1257.1	Contig40	74856	75752	79%	<p>pir B65075 probable monooxygenase (EC 1.14.13.-) visC - Escherichia coli gb AAA69074.1 (U28377) ORF_f400 [Escherichia coli] gb AAC75944.1 (AE000374) orf, hypothetical protein [Escherichia coli] Length = 400</p>
SEQ ID n°327	Prot n°PL-1258.1	Contig40	73277	74497	71%	<p>Identities = 247/392 (63%), Positives = 299/392 (76%), Gaps = 1/392 (0%) pir C65075 probable 2-octaprenyl-6-methoxyphenol 4-monooxygenase (EC 1.14.13.-) ubiH - Escherichia coli (strain K-12) gb AAA69075.1 (U28377) ORF_f392 [Escherichia coli] gb AAC75945.1 (AE000374) 2-octaprenyl-6-methoxyphenol → 2-octaprenyl-6-methoxy-1, 4-benzoquinone [Escherichia coli] Length = 392</p>
SEQ ID n°328	Prot n°PL-1259.1	Contig40	72060	73238	74%	<p>Identities = 149/201 (74%), Positives = 170/201 (84%) gb AAF93896.1 (AE004159) antioxidant, AhpC/Tsa family [Vibrio cholerae] Length = 207</p>
SEQ ID n°329	Prot n°PL-126.1	Contig41	211884	212486	84%	<p>Identities = 324/435 (74%), Positives = 373/435 (85%) gb AAB96776.1 (AF041033) aminopeptidase [Shigella flexneri] Length = 441</p>
SEQ ID n°330	Prot n°PL-1260.1	Contig40	70736	72052	84%	<p>Identities = 325/413 (78%), Positives = 368/413 (88%), Gaps = 3/413 (0%) sp P08328 SERA_ECOLI D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PGDH) pir DEECPG phosphoglycerate dehydrogenase (EC 1.1.1.95) - Escherichia coli gb AAA24625.1 (L29397) phosphoglycerate dehydrogenase [Escherichia coli] gb AAA69080.1 (U28377) D-3-phosphoglycerate dehydrogenase [Escherichia coli] gb AAC75950.1 (AE000374) D-3-phosphoglycerate dehydrogenase [Escherichia coli] Length = 410</p>
SEQ ID n°331	Prot n°PL-1261.1	Contig40	67374	68615	88%	

TABLEAU I

SEQ ID n°332	Prot n°PL-1262.1	Contig40	66442	67101	90%	<p>Identities = 180/218 (82%), Positives = 201/218 (91%) sp O52398 RPIA_EDWIC_RIBOSE_5-PHOSPHATE_ISOMERASE_A (PHOSPHORIBOISOMERASE A) gb AAB92568.1 (AF037440) ribose-5-phosphate isomerase [Edwardsiella ictaluri] Length = 219 emb CAB56657.1 (AL121596) putative hydrolase [Streptomyces coelicolor A3(2)] Length = 278</p>
SEQ ID n°333	Prot n°PL-1263.2	Contig37	365188	365994	30%	<p>Identities = 334/462 (72%), Positives = 397/462 (85%), Gaps = 3/462 (0%) sp P77429 ARCD_ECOLI_PUTATIVE_ARGININE/ORNITHINE_ANTIPORTER pir IG64916 probable membrane protein b1605 precursor - Escherichia coli dbj BAA15343.1 (D90803) Arginine/ornithine antiporter. [Escherichia coli] bj BAA15353.1 (D90804) Arginine/ornithine antiporter. [Escherichia coli] gb AAC74877.1 (AE000256) putative arginine/ornithine antiporter [Escherichia coli] Length = 460</p>
SEQ ID n°335	Prot n°PL-1265.2	Contig37	361394	362299	No Hits found	<p>Identities = 85/357 (23%), Positives = 145/357 (39%), Gaps = 69/357 (19%) sp O67185 FABH_AQUAE_3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III (BETA-KETOACYL-ACPSYNTHASE III) (KAS III) pir F70394_3-oxoacyl-[acyl-carrier-protein] synthase III - Aquifex aeolicus gb AAC07144.1 (AE000723) 3-oxoacyl-[acyl-carrier-protein] synthase III [Aquifex aeolicus] Identities = 199/317 (62%), Positives = 246/317 (76%), Gaps = 3/317 (0%) sp P76177 YDGH_ECOLI_PROTEIN_YDGH_PRECURSOR pir F64916 conserved hypothetical protein b1604 precursor - Escherichia coli gb AAC74676.1 (AE000256) orf, hypothetical protein [Escherichia coli] Length = 314</p>
SEQ ID n°336	Prot n°PL-1266.2	Contig37	360245	361393	37%	
SEQ ID n°337	Prot n°PL-1267.1	Contig37	358895	359848	69%	
SEQ ID n°338	Prot n°PL-1268.1	Contig37	356842	358371	89%	<p>Identities = 420/510 (82%), Positives = 460/510 (89%), Gaps = 1/510 (0%) sp P07001 PNTA_ECOLI_NAD(P) TRANSHYDROGENASE SUBUNIT ALPHA (PYRIDINE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT ALPHA) (NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT ALPHA) pir DDEECXA_NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) alpha chain - Escherichia coli emb CAA46884.1 (X66086) pyridine nucleotide transhydrogenase [Escherichia coli] dbj BAA15342.1 (D90803) NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) a chain [Escherichia coli] dbj BAA15362.1 (D90804) NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) a chain [Escherichia coli] gb AAC74675.1 (AE000256) pyridine nucleotide transhydrogenase, alpha subunit [Escherichia coli] emb CAB37089.1 (X04195) NAD(P)+ transhydrogenase subunit alpha [Escherichia coli] Length = 510</p>

TABLEAU I

SEQ ID n°339	Prot n°PL-1269.1	Contig37	355443	356831	94%	<p>Identities = 403/462 (87%), Positives = 437/462 (94%)</p> <p>sp P07002 PNTB_ECOLI_NAD(P) TRANSHYDROGENASE SUBUNIT BETA (PYRIDINE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA) (NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT BETA) pir DEECXB_NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) beta chain - Escherichia coli emb CAA46885.1 (X66086) pyridine nucleotide transhydrogenase [Escherichia coli] dbj BAA15336.1 (D80802) NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) b chain [Escherichia coli] dbj BAA15341.1 (D80803) NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) b chain [Escherichia coli] gb AAC74674.1 (AE000255) pyridine nucleotide transhydrogenase, beta subunit [Escherichia coli] emb CAB37080.1 (X04195) NAD(P)+ transhydrogenase</p>
SEQ ID n°340	Prot n°PL-127.1	Contig41	212706	214466	68%	<p>Identities = 325/569 (57%), Positives = 410/569 (71%), Gaps = 15/569 (2%)</p> <p>sp P36267 GGT_PSESP_GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR gb AAC80442.1 (S83255) gamma-glutamyltranspeptidase, GGT [EC 2.3.2.2] [Pseudomonas, A14, Peptide, 575 aa] pir 1920225A gamma-Glu transpeptidase [Pseudomonas sp.] Length = 575</p>
SEQ ID n°341	Prot n°PL-1270.1	Contig37	353712	354626	66%	<p>Identities = 198/285 (69%), Positives = 235/285 (81%), Gaps = 4/285 (1%)</p> <p>gb AAC05920.1 (AF029846) unknown [Salmonella typhi] Length = 284</p>
SEQ ID n°342	Prot n°PL-1271.1	Contig37	350542	352257	91%	<p>Identities = 474/571 (83%), Positives = 524/571 (91%), Gaps = 1/571 (0%)</p> <p>sp P31494 URE1_YEREN_UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE) gb AA50996.1 (L24101) urease alpha subunit [Yersinia enterocolitica] Length = 572</p>
SEQ ID n°343	Prot n°PL-1272.1	Contig37	349871	350467	68%	<p>Identities = 124/193 (64%), Positives = 153/193 (79%) gb AA87855.2 (U40842) urease accessory protein [Yersinia pseudotuberculosis] Length = 231</p>
SEQ ID n°344	Prot n°PL-1273.1	Contig37	349188	349874	72%	<p>Identities = 154/228 (67%), Positives = 174/228 (75%) gb AA87856.2 (U40842) urease accessory protein [Yersinia pseudotuberculosis] Length = 228</p>
SEQ ID n°345	Prot n°PL-1274.1	Contig37	348500	349135	91%	<p>Identities = 189/204 (92%), Positives = 200/204 (97%)</p> <p>sp P42871 UREG_YEREN_UREASE ACCESSORY PROTEIN UREG gb AA50999.1 (L24101) urease [Yersinia enterocolitica] Length = 221</p>
SEQ ID n°346	Prot n°PL-1275.1	Contig37	347538	348503	76%	<p>Identities = 215/320 (67%), Positives = 255/320 (79%), Gaps = 2/320 (0%)</p> <p>gb AA87858.2 (U40842) urease accessory protein [Yersinia pseudotuberculosis] Length = 321</p>

TABLEAU I

SEQ ID n°347	Prot n°PL-1276.1	Contig37	346536	347480	80%	Identities = 219/315 (69%), Positives = 264/315 (83%), Gaps = 1/315 (0%) sp P03807 YDAA_ECOLI 35.6 KDA PROTEIN IN TPX-FNR INTERGENIC REGION pir IQEQEX membrane protein ydaA - Escherichia coli dbj BAA14926.1 (D90771) ORF_ID:0261#5~similar to [SwissProt Accession Number P44195] [Escherichia coli] dbj BAA14936.1 (D90772) ORF_ID:0261#5~similar to [SwissProt Accession Number P44195] [Escherichia coli] gb AAC74415.1 (AE000231) orf, hypothetical protein [Escherichia coli] Length = 316
SEQ ID n°348	Prot n°PL-1277.1	Contig37	345845	348400	91%	Identities = 225/244 (92%), Positives = 233/244 (95%) sp P03019 FNR_ECOLI FUMARATE AND NITRATE REDUCTION REGULATORY PROTEIN pir RGECF transcription regulator fnr - Escherichia coli dbj BAA14927.1 (D90771) Fumarate and nitrate reduction regulatory protein. [Escherichia coli] dbj BAA14937.1 (D90772) Fumarate and nitrate reduction regulatory protein. [Escherichia coli] gb AAC74416.1 (AE000231) transcriptional regulation of aerobic, anaerobic respiration, osmotic balance [Escherichia coli] Length = 250
SEQ ID n°349	Prot n°PL-1278.1	Contig37	344473	345129	65%	Identities = 107/209 (51%), Positives = 147/209 (70%) emb CAB75340.1 (AJ250199) NikR protein [Streptomyces tendae] emb CAC11140.1 (AJ250581) NikR protein [Streptomyces tendae] Length = 226
SEQ ID n°350	Prot n°PL-1279.1	Contig37	343453	344121	56%	Identities = 104/213 (48%), Positives = 131/213 (60%) gb AAF74780.1 AF265211_5 (AF265211) indigoldine synthase protein lbgB [Pectobacterium chrysanthemi] Length = 230
SEQ ID n°351	Prot n°PL-128.1	Contig41	214597	215928	77%	Identities = 314/436 (72%), Positives = 371/436 (85%), Gaps = 1/436 (0%) sp P37011 BRNQ_ECOLI BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN (LIV-II) pir IA64769 branched-chain amino acid transport system II carrier protein brnQ - Escherichia coli gb AAB18125.1 (U73857) similar to S. typhimurium brnQ [Escherichia coli] gb AAC73504.1 (AE000146) branched chain amino acid transport system II carrier protein [Escherichia coli] Length = 439
SEQ ID n°352	Prot n°PL-1280.1	Contig37	341349	342536	18%	Identities = 44/167 (26%), Positives = 73/167 (43%), Gaps = 16/167 (9%) emb CAB45045.1 (AL078635) hypothetical protein [Amycolatopsis orientalis] Length = 353
SEQ ID n°353	Prot n°PL-1281.1	Contig37	337168	341082	64%	Identities = 613/1267 (48%), Positives = 843/1267 (66%), Gaps = 15/1267 (1%) emb CAB87990.1 (AJ277403) indigoldine synthase [Erwinia chrysanthemi] Length = 1488
SEQ ID n°354	Prot n°PL-1282.1	Contig37	336123	337091	72%	Identities = 195/294 (66%), Positives = 235/294 (79%) gb AAF74779.1 AF265211_4 (AF265211) indigoldine synthase protein lbgA [Pectobacterium chrysanthemi] Length = 316
SEQ ID n°355	Prot n°PL-1283.1	Contig37	330990	334517	25%	Identities = 218/408 (53%), Positives = 295/408 (71%) dbj BAB04638.1 (AP001510) diaminobutyric acid aminotransferase [Bacillus halodurans] Length = 427

TABLEAU I

SEQ ID n°356	Prot n°PL-1284.1	Contig37	320869	330999	26%	Identities = 66/178 (37%), Positives = 97/178 (54%), Gaps = 2/178 (1%) gb AAD00512.2 (U81376) PaaA [Erwinia herbicola] Length = 373
SEQ ID n°357	Prot n°PL-1285.1	Contig37	328851	329845	30%	Identities = 64/262 (24%), Positives = 113/262 (42%), Gaps = 18/262 (6%) gb AAG04602.1 AE004551.6 (AE004551) hypothetical protein [Pseudomonas aeruginosa] Length = 319
SEQ ID n°358	Prot n°PL-1286.1	Contig37	327225	328193	35%	Identities = 69/274 (25%), Positives = 114/274 (41%), Gaps = 45/274 (16%) gb AAF13661.1 AF189935_59 (AF189935) pXO2-56 [Bacillus anthracis] Length = 411
SEQ ID n°359	Prot n°PL-1287.1	Contig37	326029	327219	47%	Identities = 115/393 (29%), Positives = 190/393 (48%), Gaps = 22/393 (5%) emb CAC11141.1 (AJ250581) NikS protein [Streptomyces tendae] Length = 424
SEQ ID n°360	Prot n°PL-1288.1	Contig37	324726	325988	59%	Identities = 160/420 (38%), Positives = 252/420 (59%), Gaps = 12/420 (2%) emb CAB83546.1 (AL162752) phosphoribosylamine-glycine ligase [Neisseria meningitidis] Length = 423
SEQ ID n°361	Prot n°PL-1289.1	Contig37	323314	324735	52%	Identities = 146/458 (31%), Positives = 249/458 (53%), Gaps = 12/458 (2%) sp Q00538 MMR_BACSU METHYLENOMYCIN A RESISTANCE PROTEIN (MMR PEPTIDE) pir JYTBSMA methylenomycin A resistance protein mmr - Bacillus subtilis emb CAA46908.1 (X66121) methylenomycinA resistance protein [Bacillus subtilis] emb CAB15784.1 (Z99123) methylenomycin A resistance protein [Bacillus subtilis] Length = 466
SEQ ID n°362	Prot n°PL-129.1	Contig41	216279	217619	72%	Identities = 288/427 (67%), Positives = 343/427 (79%), Gaps = 1/427 (0%) sp P08400 PHOR_ECOLI PHOSPHATE REGULON SENSOR PROTEIN PHOR pir JRGECFR sensor kinase (EC 2.7.3.-) phoR - Escherichia coli emb CAA28409.1 (X04704) phoR gene product (AA 1-431) [Escherichia coli] gb AAB18124.1 (U73857) phosphate regulon sensor protein phoR [Escherichia coli] gb AAC73503.1 (AE000148) positive and negative sensor protein for pho regulon [Escherichia coli] Length = 431
SEQ ID n°363	Prot n°PL-1290.1	Contig37	321971	323317	47%	Identities = 140/460 (30%), Positives = 212/460 (45%), Gaps = 41/460 (8%) gb AAC77368.1 (AF058285) nicotinamidase/pyrazinamidase [Mycobacterium smegmatis] Length = 468
SEQ ID n°364	Prot n°PL-1291.1	Contig37	320839	321621	64%	Identities = 144/255 (56%), Positives = 183/255 (71%), Gaps = 1/255 (0%) gb AAG17135.1 AF190463_8 (AF190463) 2-oxo-4-pentenoate hydratase [Comamonas sp. JS765] Length = 262
SEQ ID n°365	Prot n°PL-1292.1	Contig37	319843	320769	60%	Identities = 139/280 (49%), Positives = 187/280 (66%), Gaps = 2/280 (0%) gb AAF81825.1 AF274045_4 (AF274045) 2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase, OhpC [Rhodococcus sp.] Length = 289 "
SEQ ID n°366	Prot n°PL-1293.1	Contig37	318869	319753	66%	Identities = 144/290 (49%), Positives = 202/290 (69%) dbj BAA16432.1 (D90883) ALS OPERON REGULATORY PROTEIN [Escherichia coli] dbj BAA16440.1 (D90884) ALS OPERON REGULATORY PROTEIN. [Escherichia coli] Length = 297

TABLEAU I

SEQ ID n°367	Prot n°PL-1294.1	Contig37	317371	318732	89%	<p>sp Q47139 HCAE_ECOLI_3-PHENYLPROPIONATE DIOXYGENASE ALPHA SUBUNIT (DIGOXIGENIN ALPHA SUBUNIT) pir JA65031 biphenyl dioxigenase (EC 1.14.-.-) terminal oxygenase component large chain - Escherichia coli gb AAC75591.1 (AE000340) large terminal subunit of phenylpropionate dioxigenase [Escherichia coli] dbj BAA16441.1 (D90884) BENZENE 1,2-DIOXYGENASE ALPHA SUBUNIT (EC 1.14.12.3).</p> <p>Identities = 367/453 (81%), Positives = 408/453 (90%)</p>
SEQ ID n°368	Prot n°PL-1295.1	Contig37	315673	316515	68%	<p>sp P77646 YFHX_ECOLI_HYPOTHETICAL OXIDOREDUCTASE IN CSIE-GLYA INTERGENIC REGION pir JD65031 hypothetical protein b2541 - Escherichia coli (strain K-12) gb AAC75594.1 (AE000340) 2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase [Escherichia coli] dbj BAA16444.1 (D90884) BIPHENYL-2,3-DIHYDRO-2,3-DIOL DEHYDROGENASE (EC 1.3.1.-) (BIPHENYL- CIS-DIOL DEHYDROGENASE) (2,3-DIHYDROXY-4-PHENYLHEXA-4,6-DIENE</p> <p>Identities = 167/268 (62%), Positives = 201/268 (74%)</p>
SEQ ID n°369	Prot n°PL-1296.1	Contig37	314730	315683	59%	<p>sp P17285 MPCT1_ALCEU METAPYROCATECHASE 1 (CATO2ASE) (CATECHOL 2,3-DIOXYGENASE I) pir S10154 catechol 2,3-dioxigenase (EC 1.13.11.2) I - Alcaligenes eutrophus emb CAA36665.1 (X52414) metapyrocatechase (AA 1-313) [Ralstonia eutropha]</p> <p>Identities = 144/311 (46%), Positives = 196/311 (62%), Gaps = 1/311 (0%)</p>
SEQ ID n°370	Prot n°PL-1287.1	Contig37	313544	314728	60%	<p>sp P77650 HCAD_ECOLI_3-PHENYLPROPIONATE DIOXYGENASE FERREDOXIN-NAD(+) REDUCTASE COMPONENT (DIGOXIGENIN SYSTEM FERREDOXIN-NAD(+)) REDUCTASE COMPONENT</p> <p>pir JE65031 hypothetical protein b2542 - Escherichia coli (strain K-12) gb AAC75595.1 (AE000340) ferredoxin reductase subunit of phenylpropionate dioxigenase [Escherichia coli] dbj BAA16445.1 (D90884) BIPHENYL DIOXYGENASE SYSTEM FERREDOXIN-NAD(+) REDUCTASE COMPONENT (EC 1.18.1.3). [Escherichia coli] dbj BAA16452.1 (D90885) BIPHENYL DIOXYGENASE SYSTEM FERREDOXIN-NAD(+) REDUCTASE COMPONENT (EC 1.18.1.3). [Escherichia coli] emb CAA71952.1 (Y11070) ferredoxin reductase [Escherichia coli]</p> <p>Identities = 174/378 (45%), Positives = 240/378 (62%), Gaps = 2/378 (0%)</p> <p>Length = 313</p>
SEQ ID n°371	Prot n°PL-1298.1	Contig37	310490	312100	66%	<p>sp P06202 OPPA_SALTY PERIPLASMIC OLIGOPEPTIDE-BINDING PROTEIN PRECURSOR pir IQREBOA oligopeptide-binding protein precursor - Salmonella typhimurium emb CAA29039.1 (X05491) Opp A (AA1-542) [Salmonella typhimurium] emb CAA27785.1 (X04194) precursor polypeptide [Salmonella typhimurium]</p> <p>Identities = 278/540 (51%), Positives = 373/540 (68%), Gaps = 9/540 (1%)</p> <p>Length = 400</p>
SEQ ID n°372	Prot n°PL-1299.1	Contig37	309069	309980	No Hits found	<p>Identities = 144/311 (46%), Positives = 196/311 (62%), Gaps = 1/311 (0%)</p> <p>Length = 542</p>

TABLEAU I

SEQ ID n°373	Prot n°PL-13.1	Contig41	23755	25203	73%	<p>Identities = 300/478 (62%), Positives = 365/478 (75%) pir D64883 hypothetical protein b1337 - Escherichia coli gb AAC74419.1 (AE000231) ori, hypothetical protein [Escherichia coli] Length = 481</p>	
SEQ ID n°374	Prot n°PL-130.1	Contig41	217843	218332	87%	<p>sp P45606 PHOB_SHIDY PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB pir J44753 phoB protein - Shigella dysenteriae gb AAA26535.1 (M31793) phosphate regulatory protein phoB Length = 189/229 (82%), Positives = 211/229 (91%)</p>	
SEQ ID n°375	Prot n°PL-1300.1	Contig37	308191	309102	38%	<p>Identities = 60/262 (22%), Positives = 117/262 (43%), Gaps = 27/262 (10%) pir T09914 protein-arginine N-methyltransferase (EC 2.1.1.23) - Arabidopsis thaliana emb CAB45311.1 (AL079344) arginine methyltransferase (pam1) [Arabidopsis thaliana] emb CAB79709.1 (AL161575) arginine methyltransferase (pam1) [Arabidopsis thaliana] Length = 390</p>	
SEQ ID n°376	Prot n°PL-1301.1	Contig37	308821	308218	43%	<p>Identities = 101/465 (21%), Positives = 204/465 (43%), Gaps = 67/465 (14%) gb AAD28497.1 (AF061787_4 (AF061787) McpD [Escherichia coli] Length = 580</p>	
SEQ ID n°377	Prot n°PL-1302.1	Contig37	304425	305690	54%	<p>Identities = 157/430 (36%), Positives = 228/430 (52%), Gaps = 33/430 (7%) pir B70448 3-oxoacyl-lacyl-carrier-protein synthase (EC 2.3.1.41) Il - Aquifex aeolicus gb AAC07574.1 (AE000752) 3-oxoacyl-lacyl-carrier-protein synthase Il [Aquifex aeolicus] Length = 415</p>	
SEQ ID n°378	Prot n°PL-1303.2	Contig37	303843	304329	No Hits found		
SEQ ID n°379	Prot n°PL-1304.2	Contig37	301738	302760	No Hits found		
SEQ ID n°380	Prot n°PL-1306.2	Contig37	298717	301486	44%	<p>Identities = 280/779 (35%), Positives = 407/779 (51%), Gaps = 37/779 (4%) gb AAD33495.1 (AF131076_21 (AF131076) hypothetical protein [Coxiella burnetii] Length = 773</p>	hypothetical toxin
SEQ ID n°381	Prot n°PL-1307.1	Contig37	294737	295810	No Hits found	<p>Identities = 251/394 (63%), Positives = 322/394 (81%) sp P43531 YNFM_ECOLI HYPOTHETICAL 45.3 KD PROTEIN IN MLC-ASR INTERGENIC REGION pir F64915 membrane protein ynfM - Escherichia coli dbj BAA15330.1 (D90802) Bicyclomycin resistance protein (Sulfonamide resistance protein) [Escherichia coli] gb AAC74668.1 (AE000255) putative transport protein [Escherichia coli] Length = 417</p>	
SEQ ID n°382	Prot n°PL-1308.1	Contig37	293355	294638	75%	<p>Identities = 152/287 (52%), Positives = 208/287 (71%), Gaps = 2/287 (0%) sp P77559 YNFL_ECOLI HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN MLC-ASR INTERGENIC REGION pir E84915 probable transcription regulator ynfL - Escherichia coli dbj BAA15319.1 (D90801) als operon regulatory protein. [Escherichia coli] dbj BAA15329.1 (D90802) als operon regulatory protein. [Escherichia coli] gb AAC74667.1 (AE000255) putative transcriptional regulator LYSR-type [Escherichia coli] Length = = 408</p>	
SEQ ID n°383	Prot n°PL-1309.1	Contig37	292323	293243	67%		
SEQ ID n°384	Prot n°PL-131.1	Contig41	218719	219954	72%	<p>Identities = 244/408 (59%), Positives = 305/408 (73%), Gaps = 7/408 (1%) gb AAB18122.1 (U73857) exonuclease SbcD [Escherichia coli] Length = 408</p>	

TABLEAU I

SEQ ID n°385	Prot n°PL-1310.1	Contig37	290980	292191	74%	Identities = 218/405 (54%), Positives = 303/405 (74%), Gaps = 1/405 (0%) spiP50456[MLC_ECOLI_MLC PROTEIN (MAKING LARGE COLONIES PROTEIN)] pir D84915 mic protein - Escherichia coli dbj BAA15318.1 (D90801) Mic protein. [Escherichia coli] dbj BAA15328.1 (D90802) Mic protein. [Escherichia coli] gb AAC74688.1 (AE000255) putative NAGC-like transcriptional regulator [Escherichia coli] Length = 408
SEQ ID n°386	Prot n°PL-1311.1	Contig37	290108	290839	59%	Identities = 109/220 (49%), Positives = 158/220 (71%), Gaps = 3/220 (1%) spiP77201[BID2_ECOLI_PUTATIVE DETHIOBIOTIN SYNTHETASE (DETHIOBIOTIN SYNTHASE) (DTB SYNTHETASE) (DTBS)] Length = 231
SEQ ID n°387	Prot n°PL-1312.2	Contig37	287078	288475		Identities = 183/247 (74%), Positives = 208/247 (84%) spiP39831[YDFG_ECOLI_PROBABLE OXIDOREDUCTASE IN DCP-NOHA INTERGENIC REGION pir F64908 probable dehydrogenase (EC 1.1.1.-) ydfG - Escherichia coli dbj BAA15241.1 (D90797) 3-oxoacyl-Hacyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase). [Escherichia coli] gb AAC74612.1 (AE000251) putative oxidoreductase [Escherichia coli] Length = 248
SEQ ID n°388	Prot n°PL-1313.1	Contig37	285241	285990	77%	Identities = 165/494 (33%), Positives = 262/494 (52%), Gaps = 23/494 (4%) emb CAC11387.1 (AL445063) probable histidine ammonia-lyase [Thermoplasma acidophilum] Length = 496
SEQ ID n°389	Prot n°PL-1314.1	Contig37	283367	285016	47%	Identities = 278/544 (51%), Positives = 350/544 (64%), Gaps = 36/544 (6%) emb CAA72201.1 (Y11391) exochitinase [Glossina morsitans S-endosymbiont] Length = 695
SEQ ID n°390	Prot n°PL-1315.1	Contig37	281314	283017	61%	Identities = 108/382 (28%), Positives = 172/382 (44%), Gaps = 44/382 (11%) pir T36402 probable monooxygenase - Streptomyces coelicolor emb CAB53314.1 (AL109974) putative monooxygenase [Streptomyces coelicolor A3(2)] Length = 388
SEQ ID n°391	Prot n°PL-1316.1	Contig37	279775	281079	39%	Identities = 80/320 (25%), Positives = 129/320 (40%), Gaps = 50/320 (15%) pir S76629 hypothetical protein - Synecocystis sp. (strain PCC 6803) dbj BAA10573.1 (D84004) hypothetical protein [Synecocystis sp.] Length = 402
SEQ ID n°392	Prot n°PL-1317.1	Contig37	278255	279253	38%	Identities = 194/255 (76%), Positives = 228/255 (88%) gb AAD43990.1 U59485_17 (U59485) Atm [Agrobacterium tumefaciens] Length = 258
SEQ ID n°393	Prot n°PL-1318.1	Contig37	277372	278142	79%	Identities = 147/338 (43%), Positives = 201/338 (58%), Gaps = 32/338 (9%) emb CAB90977.1 (AL355832) hypothetical protein SCE22.10 [Streptomyces coelicolor A3(2)] Length = 348
SEQ ID n°394	Prot n°PL-1319.1	Contig37	276235	277212	61%	

TABLEAU I

SEQ ID n°395	Prot n°PL-132.1	Contig41	219951	223637	55%	Identities = 512/1233 (41%), Positives = 680/1233 (54%), Gaps = 198/1233 (16%) sp P13458 SBCC_ECOLI EXONUCLEASE SBCC pir JBVECS exonuclease (EC 3.1.15.-) sbcC - Escherichia coli emb CAA34104.1 (X15981) SbcC (AA 1-1048) [Escherichia coli] gb AAB18121.1 (U73857) exonuclease SbcC [Escherichia coli] gb AAC73500.1 (AE000146) ATP-dependent dsDNA exonuclease [Escherichia coli] prf J2204364A sbcC gene [Escherichia coli] Length = 1048
SEQ ID n°396	Prot n°PL-1320.1	Contig37	274830	276095	56%	Identities = 199/409 (48%), Positives = 257/409 (62%), Gaps = 6/409 (1%) gb AAG04655.1 AE004556_5 (AE004556) probable oxidoreductase [Pseudomonas aeruginosa] Length = 417
SEQ ID n°397	Prot n°PL-1321.1	Contig37	273374	274549	63%	Identities = 191/360 (53%), Positives = 250/360 (69%) gb AAG04656.1 AE004556_6 (AE004556) hypothetical protein [Pseudomonas aeruginosa] Length = 371
SEQ ID n°398	Prot n°PL-1322.1	Contig37	272463	273425	74%	Identities = 200/311 (64%), Positives = 239/311 (76%), Gaps = 4/311 (1%) gb AAG04657.1 AE004556_7 (AE004556) hypothetical protein [Pseudomonas aeruginosa] Length = 314
SEQ ID n°399	Prot n°PL-1323.1	Contig37	271385	272260	66%	Identities = 127/217 (58%), Positives = 184/217 (75%) gb AAG04660.1 AE004555_10 (AE004555) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 224
SEQ ID n°400	Prot n°PL-1324.1	Contig37	270236	271166	74%	Identities = 194/303 (64%), Positives = 243/303 (80%) gb AAG04643.1 AE004555_3 (AE004555) probable dihydrodipicolinate synthetase [Pseudomonas aeruginosa] Length = 305
SEQ ID n°401	Prot n°PL-1325.1	Contig37	268611	270194	70%	Identities = 325/518 (62%), Positives = 384/518 (73%) gb AAG05605.1 AE004648_4 (AE004648) probable aldehyde dehydrogenase [Pseudomonas aeruginosa] Length = 527
SEQ ID n°402	Prot n°PL-1326.1	Contig37	266949	268550	73%	Identities = 310/515 (60%), Positives = 408/515 (78%), Gaps = 1/515 (0%) pir D70035 permease homolog yveA - Bacillus subtilis emb CAB08050.1 (Z94043) hypothetical protein [Bacillus subtilis] emb CAB15452.1 (Z89121) similar to permease [Bacillus subtilis] Length = 520
SEQ ID n°403	Prot n°PL-1327.1	Contig37	266258	266854	48%	Identities = 69/172 (40%), Positives = 99/172 (57%), Gaps = 21/172 (12%) sp Q10612 YC84_MYCTU HYPOTHETICAL 18.2 KDA PROTEIN RV1284 pir H70771 hypothetical protein Rv1284 - Mycobacterium tuberculosis (strain H37Rv) emb CAA97750.1 (Z73419) hypothetical protein Rv1284 [Mycobacterium tuberculosis] Length = 163
SEQ ID n°404	Prot n°PL-1328.1	Contig37	263296	264180	59%	Identities = 126/284 (44%), Positives = 188/284 (65%), Gaps = 4/284 (1%) gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300

TABLEAU I

SEQ ID n°405	Prot n°PL-1329.1	Contig37	259680	260865	62%	Identities = 171/375 (45%), Positives = 250/375 (66%), Gaps = 20/375 (5%) pdb 1B65 A Chain A, Structure Of L-Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold pdb 1B65 B Chain B, Structure Of L-Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold pdb 1B65 C Chain C, Structure Of L-Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold pdb 1B65 D Chain D, Structure Of L-Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold pdb 1B65 E Chain E, Structure Of L-Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold
SEQ ID n°406	Prot n°PL-133.1	Contig41	224088	224982	70%	Identities = 156/317 (49%), Positives = 220/317 (69%), Gaps = 9/317 (2%) pir T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CAB55253.1 (AL117211) hypothetical protein YPMT1.71 [Yersinia pestis]
SEQ ID n°407	Prot n°PL-1330.1	Contig37	256915	256326	43%	Identities = 252/552 (45%), Positives = 346/552 (62%), Gaps = 6/552 (1%) gb AAF33136.1 (AF196567) PdtorFL [Pseudomonas stutzeri]
SEQ ID n°408	Prot n°PL-1331.1	Contig37	255463	256794	85%	Identities = 343/436 (78%), Positives = 389/436 (88%) gb AAG03522.1 (AE004451_3 (AE004451) beta-alanine--pyruvate transaminase [Pseudomonas aeruginosa] Length = 448
SEQ ID n°409	Prot n°PL-1332.1	Contig37	254049	255206	No Hits found	
SEQ ID n°410	Prot n°PL-1333.2	Contig37	250108	263428		
SEQ ID n°411	Prot n°PL-1334.1	Contig37	248807	249778	35%	Identities = 69/256 (26%), Positives = 114/256 (43%), Gaps = 12/256 (4%) pdb 2EBN Endo-Beta-N-Acetylglucosaminidase F1 (E.C.3.2.1.96) (Endoglycosidase F1, Endo F1) Length = 289
SEQ ID n°412	Prot n°PL-1335.1	Contig37	246926	247846	52%	Identities = 117/291 (40%), Positives = 170/291 (58%), Gaps = 8/291 (2%) gb AAC38151.1 (AF034088) lipase [Pseudomonas sp. B11-1] Length = 308
SEQ ID n°413	Prot n°PL-1336.1	Contig37	245519	246589	No Hits found	
SEQ ID n°414	Prot n°PL-1337.2	Contig37	242561	243439		
SEQ ID n°415	Prot n°PL-1338.2	Contig37	241058	242371		
SEQ ID n°416	Prot n°PL-1339.1	Contig37	239577	241019	80%	Identities = 325/481 (67%), Positives = 400/481 (82%), Gaps = 3/481 (0%) gb AAF84712.1 (AE004233) 6-phospho-beta-glucosidase [Vibrio cholerae] Length = 478
SEQ ID n°417	Prot n°PL-134.1	Contig41	227240	228040	46%	Identities = 86/229 (37%), Positives = 123/229 (53%), Gaps = 4/229 (1%) db BAA25929.1 (AB007122) creatininase [Arthrobacter sp.] Length =

TABLEAU I

SEQ ID n°418	Prot n°PL-1340.1	Contig37	238355	239536	81%	Identities = 259/387 (66%), Positives = 325/387 (83%), Gaps = 3/387 (0%) sp P37390 XYLR_ECOLI_XYLOSE OPERON REGULATORY PROTEIN pir S47790 xylose operon regulatory protein - Escherichia coli gb AAB18548.1 (U00039) xyIR [Escherichia coli] gb AAC76593.1 (AE000434) putative regulator of xyl operon [Escherichia coli] Length = Identities = 328/443 (74%), Positives = 390/443 (87%) emb CAA28394.1 (X04691) xylose isomerase (AA 1-444) [Escherichia coli] Length = 444
SEQ ID n°419	Prot n°PL-1341.1	Contig37	236725	238044	87%	
SEQ ID n°420	Prot n°PL-1342.2	Contig37	235733	236326		
SEQ ID n°421	Prot n°PL-1343.1	Contig37	232444	233412	57%	Identities = 168/314 (53%), Positives = 213/314 (67%), Gaps = 4/314 (1%) emb CAB84714.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis] emb CAB84719.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis] Length = 321
SEQ ID n°422	Prot n°PL-1344.1	Contig37	228342	231956	44%	Identities = 333/1136 (29%), Positives = 538/1136 (47%), Gaps = 70/1136 (6%) sp P40330 BVGS_BORPA VIRULENCE SENSOR PROTEIN BVGS PRECURSOR pir S17946 virulence sensor protein bvgS precursor - Bordetella parapertussis emb CAA37124.1 (X52948) bvgS product, put. sensor protein [Bordetella parapertussis] Length = 1238
SEQ ID n°423	Prot n°PL-1345.1	Contig37	227715	228341	66%	Identities = 87/215 (40%), Positives = 139/215 (64%), Gaps = 12/215 (5%) gb AAG07101.1 AE004790_6 (AE004790) probable two-component response regulator [Pseudomonas aeruginosa] Length = 213
SEQ ID n°424	Prot n°PL-1346.1	Contig37	226314	227684	No Hits found	
SEQ ID n°425	Prot n°PL-1347.1	Contig37	223793	226375	61%	Identities = 389/871 (44%), Positives = 534/871 (60%), Gaps = 59/871 (6%) gb AAG03480.1 AE004447_13 (AE004447) probable ClpA/B-type chaperone [Pseudomonas aeruginosa] Length = 902
SEQ ID n°426	Prot n°PL-1348.1	Contig37	220276	223800	12%	Identities = 85/304 (27%), Positives = 146/304 (47%), Gaps = 21/304 (6%) gb AAG05058.1 AE004594_10 (AE004594) hypothetical protein [Pseudomonas aeruginosa] Length = 1175
SEQ ID n°427	Prot n°PL-1348.1	Contig37	219514	220275	29%	Identities = 38/158 (24%), Positives = 76/158 (48%), Gaps = 11/158 (6%) gb AAF96029.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 257
SEQ ID n°428	Prot n°PL-135.1	Contig41	228007	228876	49%	Identities = 103/295 (34%), Positives = 158/295 (52%), Gaps = 15/295 (5%) sp O59185 PYRD_PYRHO DIHYDROOROTATE DEHYDROGENASE (DIHYDROOROTATE OXIDASE) (DHODASE) (DHODASE) (DHOD) pir JH71027 probable dihydroorotate dehydrogenase - Pyrococcus horikoshii dbj BA330624.1 (AP000006) 303aa long hypothetical dihydroorotate dehydrogenase [Pyrococcus horikoshii] Length = 303
SEQ ID n°429	Prot n°PL-1350.1	Contig37	218255	219655	40%	Identities = 112/471 (23%), Positives = 191/471 (39%), Gaps = 34/471 (7%) gb AAF96028.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 444

TABLEAU I

SEQ ID n°430	Prot n°PL-1352.1	Contig37	216457	217584	44%	Identities = 97/345 (28%), Positives = 166/345 (48%), Gaps = 13/345 (3%) gb AAG05748.1 AE004662_3 (AE004662) hypothetical protein [Pseudomonas aeruginosa] Length = 366
SEQ ID n°431	Prot n°PL-1353.1	Contig37	215747	216442	No Hits found	Identities = 213/668 (31%), Positives = 340/668 (50%), Gaps = 39/668 (5%) gb AAG06073.1 AE004696_7 (AE004696) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 726
SEQ ID n°432	Prot n°PL-1354.1	Contig37	213531	215537	50%	Identities = 96/347 (27%), Positives = 155/347 (44%), Gaps = 28/347 (8%) gb AAG05758.1 AE004663_4 (AE004663) hypothetical protein [Pseudomonas aeruginosa] Length = 338
SEQ ID n°433	Prot n°PL-1355.1	Contig37	212460	213506	44%	Identities = 187/608 (30%), Positives = 292/608 (47%), Gaps = 37/608 (6%) gb AAG05757.1 AE004663_3 (AE004663) hypothetical protein [Pseudomonas aeruginosa] Length = 597
SEQ ID n°434	Prot n°PL-1356.1	Contig37	210604	212505	46%	Identities = 299/489 (61%), Positives = 381/489 (77%), Gaps = 1/489 (0%) gb AAB92576.1 (AF037441) putative 54.5 kDa protein [Edwardsiella ictaluri] Length = 495
SEQ ID n°435	Prot n°PL-1357.1	Contig37	208144	209643	73%	Identities = 76/157 (48%), Positives = 108/157 (68%), Gaps = 5/157 (3%) gb AAB92577.1 (AF037441) putative 19.5 kDa protein [Edwardsiella ictaluri] Length = 170
SEQ ID n°436	Prot n°PL-1358.1	Contig37	207603	208154	52%	Identities = 81/156 (51%), Positives = 102/156 (64%), Gaps = 11/156 (7%) ref NP_037718.1 tail fiber gb AAF31111.1 (AF069529) tail fiber [Bacteriophage HK97] Length = 321
SEQ ID n°437	Prot n°PL-1359.1	Contig37	205495	206378	34%	Identities = 199/508 (39%), Positives = 308/508 (60%), Gaps = 21/508 (4%) dbj BAB12211.1 (AB032549) polyketide synthase and peptide synthetase [Microcystis aeruginosa] Length = 3487
SEQ ID n°438	Prot n°PL-136.1	Contig41	228591	231399	51%	Identities = 403/618 (65%), Positives = 498/618 (80%), Gaps = 6/618 (0%) gb AAA81002.1 (U11258) extracellular lipase [Serratia marcescens] Length = 613
SEQ ID n°439	Prot n°PL-1360.1	Contig37	200248	202101	79%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°440	Prot n°PL-1361.1	Contig37	199163	200230	21%	Identities = 53/152 (34%), Positives = 83/152 (53%), Gaps = 5/152 (3%) pir S74448 regulatory protein pcrR - Synechocystis sp. (strain PCC 6803) dbj BAA16600.1 (D80889) regulatory protein PcrR [Synechocystis sp.] Length = 346
SEQ ID n°441	Prot n°PL-1362.1	Contig37	197913	198917	24%	Identities = 208/669 (31%), Positives = 335/669 (49%), Gaps = 28/669 (4%) emb CAA86212.1 (Z38065) FyuA precursor [Escherichia coli] Length = 673
SEQ ID n°442	Prot n°PL-1363.1	Contig37	195643	197661	49%	

Unknown, similar to proteins involved in antibiotic biosynthesis

TABLEAU I

SEQ ID n°443	Prot n°PL-1364.1	Contig37	194402	195682	51%	Identities = 134/404 (33%), Positives = 220/404 (54%), Gaps = 16/404 (3%) emb CAA21386.1 (AL031866) ORF63, len=462 aa, putative transmembrane protein, similarity to E. coli ECAMP3_1 E.coli ampG3 gene, 27.1% identity in 376 aa overlap, Fasta scores: opt: 311, E0: 1.1e-12 [Yersinia pestis] Length = 462
SEQ ID n°444	Prot n°PL-1365.1	Contig37	192610	194409	49%	Identities = 203/567 (35%), Positives = 296/567 (51%), Gaps = 16/567 (2%) emb CAA21388.1 (AL031866) ORF 65, len=600 aa, yersiniabactin uptake, ABC Transporter, similar to many, eg. MTCY02B10_12 M. tuberculosis (859 aa), 35.7% identity in 577 aa overlap Fasta scores: opt: 1084, E0:0 [Yersinia pestis] Length = 600
SEQ ID n°445	Prot n°PL-1366.1	Contig37	190863	192740	47%	Identities = 185/550 (33%), Positives = 299/550 (53%), Gaps = 13/550 (2%) emb CAA21388.1 (AL031866) ORF 65, len=600 aa, yersiniabactin uptake, ABC Transporter, similar to many, eg. MTCY02B10_12 M. tuberculosis (859 aa), 35.7% identity in 577 aa overlap Fasta scores: opt: 1084, E0:0 [Yersinia pestis] Length = 600
SEQ ID n°446	Prot n°PL-1368.1	Contig37	184671	190829	61%	Identities = 974/2010 (48%), Positives = 1255/2010 (61%), Gaps = 65/2010 (3%) pir T17439 peptide synthetase homolog - Yersinia pestis gb AAC69587.1 (AF091251) Ybt peptide synthetase HMWP2 [Yersinia pestis] emb CAA21390.1 (AL031866) ORF67, len=2041 aa, irp2, function=synthesis of siderophore yersiniabactin, product=HMWP2 protein 98.6% identity in 2035 aa overlap to HMP2_YEREN, also highly similar to ANGR_VIBAN, (1048 aa), 44.4% identity in 917 aa overlap, Fasta
SEQ ID n°447	Prot n°PL-1369.1	Contig37	172945	184683	23%	Identities = 686/1575 (43%), Positives = 938/1575 (59%), Gaps = 64/1575 (4%) pir T17440 probable polyketide synthase - Yersinia pestis gb AAC69588.1 (AF091251) Ybt peptide/polyketide synthetase HMWP1 [Yersinia pestis] emb CAA21391.1 (AL031866) ORF68, len=3163 aa, irp1, function=synthesis of siderophore yersiniabactin, product=HMWP1 protein, 97.9% identity in 3163 aa overlap to YEIRPOP_1 Y. enterocolitica irp1, Fasta scores: opt: 2088, E0: 0 [Yersinia pestis]
SEQ ID n°448	Prot n°PL-137.1	Contig41	231520	233379	35%	Identities = 129/459 (28%), Positives = 222/459 (48%), Gaps = 40/459 (8%) emb CAC01604.1 (AJ269505) peptide synthetase [Anabaena sp. 90] Length = 5060
SEQ ID n°449	Prot n°PL-1370.1	Contig37	171851	172948	56%	Identities = 160/347 (46%), Positives = 210/347 (60%), Gaps = 7/347 (2%) pir T30343 irp3 protein - Yersinia enterocolitica emb CAA73128.1 (Y12527) irp3 protein [Yersinia enterocolitica] Length = 365
SEQ ID n°450	Prot n°PL-1371.1	Contig37	171048	171824	56%	Identities = 120/239 (50%), Positives = 154/239 (64%), Gaps = 8/239 (3%) pir T17442 ybtT protein - Yersinia pestis gb AAC69590.1 (AF091251) YbtT [Yersinia pestis] Length = 262

Unknown, similar to proteins involved in antibiotic biosynthesis

TABLEAU I

SEQ ID n°451	Prot n°PL-1372.1	Contig37	168115	171108	35%	<p>Identities = 277/503 (55%), Positives = 352/503 (69%), Gaps = 7/503 (1%) pir T17443 salicyl-AMP ligase (EC 6.2.1.-) - Yersinia pestis gb AA093464.1 (U50364) YbIE [Yersinia pestis] gb AAC68591.1 (AF091251) salicyl-AMP ligase YbIE [Yersinia pestis] emb CAA21394.1 (AL031866) ORF 71, len=525 aa, ybIE, 100% identity in 525 aa overlap, with YPU50364_2 Yersinia pestis yersiniabactin 2,3-dihydroxybenzoate-AMP ligase (ybtE) (525 aa), Fasta scores: opt: 3451, E0: 0 Length = 525</p>	hypothetical toxin
SEQ ID n°452	Prot n°PL-1373.1	Contig37	166756	167937	52%	<p>Identities = 158/318 (49%), Positives = 206/318 (64%), Gaps = 4/318 (1%) pir E70047 conserved hypothetical protein yvrK - Bacillus subtilis emb CAB15314.1 (Z99120) similar to hypothetical proteins [Bacillus subtilis] emb CAB15328.1 (Z99121) similar to hypothetical proteins [Bacillus subtilis] emb CAA11727.1 (AJ223978) YvrK protein [Bacillus subtilis] Length =</p>	
SEQ ID n°453	Prot n°PL-1374.1	Contig37	166213	166232	No Hits found		
SEQ ID n°454	Prot n°PL-1375.1	Contig37	163799	164896	44%	<p>Identities = 79/356 (22%), Positives = 162/356 (45%), Gaps = 34/356 (9%) emb CAA07408.1 (AJ008986) transmembrane protein [Streptococcus pneumoniae] Length = 332</p>	
SEQ ID n°455	Prot n°PL-1377.1	Contig37	160361	161449	48%	<p>Identities = 116/296 (39%), Positives = 175/298 (58%) gb AAC38628.1 (AF047028) insecticidal toxin complex protein TccB [Photobacterium luminescens] Length = 1565</p>	Unknown, similar to insecticidal toxins
SEQ ID n°456	Prot n°PL-1378.1	Contig37	159714	160496	57%	<p>Identities = 114/253 (45%), Positives = 151/253 (59%), Gaps = 21/253 (8%) gb AAC38629.1 (AF047028) insecticidal toxin complex protein TccB [Photobacterium luminescens] Length = 1565</p>	Unknown, similar to insecticidal toxins
SEQ ID n°457	Prot n°PL-1379.1	Contig37	157644	159452	35%	<p>Identities = 147/448 (32%), Positives = 217/448 (47%), Gaps = 36/448 (8%) gb AAD40800.1 (AF145049) acyl-CoA oxidase [Streptomyces fradiae] Length = 841</p>	
SEQ ID n°458	Prot n°PL-138.1	Contig41	233846	234484	38%	<p>Identities = 52/173 (30%), Positives = 83/173 (47%), Gaps = 15/173 (8%) gb AAG05790.1 (AE004667) probable non-ribosomal peptide synthetase [Pseudomonas aeruginosa] Length = 5149</p>	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°459	Prot n°PL-1380.1	Contig37	156021	156689	27%	<p>Identities = 38/127 (29%), Positives = 61/127 (47%), Gaps = 9/127 (7%) sp P47666 Y427_MYCGE_HYPOTHETICAL PROTEIN MG427 pir B64247 conserved hypothetical protein MG427 - Mycoplasma genitalium gb AAC72448.1 (U39725) conserved hypothetical protein [Mycoplasma genitalium] Length = 141</p>	
SEQ ID n°460	Prot n°PL-1381.1	Contig37	154167	155375	83%	<p>Identities = 279/403 (69%), Positives = 343/403 (84%), Gaps = 1/403 (0%) sp P18199 TYRP_ECOLI_TYROSINE-SPECIFIC TRANSPORT PROTEIN (TYROSINE PERMEASE) pir GRECY tyrosine-specific transport protein - Escherichia coli db BAA15730.1 (D90832) Tyrosine-specific transport protein (Tyrosine permease) [Escherichia coli] gb AAC74977.1 (AE000284) tyrosine-specific transport system [Escherichia coli] Length = 403</p>	

TABLEAU I

SEQ ID n°461	Prot n°PL-1382.1	Contig37	152167	154122	34%	Identities = 137/570 (24%), Positives = 223/570 (39%), Gaps = 128/570 (22%) gb AAAF94308.1 (AE004195) glutamate decarboxylase, putative [Vibrio cholerae] Length = 548
SEQ ID n°462	Prot n°PL-1383.2	Contig37	150761	151756		
SEQ ID n°463	Prot n°PL-1384.2	Contig37	149780	150517		
SEQ ID n°464	Prot n°PL-1385.1	Contig37	148856	149626	49%	Identities = 87/255 (34%), Positives = 140/255 (54%), Gaps = 14/255 (5%) gb AAG10092.1 (U79570_1) (U79570) glucose dehydrogenase [Bacillus licheniformis] Length = 261
SEQ ID n°465	Prot n°PL-1386.1	Contig37	147089	148657	37%	Identities = 131/389 (33%), Positives = 195/389 (49%), Gaps = 10/389 (2%) gb AAG03923.1 (AE004490_3 (AE004490) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 429
SEQ ID n°466	Prot n°PL-1387.1	Contig37	145374	146651	73%	Identities = 255/421 (60%), Positives = 316/421 (74%) sp P50457 GOAG_ECOLI 4-AMINO-BUTYRATE AMINOTRANSFERASE (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA TRANSAMINASE) (GLUTAMATE-SUCCINIC SEMIALDEHYDE TRANSAMINASE) (GABA AMINOTRANSFERASE) (GABA-AT) pir J064879 4-aminobutyrate transaminase (EC 2.6.1.19) goaG - Escherichia coli gb AAC45301.1 (U38543) GABA-aminotransferase [Escherichia coli] db BAA14871.1 (D90768) 4-aminobutyrate aminotransferase (EC 2.6.1.19) (Gamma-amino-N-butyrate transaminase) (GABA transaminase) (Glutamate-succinic semialdehyde transaminase) (GABA aminotransferase) [Escherichia coli] gb AAC74384.1 (AE002228) 4-aminobutyrate transaminase (EC 2.6.1.19) goaG - Escherichia coli Identities = 34/104 (32%), Positives = 51/104 (48%), Gaps = 9/104 (8%) gb AA097824.1 (AF013216) unknown [Mycococcus xanthus] Length = 501
SEQ ID n°467	Prot n°PL-1388.1	Contig37	144291	145079	19%	
SEQ ID n°468	Prot n°PL-1389.2	Contig37	142860	144290		
SEQ ID n°469	Prot n°PL-139.1	Contig41	234979	236502	63%	Identities = 238/480 (49%), Positives = 324/480 (66%), Gaps = 3/480 (0%) gb AAG04671.1 (AE004557_12 (AE004557) probable MFS transporter [Pseudomonas aeruginosa] Length = 501
SEQ ID n°470	Prot n°PL-1390.2	Contig37	140619	142229		
SEQ ID n°471	Prot n°PL-1391.1	Contig37	139703	140536	54%	Identities = 103/281 (36%), Positives = 155/281 (54%), Gaps = 4/281 (1%) pir J069795 conserved hypothetical protein yefF - Bacillus subtilis emb CAB12507.1 (Z99107) alternate gene name: yefM, yfxB--similar to hypothetical proteins [Bacillus subtilis] Length = 286
SEQ ID n°472	Prot n°PL-1392.1	Contig37	138911	139510	54%	Identities = 92/189 (48%), Positives = 120/189 (62%), Gaps = 3/189 (1%) pir J060070 chitin binding protein 21 precursor - Serratia marcescens db BAA31568.1 (AB015988) CBP21 precursor [Serratia marcescens] Length = 197
SEQ ID n°473	Prot n°PL-1393.1	Contig37	137578	138690	80%	Identities = 246/370 (66%), Positives = 305/370 (81%) gb AAG07161.1 (AE004796_6 (AE004796) probable acetylcholine aminohydrolase [Pseudomonas aeruginosa] Length = 380

TABLEAU I

SEQ ID n°474	Prot n°PL-1394.1	Contig37	134877	135803	72%	Identities = 181/310 (58%), Positives = 239/310 (76%), Gaps = 1/310 (0%) gb AAF68950.1 (AF231032) DNA replication terminus site-binding protein [Yersinia pestis] Length = 311
SEQ ID n°475	Prot n°PL-1395.1	Contig37	132429	133823	89%	Identities = 387/464 (83%), Positives = 418/464 (89%) pdb 1FUQJ Chain A, Fumarate With Bound Pyromellitic Acid pdb 1FUPI Chain A, Fumarate With Bound Pyromellitic Acid pdb 1FUQB Chain B, Fumarate With Bound Pyromellitic Acid Length = 472
SEQ ID n°476	Prot n°PL-1396.1	Contig37	130852	132124	74%	Identities = 234/391 (59%), Positives = 297/391 (75%), Gaps = 1/391 (0%) spiP00946 MANA_ECOLI MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNANOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) pir ISECMP mannose-6-phosphate isomerase (EC 5.3.1.8) - Escherichia coli gb AAA24109.1 (M15380) phosphomannose isomerase [Escherichia coli] dbj BAA15361.1 (D90804) Mannose-6- phosphate isomerase (EC 5.3.1.8) (Phosphomannose isomerase) (PMI) (Phosphohexomutase). [Escherichia coli] dbj BAA15365.1 (D90805) Mannose- 6-phosphate isomerase (EC 5.3.1.8) (Phosphomannose isomerase) (PMI) (Phosphohexomutase). [Escherichia coli] gb AAC74685.1 (AE000257) mannose-6-phosphate isomerase [Escherichia coli] prf 1102208A isomerase-phosphomannose [Escherichia coli] Length = 391
SEQ ID n°477	Prot n°PL-1397.1	Contig37	129265	130812	54%	Identities = 179/506 (35%), Positives = 300/506 (58%), Gaps = 18/506 (3%) spiP77804 YDGA_ECOLI HYPOTHETICAL 54.7 KDA PROTEIN IM MANA- GUSC INTERGENIC REGION pir H64917 probable membrane protein ydgA - Escherichia coli dbj BAA15362.1 (D90804) ORF_ID:o312#14; similar to [SwissProt Accession Number P32128] [Escherichia coli] dbj BAA15366.1 (D90805) ORF_ID:o312#14; similar to [SwissProt Accession Number P32128] [Escherichia coli] gb AAC74686.1 (AE000257) orf, hypothetical protein [Escherichia coli] Length = 502 "
SEQ ID n°478	Prot n°PL-1398.1	Contig37	128186	129187	69%	Identities = 238/331 (71%), Positives = 268/331 (80%) spiP22333 ADD_ECOLI ADENOSINE DEAMINASE (ADENOSINE AMINOHYDROLASE) pir A64919 adenosine deaminase (EC 3.5.4.4) - Escherichia coli dbj BAA15374.1 (D90805) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase). [Escherichia coli] dbj BAA15381.1 (D90806) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase). [Escherichia coli] dbj BAA15411.1 (D90808) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase). [Escherichia coli] gb AAC74695.1 (AE000258) adenosine deaminase [Escherichia coli] Length = 333
SEQ ID n°479	Prot n°PL-1399.1	Contig37	122062	123033	79%	Identities = 206/316 (65%), Positives = 257/316 (81%), Gaps = 2/316 (0%) dbj BAA16281.1 (D90870) similar to [SwissProt Accession Number P39836]-start codon is not identified yet [Escherichia coli] Length = 340

TABLEAU I

SEQ ID n°480	Prot n°PL-14.1	Contig41	25196	26518	75%	<p>Identities = 268/428 (62%), Positives = 339/429 (78%), Gaps = 1/429 (0%) spiP77357YDAJ_ECOLI_HYPOTHETICAL 47.1 KD PROTEIN IN OGT-DBPA INTERGENIC REGION pir E64883 probable amidohydrolase (EC 3.5.-.-) ydaJ - Escherichia coli dbj BAA14940.1 (D90772) Thermostable carboxypeptidase (EC 3.4.17.-) [Escherichia coli] gb AAC74420.1 (AE000231) putative aminohydrolase (EC 3.5.1.14) [Escherichia coli]</p> <p>Identities = 47/180 (26%), Positives = 85/180 (47%), Gaps = 4/180 (2%) pir T35714 hypothetical protein SC7H1.19 - Streptomyces coelicolor emb CAA16206.1 (AL021411) hypothetical protein [Streptomyces coelicolor A3(2)] Length = 182</p>
SEQ ID n°481	Prot n°PL-140.1	Contig41	236542	237174	40%	<p>Identities = 224/345 (64%), Positives = 270/345 (77%) spiP77376YDGJ_ECOLI_HYPOTHETICAL OXIDOREDUCTASE IN ADD-NTH INTERGENIC REGION Length = 346</p>
SEQ ID n°482	Prot n°PL-1400.1	Contig37	120816	121853	77%	<p>Identities = 139/189 (73%), Positives = 162/189 (85%) spiP77223YDGM_ECOLI_PUTATIVE FERREDOXIN-LIKE PROTEIN IN ADD-NTH INTERGENIC REGION pir F64919 probable iron-sulfur protein b1628 precursor - Escherichia coli dbj BAA15383.1 (D90806) Ferredoxin II. [Escherichia coli] dbj BAA15390.1 (D90807) Ferredoxin II. [Escherichia coli] dbj BAA15413.1 (D90808) Ferredoxin II. [Escherichia coli] gb AAC74700.1 (AE000258) orf, hypothetical protein [Escherichia coli] Length = 192</p>
SEQ ID n°484	Prot n°PL-1402.1	Contig37	116301	118859	63%	<p>Identities = 47/173 (60%), Positives = 565/773 (72%), Gaps = 37/773 (4%) pir G64919 probable iron-sulfur protein b1628 - Escherichia coli dbj BAA15384.1 (D90806) Glucose repression mediator protein. [Escherichia coli] dbj BAA15391.1 (D90807) Glucose repression mediator protein. [Escherichia coli] dbj BAA15414.1 (D90808) Glucose repression mediator protein. [Escherichia coli] gb AAC74701.1 (AE000258) putative membrane protein [Escherichia coli] Length = 740</p>
SEQ ID n°485	Prot n°PL-1403.1	Contig37	115209	116198	76%	<p>Identities = 221/348 (63%), Positives = 277/348 (79%), Gaps = 1/348 (0%) spiP76182YDGO_ECOLI_HYPOTHETICAL 38.1 KD PROTEIN IN ADD-NTH INTERGENIC REGION pir H64919 probable membrane protein ydgo precursor - Escherichia coli gb AAC74702.1 (AE000258) orf, hypothetical protein [Escherichia coli] Length = 352</p>

TABLEAU I

SEQ ID n°486	Prot n°PL-1404.1	Contig37	114570	115189	78%	<p>Identities = 140/207 (67%), Positives = 168/207 (80%), Gaps = 1/207 (0%) sp P77285 YDGP_ECOLI_HYPOTHETICAL_21.9_KDA_PROTEIN_IN_ADD-NTH_INTERGENIC_REGION pir J64920 conserved hypothetical protein b1631 - Escherichia coli dbj BAA15385.1 (D90806) ORF_ID:0316#10; similar to [SwissProt Accession Number P44291] [Escherichia coli] dbj BAA15392.1 (D90807) ORF_ID:0316#10; similar to [SwissProt Accession Number P44291] [Escherichia coli] dbj BAA15415.1 (D90808) ORF_ID:0316#10; similar to [SwissProt Accession Number P44291] [Escherichia coli] gb AAC74703.1 (AE000258) orf, hypothetical protein [Escherichia coli] Length = 206 "</p>
SEQ ID n°487	Prot n°PL-1405.1	Contig37	113875	114573	78%	<p>Identities = 170/213 (79%), Positives = 192/213 (89%) sp P77179 YDGP_ECOLI_HYPOTHETICAL_24.5_KDA_PROTEIN_IN_ADD-NTH_INTERGENIC_REGION pir J64920 probable membrane protein ydgQ - Escherichia coli dbj BAA15386.1 (D90806) ORF_ID:0316#11; similar to [SwissProt Accession Number P43959] [Escherichia coli] dbj BAA15393.1 (D90807) ORF_ID:0316#11; similar to [SwissProt Accession Number P43959] [Escherichia coli] dbj BAA15416.1 (D90808) ORF_ID:0316#11; similar to [SwissProt Accession Number P43959] [Escherichia coli] gb AAC74704.1 (AE000258) orf, hypothetical protein [Escherichia coli] Length = 231 "</p>
SEQ ID n°488	Prot n°PL-1406.1	Contig37	113235	113873	88%	<p>Identities = 184/209 (88%), Positives = 199/209 (95%) sp P20825 END3_ECOLI_ENDONUCLEASE_III (DNA-APURINIC OR APYRIMIDINIC SITE) LYASE pir J32412 DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) endonuclease III - Escherichia coli pdb 2ABK Refinement Of The Native Structure Of Endonuclease III To A Resolution Of 1.85 Angstrom gb AA24227.1 (J02857) endonuclease III [Escherichia coli] dbj BAA15387.1 (D90806) Deoxyribonuclease (pyrimidine dimer) (EC 3.1.25.1) [Escherichia coli] dbj BAA15394.1 (D90807) Deoxyribonuclease (pyrimidine dimer) (EC 3.1.25.1) [Escherichia coli] dbj BAA15417.1 (D90808) Deoxyribonuclease (pyrimidine dimer) (EC 3.1.25.1) [Escherichia coli] gb AAC74705.1 (AE000258) endonuclease III; specific for apurinic and/or apyrimidinic sites [Escherichia coli]</p>
SEQ ID n°489	Prot n°PL-1407.1	Contig37	111152	113095	80%	<p>Identities = 447/647 (69%), Positives = 525/647 (81%), Gaps = 3/647 (0%) sp P30850 RNB_ECOLI_EXORIBONUCLEASE_II (RIBONUCLEASE II) (RNASE II) pir J64877 exoribonuclease II (EC 3.1.13.1) - Escherichia coli dbj BAA14840.1 (D90766) Exoribonuclease II (EC 3.1.13.1) (Ribonuclease II) (RNase II) [Escherichia coli] dbj BAA14848.1 (D90767) Exoribonuclease II (EC 3.1.13.1) (Ribonuclease II) (RNase II) [Escherichia coli] gb AAC74368.1 (AE000228) RNase II, mRNA degradation</p>

TABLEAU I

SEQ ID n°490	Prot n°PL-1408.1	Contig37	109024	110160	30%	Identities = 78/204 (38%), Positives = 115/204 (56%), Gaps = 2/204 (0%) emb[CAB77347.1] (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°491	Prot n°PL-1409.1	Contig37	107674	108968	24%	Identities = 73/181 (40%), Positives = 108/181 (59%), Gaps = 2/181 (1%) emb[CAB77347.1] (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°492	Prot n°PL-141.1	Contig41	237618	238466	45%	Identities = 83/207 (40%), Positives = 128/207 (61%), Gaps = 20/207 (9%) sp P44012 RN26_HAEIN PROBABLE RIBONUCLEASE H10526 PRECURSOR pir J064009 Hbnuclease homolog H10526 - Haemophilus influenzae (strain Rd KW20) gb AAC22192.1 (U32735) H. influenzae predicted coding region H10526 [Haemophilus influenzae Rd] Length = 272
SEQ ID n°493	Prot n°PL-1410.1	Contig37	106453	107652	26%	Identities = 67/203 (33%), Positives = 107/203 (52%), Gaps = 6/203 (2%) emb[CAB77347.1] (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°494	Prot n°PL-1411.1	Contig37	105130	105840	No Hits found	Identities = 120/568 (21%), Positives = 219/568 (38%), Gaps = 65/568 (11%) emb[CAB77340.1] (AL160331) hypothetical protein SCD8A.19c [Streptomyces coelicolor A3(2)] Length = 643
SEQ ID n°495	Prot n°PL-1412.1	Contig37	103529	105172	39%	
SEQ ID n°496	Prot n°PL-1413.1	Contig37	98545	102651	No Hits found	
SEQ ID n°497	Prot n°PL-1414.1	Contig37	95484	98555	No Hits found	
SEQ ID n°498	Prot n°PL-1415.2	Contig37	94011	95441	No Hits found	
SEQ ID n°499	Prot n°PL-1416.2	Contig37	91920	94001	No Hits found	Identities = 112/258 (43%), Positives = 159/258 (61%), Gaps = 3/258 (1%) emb[CAB77353.1] (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)] Length = 690
SEQ ID n°500	Prot n°PL-1417.1	Contig37	90993	91919	23%	Identities = 45/177 (25%), Positives = 73/177 (40%), Gaps = 32/177 (18%) emb[CAB77354.1] (AL160331) hypothetical protein SCD8A.33c (fragment) [Streptomyces coelicolor A3(2)] Length = 224
SEQ ID n°501	Prot n°PL-1418.1	Contig37	89072	90862	36%	Identities = 123/522 (23%), Positives = 216/522 (40%), Gaps = 59/522 (11%) emb[CAA36717.1] (X52478) dermonecrotic toxin (AA 1-1285) [Pasteurella multocida] Length = 1285
SEQ ID n°502	Prot n°PL-1419.1	Contig37	87824	88819	56%	Identities = 139/282 (49%), Positives = 187/282 (66%), Gaps = 1/282 (0%) gb AAC62582.1 (AF053946) unknown [Yersinia pestis] gb AAC69833.1 (AF074612) Yop targeted effector [Yersinia pestis] emb[CAB54897.1] (AL117189) putative cytotoxic effector protein [Yersinia pestis] Length = 1285
SEQ ID n°503	Prot n°PL-142.1	Contig41	238476	240431	81%	Identities = 442/640 (69%), Positives = 540/640 (84%) sp P53052 CN16_YEREN 2',3'-CYCLIC-NUCLEOTIDE 2'- PHOSPHODIESTERASE PRECURSOR pir S52695.2 3'-cyclic-nucleotide 2'- phosphodiesterase (EC 3.1.4.16) precursor - Yersinia enterocolitica emb[CAA59745.1] (X85742) 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Yersinia enterocolitica] Length = 652

TABLEAU I

SEQ ID n°504	Prot n°PL-1420.1	Contig37	85715	88815	48%	Identities = 110/359 (30%), Positives = 178/359 (48%), Gaps = 30/359 (8%) pir D75096 aspartate aminotransferase (aspb-like1) PAB0774 - Pyrococcus abyssi (strain Orsay) emb CAB50073.1 (AJ248288) aspartate aminotransferase (aspb-like1) [Pyrococcus abyssi] Length = 366
SEQ ID n°505	Prot n°PL-1421.1	Contig37	84951	85733	No Hits found	
SEQ ID n°506	Prot n°PL-1422.1	Contig37	83861	84976	No Hits found	
SEQ ID n°507	Prot n°PL-1423.1	Contig37	81990	83405	37%	Identities = 108/375 (28%), Positives = 178/375 (48%), Gaps = 34/375 (9%) gb AAF94733.1 (AE004235) enterobactin synthetase component F-related protein [Vibrio cholerae] Length = 556
SEQ ID n°508	Prot n°PL-1424.1	Contig37	81151	82035	No Hits found	
SEQ ID n°509	Prot n°PL-1425.2	Contig37	79974	81161		
SEQ ID n°510	Prot n°PL-1426.1	Contig37	79099	79896	40%	Identities = 58/216 (26%), Positives = 109/216 (48%), Gaps = 8/216 (3%) dbj BAB07432.1 (AP001519) glycosyltransferase [Bacillus halodurans] Length = 303
SEQ ID n°511	Prot n°PL-1427.1	Contig37	77173	78264	No Hits found	
SEQ ID n°512	Prot n°PL-1428.1	Contig37	75821	76899	70%	Identities = 167/285 (58%), Positives = 206/285 (71%) sp P16943 YIS5_SHISO INSERTION ELEMENT IS630 HYPOTHETICAL 39 KD PROTEIN (ISO-IS200 39 KD PROTEIN) pir S03415 hypothetical protein - Shigella sonnei insertion sequence IS630 emb CAA29388.1 (X05955) ORF (343 AA) [Shigella sonnei] Length = 343
SEQ ID n°513	Prot n°PL-1429.1	Contig37	74666	75757	45%	Identities = 91/347 (26%), Positives = 184/347 (47%), Gaps = 23/347 (6%) gb AAF94782.1 (AE004241) conserved hypothetical protein [Vibrio cholerae] Length = 458
SEQ ID n°514	Prot n°PL-143.1	Contig41	241003	243915	23%	Identities = 127/509 (24%), Positives = 227/509 (43%), Gaps = 58/509 (11%) sp Q9ZDF8 SYK_RICPR LYSYL-TRNA SYNTHETASE (LYSINE-TRNA LIGASE) (LYSRS) pir D71694 lysine-tRNA ligase (EC 6.1.1.6) (lys) RP371-Rickettsia prowazekii emb CAA14830.1 (AJ236271) LYSYL-TRNA SYNTHETASE (lysS) [Rickettsia prowazekii] Length = 528
SEQ ID n°515	Prot n°PL-1430.1	Contig37	72300	73367	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°516	Prot n°PL-1431.1	Contig37	67156	72096	14%	Identities = 143/527 (27%), Positives = 235/527 (44%), Gaps = 84/527 (15%) dbj BAA34597.1 (AB020025) demonecrotizing toxin [Bordetella bronchiseptica] Length = 1464
SEQ ID n°517	Prot n°PL-1432.1	Contig37	65719	67068	58%	Identities = 180/439 (41%), Positives = 266/439 (60%), Gaps = 8/439 (1%) gb AAF42100.1 (AE002525) conserved hypothetical protein [Neisseria meningitidis MC58] Length = 454
SEQ ID n°518	Prot n°PL-1433.1	Contig37	63812	65194	18%	Identities = 55/191 (28%), Positives = 85/191 (43%), Gaps = 30/191 (15%) sp P56412 Y4DM_RHISN HYPOTHETICAL 45.3 KD PROTEIN Y4DM pir J02776 y4dm protein - Rhizobium sp. plasmid pNGR234a gb AAB91642.1 (AE000069) Y4dm [Rhizobium sp. NGR234] Length =

Unknown, similar to
toxins

TABLEAU I

SEQ ID n°519	Prot n°PL-1434.1	Contig37	62667	63208	40%	<p>Identities = 61/182 (33%), Positives = 87/182 (47%), Gaps = 2/182 (1%) gb AAC25764.1 (AF072709) putative transcriptional regulator [Streptomyces lividans] Length = 192</p> <p>Identities = 174/238 (73%), Positives = 202/238 (84%), Gaps = 1/238 (0%) sp P08244 DCOP_ECOLI ORODINE 5'-PHOSPHATE DECARBOXYLASE (OMP DECARBOXYLASE) (OMPDCase) pir DCECOP orotidine-5-phosphate decarboxylase (EC 4.1.1.23) - Escherichia coli pdb 1EIX C Chain C, Structure Of Orotidine 5'-Monophosphate Decarboxylase From E. Coli, Co-Crystallised With The Inhibitor Bmp pdb 1EIX A Chain A, Structure Of Orotidine 5'-Monophosphate Decarboxylase From E. Coli, Co-Crystallised With The Inhibitor Bmp pdb 1EIX B Chain B, Structure Of Orotidine 5'-Monophosphate Decarboxylase From E. Coli, Co-Crystallised With The Inhibitor Bmp pdb 1EIX D Chain D, Structure Of Orotidine 5'-Monophosphate Decarboxylase From E. Coli, Co-Crystallised With The Inhibitor Bmp gb AAA24483.1 (J02768) orotidine 5'-monophosphate (OMP) decarboxylase (E.C. 4.1.1.23) [Escherichia coli] dbj BAA14835.1 (D90766) Orotidine 5'-phosphate decarboxylase (EC</p>
SEQ ID n°520	Prot n°PL-1435.1	Contig37	61151	61897	80%	
SEQ ID n°521	Prot n°PL-1436.2	Contig37	59937	61106		<p>Identities = 170/196 (86%), Positives = 184/196 (93%) sp P25523 GCH2_ECOLI GTP CYCLOHYDROLASE II pir A40654 GTP cyclohydrolase II (EC 3.5.4.25) - Escherichia coli emb CAA48075.1 (X67876) GTP cyclohydrolase II [Escherichia coli] dbj BAA14831.1 (D90766) GTP cyclohydrolase II (EC 3.5.4.25) [Escherichia coli] gb AAC74359.1 (AE000226) GTP cyclohydrolase II [Escherichia coli] Length = 196</p> <p>Identities = 674/891 (75%), Positives = 762/891 (84%) pir G64875 aconitate hydratase (EC 4.2.1.3) - Escherichia coli gb AAC74358.1 (AE000225) aconitate hydratase 1 [Escherichia coli] Length = 891</p>
SEQ ID n°522	Prot n°PL-1437.1	Contig37	58505	59125	81%	
SEQ ID n°523	Prot n°PL-1438.1	Contig37	55680	58355	84%	
SEQ ID n°524	Prot n°PL-1439.1	Contig37	54600	55427	No Hits found	
SEQ ID n°525	Prot n°PL-144.1	Contig41	244121	245032	87%	<p>Identities = 236/303 (77%), Positives = 271/303 (89%) gb AAB18117.1 (U73857) hypothetical 34.0 kd protein in araJ-aroM intergenic region [Escherichia coli] Length = 325</p> <p>Identities = 277/322 (86%), Positives = 305/322 (94%)</p>
SEQ ID n°526	Prot n°PL-1440.1	Contig37	53450	54424	83%	<p>sp P06613 CYSB_ECOLI CYS REGULON TRANSCRIPTIONAL ACTIVATOR pir RGECB regulatory protein cysB - Escherichia coli gb AAA23642.1 (M15041) cysB regulatory protein [Escherichia coli] gb AAA23643.1 (M34332) cysteine regulatory protein (cysB) [Escherichia coli] dbj BAA14827.1 (D90765) Regulatory protein CysB [Escherichia coli] gb AAC74357.1 (AE000225) positive transcriptional regulator for cysteine regulon</p>

TABLEAU I

SEQ ID n°535	Prot n°PL-1449.1	Contig37	31258	32190	80%	<p>Identities = 231/288 (80%), Positives = 261/288 (90%), Gaps = 4/288 (1%) sp P37766 YCIL_ECOWI_HYPOTHETICAL_32.7_KD_PROTEIN_IN_TRPL-BTUR INTERGENIC_REGION (ORF4) pir H64874 probable pseudouridylylate synthase yciL - Escherichia coli dbj BAA14806.1 (D90764) ORF_ID:0253#9; similar to [SwissProt Accession Number P37765] [Escherichia coli] dbj BAA14821.1 (D90765) ORF_ID:0253#9; similar to [SwissProt Accession Number P37765] [Escherichia coli] gb AAC74351.1 (AE000225) orf, hypothetical protein [Escherichia coli] Length = 291 "</p>
SEQ ID n°538	Prot n°PL-145.1	Contig41	245005	246312	25%	<p>Identities = 69/246 (28%), Positives = 113/246 (45%), Gaps = 30/246 (12%) pir T27927 hypothetical protein ZK593.8 - Caenorhabditis elegans emb CAA93429.1 (Z69385) cDNA EST yk170b8.3 comes from this gene-cDNA EST yk170b8.5 comes from this gene [Caenorhabditis elegans] Length = 517</p>
SEQ ID n°537	Prot n°PL-1450.1	Contig37	25876	30841	34%	<p>Identities = 341/1423 (23%), Positives = 598/1423 (41%), Gaps = 220/1423 (15%) gb AAG05850.1 AE004673_10 (AE004673) hypothetical protein [Pseudomonas aeruginosa] Length = 5627</p>
SEQ ID n°538	Prot n°PL-1451.1	Contig37	23658	24824	33%	<p>Identities = 87/287 (30%), Positives = 130/287 (44%), Gaps = 43/287 (14%) gb AAC61764.1 (AF091998) calpain Lp82 [Mus musculus] Length = 709</p>
SEQ ID n°539	Prot n°PL-1452.1	Contig37	22736	23356	90%	<p>Identities = 159/206 (77%), Positives = 189/206 (91%) sp P45847 YCIO_ECOWI_23.2_KDA_PROTEIN_IN_TRPL-BTUR_INTERGENIC Length = 289</p>
SEQ ID n°540	Prot n°PL-1453.1	Contig37	21848	22708	72%	<p>Identities = 187/281 (66%), Positives = 214/281 (75%) sp O54453 TRPH_SALTY_TRPH_PROTEIN Length = 289</p>
SEQ ID n°541	Prot n°PL-1454.1	Contig37	19778	21646	48%	<p>Identities = 219/530 (41%), Positives = 303/530 (56%), Gaps = 39/530 (7%) emb CAA72201.1 (Y11391) exochitinase [Glossina morsitans S- endosymbiont] Length = 695</p>
SEQ ID n°542	Prot n°PL-1455.1	Contig37	15541	19650	36%	<p>Identities = 341/830 (41%), Positives = 497/830 (59%), Gaps = 34/830 (4%) gb AAC38629.1 (AF047028) insecticidal toxin complex protein TccB [Photobacterium luminescens] Length = 1565</p>
SEQ ID n°543	Prot n°PL-1456.2	Contig37	12048	15569		Unknown, similar to insecticidal toxins
SEQ ID n°544	Prot n°PL-1457.1	Contig37	10314	11951	56%	<p>Identities = 221/521 (42%), Positives = 309/521 (58%), Gaps = 47/521 (9%) emb CAA72201.1 (Y11391) exochitinase [Glossina morsitans S- endosymbiont] Length = 695</p>
SEQ ID n°545	Prot n°PL-1458.1	Contig37	7886	9460	77%	<p>Identities = 342/524 (65%), Positives = 409/524 (77%), Gaps = 4/524 (0%) sp P00895 TRPE_ECOWI_14799.1 (D90764) Anthranilate synthase component I pir NNEC1 anthranilate synthase (EC 4.1.3.27) component I - Escherichia coli dbj BAA14799.1 (D90764) Anthranilate synthase component I (EC 4.1.3.27). [Escherichia coli] dbj BAA14814.1 (D90765) Anthranilate synthase component I (EC 4.1.3.27). [Escherichia coli] gb AAC74346.1 (AE000224) anthranilate synthase component I [Escherichia coli] Length</p>

TABLEAU I

SEQ ID n°546	Prot n°PL-1459.1	Contig37	6296	7294	81%	<p>Identities = 238/331 (71%), Positives = 276/331 (82%)</p> <p>spiP00904 TRPG_ECOLI ANTHRANILATE SYNTHASE COMPONENT II [INCLUDES: GLUTAMINE AMIDOTRANSFERASE; ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE] pir INNEC2 anthranilate synthase (EC 4.1.3.27) component II - Escherichia coli dbj BAA14798.1 (D90784) Anthranilate synthase (EC 4.1.3.27) component II [Escherichia coli] gb AAC74345.1 (AE000224) anthranilate synthase component II, glutamine amidotransferase and phosphoribosylanthranilate transferase [Escherichia coli]</p>	Length
SEQ ID n°547	Prot n°PL-146.1	Contig41	247069	248007	No Hits found	<p>Identities = 289/450 (64%), Positives = 355/450 (78%)</p> <p>spiP00910 TRPC_SALTY TRYPTOPHAN BIOSYNTHESIS PROTEIN TRPCF [INCLUDES: INDOL-3-GLYCEROL PHOSPHATE SYNTHASE (GPS); N-(5'-PHOSPHO-RIBOSYL)ANTHRANILATE ISOMERASE (PRAI)] pir GWEBT indole-3-glycerol-phosphate synthase (EC 4.1.1.48) / phosphoribosylanthranilate isomerase (EC 5.3.1.24) - typhimurium gb AAA27237.1 (M30286) N-(5'-phosphoribosyl)-anthranilic acid isomerase/indole-3-glycerol phosphate synthetase [Salmonella typhimurium] Length = 452 "</p>	
SEQ ID n°548	Prot n°PL-1460.1	Contig37	4929	6293	76%	<p>Identities = 337/393 (85%), Positives = 369/393 (93%) pir TSEBBT tryptophan synthase (EC 4.2.1.20) beta chain - Salmonella typhimurium pdb 1A50 B Chain B, Crystal Structure Of Wild-Type Tryptophan Synthase Complexed With 5-Fluoroindole Propanol Phosphate pdb 2WSY B Chain B, Crystal Structure Of Wild-Type Tryptophan Synthase Length = 396</p>	
SEQ ID n°550	Prot n°PL-1482.2	Contig37	2856	3662		<p>Identities = 819/3041 (26%), Positives = 1369/3041 (44%), Gaps = 448/3041 (14%) gb AAG05850.1 AE004673_10 (AE004673) hypothetical protein [Pseudomonas aeruginosa] Length = 5627</p>	Unknown, similar to toxins
SEQ ID n°551	Prot n°PL-1463.1	Contig39	249	13928	30%	<p>Identities = 240/539 (44%), Positives = 325/539 (59%), Gaps = 12/539 (2%) gb AAF85347.1 AE004062_2 (AE004062) outer membrane hemolysin activator protein [Xylella fastidiosa] Length = 597</p>	
SEQ ID n°552	Prot n°PL-1464.1	Contig39	13975	15681	57%	<p>Identities = 126/215 (58%), Positives = 158/215 (72%), Gaps = 2/215 (0%) spiP18838 SMP_ECOLI SMP PROTEIN PRECURSOR pir A26227 emp protein - Escherichia coli emb CAA26853.1 (X03046) Smp protein [Escherichia coli] gb AAA24635.1 (M30784) ORF [Escherichia coli] gb AAA97283.1 (U14003) smp gene product [Escherichia coli] gb AAC77340.1 (AE000508) orf, hypothetical protein [Escherichia coli]</p>	
SEQ ID n°553	Prot n°PL-1465.1	Contig39	16403	17047	64%		

THIS PAGE BLANK (USPTO)

TABLEAU I

SEQ ID n°554	Prot n°PL-1466.1	Contig39	17163	18140	82%	<p>Identities = 223/320 (69%), Positives = 271/320 (84%)</p> <p>sp P06862 SERB_ECOLI PHOSPHOSERINE PHOSPHATASE (PSP) (O-PHOSPHOSERINE PHOSPHOHYDROLASE) pir PAECS phosphoserine phosphatase (EC 3.1.3.3) - Escherichia coli emb CAA26852.1 (X03046) phosphoserine phosphatase (EC 3.1.3.3) [Escherichia coli] gb AA97284.1 (U14003) phosphoserine phosphatase [Escherichia coli] gb AAC77341.1 (AE000509) 3-phosphoserine phosphatase [Escherichia coli] Length =</p>
SEQ ID n°555	Prot n°PL-1467.1	Contig39	18287	19669	98%	<p>Identities = 423/459 (92%), Positives = 448/459 (97%), Gaps = 1/459 (0%)</p> <p>sp P24554 RADA_ECOLI DNA REPAIR PROTEIN RADA (DNA REPAIR PROTEIN SMS) pir JC1417 DNA repair protein sms - Escherichia coli gb AA97285.1 (U14003) sms gene product [Escherichia coli] emb CAA44856.1 (X63155) sms [Escherichia coli] gb AAC44380.1 (U59449) Rada [Escherichia coli] gb AAC77342.1 (AE000509) probable ATP-dependent protease [Escherichia coli] Length = 460</p>
SEQ ID n°556	Prot n°PL-1468.1	Contig39	19662	20918	85%	<p>Identities = 329/408 (80%), Positives = 367/408 (89%) pir S56614 transcription regulator nadR - Escherichia coli gb AA97286.1 (U14003) nadR gene product [Escherichia coli] gb AAC77343.1 (AE000509) probable nadAB transcriptional regulator [Escherichia coli] Length = 417</p>
SEQ ID n°557	Prot n°PL-1469.1	Contig39	21599	22339	46%	<p>Identities = 84/211 (39%), Positives = 121/211 (56%), Gaps = 3/211 (1%)</p> <p>pir H72342 ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8) gb AAD35787.1 (AE001742) 2 (AE001742) ABC transporter, ATP-binding protein [Thermotoga maritima] Length =</p>
SEQ ID n°558	Prot n°PL-147.1	Contig41	249159	250846	15%	<p>Identities = 58/201 (28%), Positives = 93/201 (45%), Gaps = 36/201 (17%)</p> <p>sp Q9ZFM2 XYNB_BACST BETA-XYLOSIDASE (1,4-BETA-D-XYLAN 1,4-BETA-XYLOSIDASE) (XYLAN 1,4-BETA-XYLOSIDASE) gb AAC98129.1 (AF098273) beta-xylosidase [Bacillus stearothermophilus] Identities = 497/555 (89%), Positives = 530/555 (94%)</p>
SEQ ID n°559	Prot n°PL-1470.1	Contig39	22378	24045	90%	<p>sp P37797 YJUK_ECOLI ABC TRANSPORTER ATP-BINDING PROTEIN YJUK pir F65254 ABC transporter in nadR-sit intergenic region - Escherichia coli (strain K-12) gb AAC77344.1 (AE000509) putative ATP-binding component of a transport system [Escherichia coli] Length = 555</p>
SEQ ID n°560	Prot n°PL-1471.1	Contig39	24518	26458	69%	<p>Identities = 354/637 (55%), Positives = 462/637 (71%), Gaps = 2/637 (0%)</p> <p>pir S56616 soluble lytic transglycosylase - Escherichia coli pir QCECW1 soluble lytic transglycosylase (EC 3.2.1.-) precursor - Escherichia coli gb AA97288.1 (U14003) soluble lytic transglycosylase [Escherichia coli] gb AAC77345.1 (AE000509) soluble lytic murein transglycosylase [Escherichia coli] Length = 654</p>
SEQ ID n°561	Prot n°PL-1472.1	Contig39	27459	28106	85%	<p>Identities = 166/215 (77%), Positives = 188/215 (87%) pir S56619 gpmb protein - Escherichia coli gb AA97291.1 (U14003) Kenn Rudd identifies as gpmb [Escherichia coli] gb AAC77348.1 (AE000509) phosphoglyceromutase 2 [Escherichia coli] Length = 215</p>

TABLEAU I

SEQ ID n°562	Prot n°PL-1473.1	Contig39	28103	28978	72%	<p>Identities = 178/290 (61%), Positives = 214/290 (73%), Gaps = 2/290 (0%) sp P27292 ROB_ECOLI RIGHT ORIGIN-BINDING PROTEIN pir JU0158 right oriC-binding protein - Escherichia coli gb AAA24569.1 (M97495) right origin- binding protein [Escherichia coli] gb AAA97292.1 (U14003) rob gene product [Escherichia coli] gb AAC77349.1 (AE000509) right origin-binding protein [Escherichia coli] Length = 289</p>
SEQ ID n°563	Prot n°PL-1474.1	Contig39	29911	30627	93%	<p>Identities = 221/237 (93%), Positives = 226/237 (95%) sp P03026 ARCA_ECOLI AEROBIC RESPIRATION CONTROL PROTEIN ARCA (DYE RESISTANCE PROTEIN) pir JYECR dye resistance protein - Escherichia coli gb AAA23718.1 (M10044) dye [Escherichia coli] gb AAA97297.1 (U14003) alternate gene names arca, fexA, msp, seg, sfrA; CG Site No. 831 [Escherichia coli] gb AAC77354.1 (AE000610) negative response regulator of genes in aerobic pathways, (sensors, Identities = 667/819 (81%), Positives = 727/819 (88%) dbj BAA38477.1 (D10386) aspartokinase l-homoserine dehydrogenase I [Serratia marcescens] Length = 819</p>
SEQ ID n°564	Prot n°PL-1475.1	Contig39	31438	33897	86%	<p>Identities = 232/309 (75%), Positives = 274/309 (88%) sp P27722 KHSE_SERMA HOMOSERINE KINASE (HK) pir CA7057 homoserine kinase [EC 2.7.1.39] - Serratia marcescens emb CAA43213.1 (X60821) homoserine kinase [Serratia marcescens] dbj BAA38482.1 (D10387) homoserine kinase [Serratia marcescens] Length = 309</p>
SEQ ID n°565	Prot n°PL-1476.1	Contig39	33900	34829	82%	<p>Identities = 349/425 (82%), Positives = 381/425 (89%) sp P27735 THRC_SERMA THREONINE SYNTHASE pir S16043 threonine synthase [EC 4.2.99.2] - Serratia marcescens emb CAA43214.1 (X60821) threonine synthase [Serratia marcescens] dbj BAA01222.1 (D10387) threonine synthase [Serratia marcescens] Length = 429</p>
SEQ ID n°566	Prot n°PL-1477.1	Contig39	34833	36131	87%	<p>Identities = 194/257 (75%), Positives = 219/257 (84%) sp P11288 YAAA_ECOLI PROTEIN YAAA pir Q3ECTC yaaA protein - Escherichia coli dbj BAA01289.1 (D10483) Hypothetical protein 126: PIR:Q3ECTC [Escherichia coli] gb AAC73117.1 (AE000111) orf, hypothetical protein [Escherichia coli] Length = 258</p>
SEQ ID n°567	Prot n°PL-1478.1	Contig39	36182	36958	70%	<p>Identities = 77/381 (20%), Positives = 187/381 (43%), Gaps = 40/381 (10%) emb CAB75089.1 (AL139076) putative integral membrane protein [Campylobacter jejuni] Length = 395</p>
SEQ ID n°568	Prot n°PL-1479.1	Contig39	37456	38670	41%	<p>Identities = 55/200 (27%), Positives = 94/200 (46%), Gaps = 40/200 (20%) sp Q9ZFM2 XYNB_BACST BETA-XYLOSIDASE (1,4-BETA-D-XYLAN XYLOHYDROLASE) (XYLAN 1,4-BETA-XYLOSIDASE) gb AAC98129.1 (AF098273) beta-xylosidase [Bacillus stearothermophilus]</p>

TABLEAU I

SEQ ID n°570	Prot n°PL-1480.1	Contig39	39394	40347	85%	<p>Identities = 269/317 (84%), Positives = 300/317 (93%)</p> <p>sp P30148 TALB_ECOLI_TRANSALDOLASE B pir S40535 transaldolase (EC 2.2.1.2) B - Escherichia coli dbj BAA01290.1 (D10483) transaldolase homolog (SWISS:P15019) [Escherichia coli] gb AAC73119.1 (AE000111) transaldolase B [Escherichia coli] gb AAB47022.1 (S80045) transaldolase B, D-sedoneptulose-7-phosphate:D-glyceraldehyde-3-phosphate dihydroxyacetone transferase (EC 2.2.1.2) [Escherichia coli, K-12, Peptide, 317 aa] dbj BAA21822.1 (D13161) transaldolase [Escherichia coli]</p> <p>Identities = 197/370 (53%), Positives = 274/370 (73%), Gaps = 1/370 (0%)</p> <p>dbj BAB16259.1 (AP002086) similar to orf300 gene (putative AAA-family ATPase gene) In Escherichia coli [Agrobacterium rhizogenes]</p> <p>Identities = 99/287 (34%), Positives = 149/287 (51%), Gaps = 15/287 (5%)</p> <p>dbj BAB16260.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]</p> <p>Length = 752</p>
SEQ ID n°571	Prot n°PL-1481.1	Contig39	42138	43244	68%	
SEQ ID n°572	Prot n°PL-1482.1	Contig39	43214	44191	45%	
SEQ ID n°573	Prot n°PL-1483.1	Contig39	44179	45063	59%	<p>Identities = 133/285 (46%), Positives = 189/285 (65%), Gaps = 4/285 (1%)</p> <p>gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]</p> <p>Length = 300</p>
SEQ ID n°574	Prot n°PL-1484.1	Contig39	45003	46481	61%	<p>Identities = 224/465 (48%), Positives = 301/465 (64%), Gaps = 6/465 (1%)</p> <p>dbj BAB16280.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]</p> <p>Length = 752</p>
SEQ ID n°575	Prot n°PL-1485.1	Contig39	46890	47963	84%	<p>Identities = 271/350 (77%), Positives = 305/350 (86%), gb AAF94749.1 (AE004236) galactose-1-phosphate uridylyltransferase [Vibrio cholerae]</p> <p>Length = 372</p>
SEQ ID n°576	Prot n°PL-1486.1	Contig39	47956	49146	74%	<p>Identities = 268/384 (69%), Positives = 307/384 (79%), gb AAF94749.1 (AE004236) galactokinase [Vibrio cholerae]</p> <p>Length = 405</p>
SEQ ID n°577	Prot n°PL-1487.1	Contig39	49179	50240	64%	<p>Identities = 186/345 (53%), Positives = 236/345 (67%), gb AAF94748.1 (AE004236) aldose 1-epimerase [Vibrio cholerae]</p> <p>Length = 350</p>
SEQ ID n°578	Prot n°PL-1488.1	Contig39	51275	52234	41%	<p>Identities = 84/281 (29%), Positives = 133/281 (46%), Gaps = 9/281 (3%)</p> <p>sp P41755 DHE2_ACHKL_NAD-SPECIFIC GLUTAMATE DEHYDROGENASE (NAD-GDH) pir A53184 glutamate dehydrogenase (EC 1.4.1.2) - Achlya klebsiana gb AAA17563.1 (U02505) NAD-specific glutamate dehydrogenase [Achlya klebsiana]</p> <p>Length = 1063</p>
SEQ ID n°579	Prot n°PL-1489.1	Contig39	51317	53227	94%	<p>Identities = 577/638 (90%), Positives = 602/638 (93%), Gaps = 2/638 (0%)</p> <p>sp Q56073 DNAK_SALTY_DNAK_PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70) gb AAB02910.1 (U58360) DnaK [Salmonella typhimurium]</p> <p>Length = 638</p>
SEQ ID n°580	Prot n°PL-149.1	Contig41	253571	254484	50%	<p>Identities = 106/240 (44%), Positives = 152/240 (63%)</p> <p>gb AAD55884.1 AF130250.1 (AF130250) hypothetical protein [Ralstonia eutropha]</p> <p>Length = 249</p>

TABLEAU I

SEQ ID n°581	Prot n°PL-1490.1	Contig39	52304	53233	33%	<p>Identities = 69/197 (35%), Positives = 105/197 (53%), Gaps = 7/197 (3%) sp P41755 DHE2_ACHKL_NAD-SPECIFIC GLUTAMATE DEHYDROGENASE (NAD-GDH) pir A53184 glutamate dehydrogenase (EC 1.4.1.2) - Achlya klebsiana gb AAA17563.1 (U02505) NAD-specific glutamate dehydrogenase [Achlya klebsiana] Length = 1063</p>
SEQ ID n°582	Prot n°PL-1491.1	Contig39	53341	54459	91%	<p>Identities = 316/376 (84%), Positives = 342/376 (90%), Gaps = 4/376 (1%) sp P08622 DNAJ_ECOLI_DNAJ PROTEIN (HSP40) pir JHHECDJ heat shock protein dnaJ - Escherichia coli gb AAA23693.1 (M12566) heat shock protein dnaJ [Escherichia coli] db JBA001282.1 (D10483) DnaJ [Escherichia coli] gb AAC73126.1 (AE000112) chaperone with DnaK; heat shock protein [Escherichia coli] Length = 376 "</p>
SEQ ID n°583	Prot n°PL-1492.1	Contig39	54556	55863	15%	<p>Identities = 37/149 (24%), Positives = 69/149 (45%), Gaps = 18/149 (12%) sp Q43923 QUIX_ACICA_PUTATIVE PORIN QUIX PRECURSOR pir J39524 probable porin - Acinetobacter calcoaceticus gb AAC37160.1 (L05770) putative porin [Acinetobacter sp. ADP1] Length = 439</p>
SEQ ID n°584	Prot n°PL-1493.1	Contig39	55844	57265	79%	<p>Identities = 333/463 (71%), Positives = 385/463 (82%), Gaps = 1/463 (0%) sp P26206 ARBB_ERWCH_6-PHOSPHO-BETA-GLUCOSIDASE gb AAA24815.1 (M81772) phospho-beta-glucosidase [Pectobacterium chrysanthemi] Length = 465</p>
SEQ ID n°585	Prot n°PL-1494.1	Contig39	57341	58783	69%	<p>Identities = 254/474 (53%), Positives = 335/474 (70%), Gaps = 23/474 (4%) sp P26207 PTBA_ERWCH_PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (EIABC-BGL) (BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EI-BGL) pir B42603 beta-glucoside-specific phosphotransferase system-dependent permease - Erwinia chrysanthemi gb AAA24814.1 (M81772) beta-glucoside permease [Pectobacterium chrysanthemi] Length = 631</p>
SEQ ID n°586	Prot n°PL-1495.1	Contig39	59356	60210	53%	<p>Identities = 102/280 (36%), Positives = 172/280 (61%), Gaps = 6/280 (2%) sp P39805 LIC1_BACSU_TRANSCRIPTION ANTI-TERMINATOR LIC1 pir S47216 transcription antiterminator licT - Bacillus subtilis emb CAA82194.1 (Z28340) antiterminator [Bacillus subtilis] Length = 631</p>
SEQ ID n°587	Prot n°PL-1496.1	Contig39	60398	61450	56%	<p>Identities = 131/326 (40%), Positives = 198/326 (60%), Gaps = 6/326 (1%) sp P40739 PTBA_BACSU_PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (EIABC-BGL) (BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EI-BGL) pir J40406 beta-glucoside permease - Bacillus subtilis emb CAA84286.1 (Z34526) beta-glucoside permease [Bacillus subtilis] Length = 609</p>
SEQ ID n°588	Prot n°PL-1497.1	Contig39	61634	62287	53%	<p>Identities = 70/200 (35%), Positives = 117/200 (58%), Gaps = 10/200 (5%) gb AAAF89975.1 (AF206272_1 (AF206272) beta-glucoside-specific Eli permease [Streptococcus mutans] Length = 644</p>

TABLEAU I

SEQ ID n°589	Prot n°PL-1498.1	Contig39	63402	64568	71%	Identities = 244/386 (63%), Positives = 299/386 (77%), Gaps = 9/386 (2%) gb AAC33562.1 (AF051158) sodium-proton antiporter affecting protein [Vibrio cholerae] gb AAF94778.1 (AE004240) Na ⁺ /H ⁺ antiporter protein [Vibrio cholerae] Length = 382
SEQ ID n°590	Prot n°PL-1499.1	Contig39	64792	65706	81%	Identities = 234/297 (78%), Positives = 263/297 (87%) transcription activator nhaR - Escherichia coli gb AAC73131.1 (AE000112) transcriptional activator of nhaA [Escherichia coli] Length = 301
SEQ ID n°591	Prot n°PL-15.1	Contig41	26793	27692	68%	Identities = 150/297 (50%), Positives = 211/297 (70%) sp P7744 YDAK_ECOLI_HYPOTHETICAL_TRANSCRIPTIONAL REGULATOR_IN_OGT-DBPA_INTERGENIC REGION pir F64883 probable transcription regulator ydaK - Escherichia coli db BAA14941.1 (D90772) tdcABC operon transcriptional activator. [Escherichia coli] db BAA14944.1 (D90773) tdcABC operon transcriptional activator. [Escherichia coli] gb AAC74421.1 (AE000232) putative transcriptional regulator ydaK - Escherichia coli
SEQ ID n°592	Prot n°PL-150.1	Contig41	254456	255826	47%	Identities = 152/374 (40%), Positives = 217/374 (57%), Gaps = 13/374 (3%) pir D68779 antibiotic resistance protein homolog ydaR - Bacillus subtilis db BAA19365.1 (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE. [Bacillus subtilis] emb CAB12338.1 (Z99106) similar to antibiotic resistance protein [Bacillus subtilis] Length = 395
SEQ ID n°593	Prot n°PL-1500.1	Contig39	66391	67335	78%	Identities = 216/307 (70%), Positives = 255/307 (82%), Gaps = 1/307 (0%) sp P08391 RIBF_ECOLI_RIBOFLAVIN_BIOSYNTHESIS_PROTEIN_RIBF [INCLUDES: RIBOFLAVIN KINASE (FLAVOKINASE); FMN ADENYLTRANSFERASE (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE)] pir QQECIL conserved hypothetical protein, 34.8K (rpsT-les intergenic region) - Escherichia coli gb AAC73136.1 (AE000113) putative regulator [Escherichia coli] Length = 313
SEQ ID n°594	Prot n°PL-1501.1	Contig39	67360	70173	88%	Identities = 756/938 (80%), Positives = 837/938 (88%), Gaps = 1/938 (0%) sp P00956 SYL_ECOLI_ISOLEUCYL-TRNA_SYNTHETASE (ISOLEUCINE- TRNA LIGASE) (ILERS) pir ISYECIT isoleucine-tRNA ligase (EC 6.1.1.5) - Escherichia coli gb AAC73137.1 (AE000113) isoleucine tRNA synthetase [Escherichia coli] Length = 938
SEQ ID n°595	Prot n°PL-1502.1	Contig39	71133	72086	83%	Identities = 255/316 (80%), Positives = 283/316 (88%), Gaps = 1/316 (0%) sp P22565 LYTB_ECOLI_LYTB_PROTEIN pir JEO403 lyb protein - Escherichia coli emb CAA38707.1 (X54945) ORF 2 [Escherichia coli] db BAA01307.1 (D10483) hypothetical 34.8K protein (PIR:JEO403) [Escherichia coli] gb AAC73140.1 (AE000113) control of stringent response; involved in penicillin tolerance [Escherichia coli] Length = 316
SEQ ID n°596	Prot n°PL-1503.1	Contig38	72700	73731	No Hits found	

TABLEAU I

SEQ ID n°597	Prot n°PL-1504.1	Contig39	73716	75296	6%	Identities = 23/49 (46%), Positives = 36/49 (72%) pir C71083 probable purine NTPase - Pyrococcus horikoshii dbj BAA30025.1 (AP000004) 870aa long hypothetical purine NTPase [Pyrococcus horikoshii] Length = 879
SEQ ID n°598	Prot n°PL-1505.1	Contig39	75339	76334	No Hits found	Identities = 58/161 (36%), Positives = 86/161 (53%), Gaps = 7/161 (4%) sp P43420 MTB6_BACSP MODIFICATION METHYLASE BSP61 (CYTOSINE-SPECIFIC METHYLTRANSFERASE BSP61) (M.BSP61) pir J40138 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) - Bacillus sp emb CAA57293.1 (X81638) site-specific DNA-methyltransferase (cytosine-specific) [Bacillus sp.] prf J2115288B methyltransferase (Bsp61M [Bacillus sp.]) Length = 315
SEQ ID n°599	Prot n°PL-1506.1	Contig39	76327	77478	22%	Identities = 216/270 (80%), Positives = 242/270 (89%) sp P04036 DAPB_ECOLI DIHYDRODIPICOLINATE REDUCTASE (DHPR) pir JRDCEPD dihydrodipicolinate reductase (EC 1.3.1.26) - Escherichia coli pdb 1ARZ D Chain D, Escherichia coli Dihydrodipicolinate Reductase In Complex With NADH And 2,6 Pyridine Dicarboxylate pdb 1ARZ B Chain B, Escherichia coli Dihydrodipicolinate Reductase In Complex With NADH And 2,6 Pyridine Dicarboxylate pdb 1ARZ C Chain C, Escherichia coli Dihydrodipicolinate Reductase In Complex With NADH And 2,6 Pyridine Dicarboxylate Reductase; Dicarboxylate pdb 1D1H Mol_id: 1; Molecule: Dihydrodipicolinate Reductase; Chain: Null; Ec: 1.3.1.26; Engineered: Yes pdb 1DRW Escherichia coli DhpriNHDH COMPLEX pdb 1DRV Escherichia coli DhpriACNADH COMPLEX pdb 1ARZ A Chain A, Escherichia coli Dihydrodipicolinate Reductase In Complex With NADH And 2,6 Pyridine Dicarboxylate gb AA23666.1
SEQ ID n°600	Prot n°PL-1507.1	Contig39	78237	79076	85%	Identities = 320/377 (84%), Positives = 345/377 (90%) sp P00907 CARA_ECOLI CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN (CARBAMOYL-PHOSPHATE SYNTHETASE GLUTAMINE CHAIN) pir SYECCS carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) small chain - Escherichia coli dbj BAA01310.1 (D10483) carbamoyl-phosphate synthase small chain [Escherichia coli] gb AA23538.1 (J01597) carbamoyl-phosphate synthetase subunit A (tgg start codon) [Escherichia coli] gb AAC73143.1 (AE000113) carbamoyl-phosphate synthetase, glutamine (small) subunit [Escherichia coli] Identities = 98/1072 (92%), Positives = 1029/1072 (95%)
SEQ ID n°601	Prot n°PL-1508.1	Contig39	79495	80658	86%	sp P14846 CARB_SALTY CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN (CARBAMOYL-PHOSPHATE SYNTHETASE AMMONIA CHAIN) gb AAB39256.1 (U81260) carbamoylphosphate synthetase large subunit [Salmonella typhimurium] Length = 1075
SEQ ID n°602	Prot n°PL-1509.1	Contig39	80674	83898	95%	
SEQ ID n°603	Prot n°PL-151.1	Contig41	256148	256759	No Hits found	

TABLEAU I

SEQ ID n°604	Prot n°PL-1510.1	Contig39	83995	84609	70%	<p>Identities = 135/203 (68%), Positives = 165/203 (80%) gb AAG06098.1 AE004699_3 (AE004699) hypothetical protein [Pseudomonas aeruginosa] Length = 204</p>
SEQ ID n°605	Prot n°PL-1511.1	Contig39	85318	86145	79%	<p>Identities = 196/268 (73%), Positives = 221/268 (82%) sp P05637 APAH_ECOLI BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE) (DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE PYROPHOSPHOHYDROLASE) pir J064726 bis(5'-nucleosyl)-tetraphosphatase (symmetrical) (EC 3.6.1.41) - Escherichia coli gb AAC73160.1 (AE000115) diadenosine tetraphosphatase [Escherichia coli]</p>
SEQ ID n°606	Prot n°PL-1512.1	Contig39	86538	87356	89%	<p>Identities = 220/271 (81%), Positives = 247/271 (90%) sp P06992 KSGA_ECOLI DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (16S RRNA DIMETHYLASE) (HIGH LEVEL KASUGAMYCIN RESISTANCE PROTEIN KSGA) (KASUGAMYCIN DIMETHYLTRANSFERASE) pir JX5ECRO rRNA (adenine-N6,N6'-dimethyltransferase (EC 2.1.1.-) - Escherichia coli emb CAA28417.1 (X04711) put. 16S rRNA methyltransferase (ksgA) (AA 1-273) [Escherichia coli] gb AA24049.1 (M11054) methyltransferase (ksgA) [Escherichia coli] db BAA01327.1 (D10483) rRNA (adenosine-N6,N6'-dimethyltransferase [Escherichia coli] gb AAC73162.1 (AE000115) S-adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase [Escherichia coli] prf 1112172A methyltransferase [Escherichia coli]</p>
SEQ ID n°607	Prot n°PL-1513.1	Contig39	87349	88368	79%	<p>Identities = 240/322 (74%), Positives = 271/322 (83%) sp P19624 PDXA_ECOLI PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN PDXA pir JBVECA pyridoxal phosphate biosynthetic protein pdxA - Escherichia coli gb AAA24305.1 (M68521) pdxA [Escherichia coli] gb AAC73163.1 (AE000115) pyridoxine biosynthesis [Escherichia coli]</p>
SEQ ID n°608	Prot n°PL-1514.1	Contig39	88346	88647	79%	<p>Identities = 294/426 (69%), Positives = 361/426 (84%) sp P21202 SURA_ECOLI SURVIVAL PROTEIN SURA PRECURSOR (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SURA) (PPIASE) (ROTAMASE C) pir J064726 probable peptidylprolyl isomerase (EC 5.2.1.8) surA precursor - Escherichia coli gb AAC73164.1 (AE000115) survival protein [Escherichia coli] Length = 428</p>
SEQ ID n°609	Prot n°PL-1515.1	Contig39	89717	92041	79%	<p>Identities = 497/788 (63%), Positives = 616/788 (78%), Gaps = 24/788 (3%) sp P31654 IOSTA_ECOLI ORGANIC SOLVENT TOLERANCE PROTEIN PRECURSOR pir J064726 organic solvent tolerance protein precursor - Escherichia coli gb AAC73165.1 (AE000115) organic solvent tolerance [Escherichia coli] db BAA34130.1 (AB013134) ostA/imp [Escherichia coli] Length = 784</p>

TABLEAU I

SEQ ID n°610	Prot n°PL-1518.1	Contig39	92351	93172	79%	Identities = 187/273 (68%), Positives = 222/273 (80%), Gaps = 2/273 (0%) sp P31680 DULA_ECOLI DNAJ-LIKE PROTEIN DULA pir G64726 yabH protein - Escherichia coli gb AAC73166.1 (AE000116) putative DNA binding protein [Escherichia coli] Length = 271
SEQ ID n°611	Prot n°PL-1517.1	Contig39	93408	94058	80%	Identities = 164/217 (75%), Positives = 181/217 (82%), Gaps = 1/217 (0%) sp P39219 RLUA_ECOLI RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) pir G64727 yabO protein - Escherichia coli gb AAC73169.1 (AE000116) pseudouridylate synthase [Escherichia coli] Length = 219
SEQ ID n°612	Prot n°PL-1518.1	Contig39	94155	97067	88%	Identities = 755/970 (77%), Positives = 872/970 (89%), Gaps = 2/970 (0%) sp P23852 HEPA_ECOLI RNA POLYMERASE ASSOCIATED PROTEIN (ATP-DEPENDENT HELICASE HEPA) pir G64727 probable ATP-dependent helicase hepa - Escherichia coli gb AAC73170.1 (AE000116) probable ATP-dependent RNA helicase [Escherichia coli] Length = 968
SEQ ID n°613	Prot n°PL-1519.1	Contig39	97725	98654	60%	Identities = 141/230 (61%), Positives = 186/230 (80%) sp P31548 YABJ_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YABJ pir G64728 probable ABC-type transport protein - Escherichia coli gb AAC73177.1 (AE000117) putative ATP-binding component of a transport system [Escherichia coli] Length = 232
SEQ ID n°614	Prot n°PL-152.1	Contig41	256767	257885	43%	Identities = 102/352 (28%), Positives = 164/352 (45%), Gaps = 27/352 (7%) pir T36177 probable DNA-binding protein - Streptomyces coelicolor emb CAB41077.1 (AL049645) putative DNA-binding protein [Streptomyces coelicolor A3(2)] Length = 390
SEQ ID n°615	Prot n°PL-1520.1	Contig39	98419	100029	83%	Identities = 380/537 (70%), Positives = 452/537 (83%), Gaps = 1/537 (0%) sp P31549 YABK_ECOLI HYPOTHETICAL 59.6 KD PROTEIN IN ARAC-TBPA INTERGENIC REGION (ORF101) pir G64728 probable membrane protein yabK - Escherichia coli gb AAC73178.1 (AE000117) putative transport system permease protein [Escherichia coli] Length = 536
SEQ ID n°616	Prot n°PL-1521.1	Contig39	100005	100985	77%	Identities = 223/323 (69%), Positives = 265/323 (82%) pir S40584 hypothetical protein - Escherichia coli dbj BAA01338.1 (D10483) sfuA protein homolog (PIR-A35108) [Escherichia coli] gb AAA18833.1 (U09984) thiamin binding protein [Escherichia coli] Length = 323
SEQ ID n°617	Prot n°PL-1522.2	Contig39	101849	103915		
SEQ ID n°618	Prot n°PL-1523.2	Contig39	104168	105043		

TABLEAU I

SEQ ID n°623	Prot n°PL-1528.1	Contig39	119055	120911	68%	<p>Identities = 343/609 (56%), Positives = 428/609 (69%), Gaps = 10/609 (1%) sp P04993 EX5A_ECOLI EXODEOXYRIBONUCLEASE V ALPHA CHAIN (EXODEOXYRIBONUCLEASE V 67 KDA POLYPEPTIDE) pir JNCECF exodeoxyribonuclease V (EC 3.1.11.5) 87K chain - Escherichia coli gb AAB40466.1 (U29581) exonuclease V alpha-subunit [Escherichia coli] gb AAC75858.1 (AE000365) DNA helicase, ATP-dependent dsDNA/ssDNA subunit, ssDNA endonuclease [Escherichia coli] Length = 608</p>
SEQ ID n°624	Prot n°PL-1529.1	Contig39	121777	123912	77%	<p>Identities = 435/704 (61%), Positives = 557/704 (78%), Gaps = 1/704 (0%) gb AAF85196.1 AE004049_1 (AE004049) toxin secretion ABC transporter ATP-binding protein [Xyella fastidiosae] Length = 720 Identities = 151/222 (68%), Positives = 177/222 (79%)</p>
SEQ ID n°625	Prot n°PL-153.1	Contig41	258461	259522	50%	<p>sp P18783 EXBB_ECOLI BIOPOLYMER TRANSPORT EXBB PROTEIN pir BVECBX biopolymer transport exbB protein - Escherichia coli gb AAA69173.1 (U28377) exbB gene product [Escherichia coli] gb AAC76042.1 (AE000383) uptake of enterochelin; tonB-dependent uptake Identities = 199/467 (42%), Positives = 307/467 (63%), Gaps = 8/467 (1%) gb AAF85197.1 AE004049_2 (AE004049) hemolysin secretion protein D [Xyella fastidiosae] Length = 473</p>
SEQ ID n°626	Prot n°PL-1530.1	Contig39	124054	125469	63%	
SEQ ID n°627	Prot n°PL-1531.1	Contig39	124834	125538	No Hits found	
SEQ ID n°628	Prot n°PL-1533.1	Contig39	133735	134490	No Hits found	
SEQ ID n°629	Prot n°PL-1534.1	Contig39	134664	135842	17%	<p>Identities = 47/166 (28%), Positives = 67/166 (40%), Gaps = 29/166 (17%) gb AAD26911.1 AC006429_1 (AC006429) unknown protein [Arabidopsis thaliana] Length = 291</p>
SEQ ID n°630	Prot n°PL-1535.1	Contig39	129589	135981	11%	<p>Identities = 150/522 (28%), Positives = 242/522 (45%), Gaps = 78/522 (14%) gb AAB63525.1 (U12682) celfur protein [Caenorhabditis elegans] Length = 692 Identities = 356/442 (80%), Positives = 397/442 (89%)</p>
SEQ ID n°631	Prot n°PL-1537.1	Contig39	138213	137559	87%	<p>sp P08205 ARGA_ECOLI AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS) pir XYECAG amino acid N-acetyltransferase (EC 2.3.1.1) - Escherichia coli emb CAA68547.1 (Y00492) N-acetylglutamate synthase (AA 1 - 443) [Escherichia coli] gb AAB40465.1 (U29581) N-acetylglutamate synthase [Escherichia coli] gb AAC75857.1 (AE000365) N-acetylglutamate synthase; amino acid Identities = 293/415 (70%), Positives = 351/415 (83%), Gaps = 3/415 (0%) sp Q46929 AMIC_ECOLI N-ACETYL MURAMOYL-L-ALANINE AMIDASE AMIC PRECURSOR Length = 417</p>
SEQ ID n°632	Prot n°PL-1538.1	Contig39	137804	139048	84%	
SEQ ID n°633	Prot n°PL-1539.1	Contig39	140322	141419	77%	<p>Identities = 242/371 (65%), Positives = 298/371 (79%), Gaps = 2/371 (0%) gb AAB40463.1 (U29581) ORF_f432 [Escherichia coli] Length = 432</p>

TABLEAU I

SEQ ID n°634	Prot n°PL-154.1	Contig41	259779	260969	77%	<p>Identities = 253/394 (64%), Positives = 313/394 (79%)</p> <p>sp P08721 METC_ECOLI_CYSTATHIONINE BETA-LYASE (CBL) (BETA-CYSTATHIONINASE) [CYSTEINE LYASE] pir WZECB cystathionine beta-lyase (EC 4.4.1.8) - Escherichia coli pdb 1CL2 A Chain A, Cystathionine Beta-Lyase (Cbl) From Escherichia Coli In Complex With Aminoethoxyvinylglycine pdb 1CL2 B Chain B, Cystathionine Beta-Lyase (Cbl) From Escherichia Coli In Complex With Aminoethoxyvinylglycine gb AA24158.1 (M12858) beta-cystathionase [Escherichia coli] gb AAC76044.1 (AE000383) cystathionine beta-lyase (beta-cystathionase) [Escherichia coli] Identities = 218/268 (81%), Positives = 243/268 (90%)</p>
SEQ ID n°635	Prot n°PL-1540.1	Contig39	141468	142280	88%	<p>sp Q48927 YGD_L_ECOLI_HYPOTHETICAL 28.6 KD PROTEIN IN GCVA-MLTA INTERGENIC REGION pir H65063 hypothetical protein b2812 - Escherichia coli (strain K-12) gb AAB40462.1 (U29581) ORF_268 [Escherichia coli] gb AAC75854.1 (AE000364) putative enzyme [Escherichia coli] Identities = 238/416 (57%), Positives = 299/416 (70%), Gaps = 15/416 (3%)</p>
SEQ ID n°636	Prot n°PL-1541.1	Contig39	142759	144012	69%	<p>pir F65063 hypothetical protein b2810 - Escherichia coli (strain K-12) gb AAB40460.1 (U29581) ORF_0401 [Escherichia coli] gb AAC75852.1 (AE000364) orf, hypothetical protein [Escherichia coli] emb CAB77085.1 (AX000470) unnamed protein product [Escherichia coli] emb CAB77087.1 (AX000474) unnamed protein product [unidentified] emb CAB77089.1 (AX000478) unnamed protein product [unidentified] emb CAC07715.1 (AX018962) unnamed protein product [Escherichia coli] emb CAC07719.1 (AX018970) unnamed protein product [Escherichia coli] emb CAC07721.1 (AX018972) unnamed protein product [Escherichia coli] Length = 401</p>
SEQ ID n°637	Prot n°PL-1542.1	Contig39	144565	145485	87%	<p>Identities = 263/302 (87%), Positives = 284/302 (93%), Gaps = 1/302 (0%)</p> <p>sp P32064 GCVA_ECOLI_GLYCINE CLEAVAGE SYSTEM TRANSCRIPTIONAL ACTIVATOR (GCV OPERON ACTIVATOR) pir J41085 glycine cleavage system transcription activator - Escherichia coli emb CAA51813.1 (X73413) glycine cleavage activator protein [Escherichia coli] gb AAC13742.1 (U01030) GcvA [Escherichia coli] gb AAB40458.1 (U29581) CG Site No. 28676 [Escherichia coli] gb AAC75850.1 (AE000364) positive regulator of gcv operon [Escherichia coli] Length = 305</p>
SEQ ID n°638	Prot n°PL-1543.1	Contig39	145934	147034	84%	<p>Identities = 278/365 (76%), Positives = 315/365 (86%)</p> <p>sp P32066 YGDE_ECOLI_HYPOTHETICAL 41.9 KD PROTEIN IN FUCR-GCVA INTERGENIC REGION (ORF3) pir J41067 hypothetical 41.9K protein (fucR-gcvA intergenic region) - Escherichia coli emb CAA51815.1 (X73413) ORF3 [Escherichia coli] gb AAB40456.1 (U29581) alternate name Orf2 of X73413 and U01030; ORF_266 [Escherichia coli] gb AAC75848.1 (AE000364) orf, hypothetical protein [Escherichia coli]</p>

TABLEAU I

SEQ ID n°639	Prot n°PL-1544.1	Contig39	148207	149661	63%	Identities = 245/468 (52%), Positives = 313/468 (66%), Gaps = 21/468 (4%) pdb 1AKL Alkaline Protease From Pseudomonas Aeruginosa Ifc3080 Length = 470
SEQ ID n°640	Prot n°PL-1545.1	Contig39	150180	151910	83%	Identities = 410/560 (73%), Positives = 483/560 (86%), Gaps = 5/560 (1%) (D49826) LipB [Serratia marcescens] Length = 588
SEQ ID n°641	Prot n°PL-1546.1	Contig39	151950	153305	75%	Identities = 275/428 (64%), Positives = 341/428 (79%), Gaps = 5/428 (1%) (D49826) LipC [Serratia marcescens] Length = 443
SEQ ID n°642	Prot n°PL-1547.1	Contig39	153305	154681	71%	Identities = 239/455 (52%), Positives = 339/455 (73%), Gaps = 5/455 (1%) dbj BAA25796.1 (D49826) LipD [Serratia marcescens] Length = 464
SEQ ID n°643	Prot n°PL-1548.1	Contig39	154678	155442	81%	Identities = 175/247 (70%), Positives = 209/247 (83%), Gaps = 5/247 (2%) EXODEOXYRIBONUCLEASE IX (EXONUCLEASE IX) (EXO IX) pir J65062 potential 5'-3' exonuclease (EC 3.1.11.-) - Escherichia coli (strain K-12) gb AAB40448.1 (U29581) TTG start; ORF_o281 [Escherichia coli] gb AAC76840.1 (AE000363) 5'-3' exonuclease [Escherichia coli] Length = 281 "
SEQ ID n°644	Prot n°PL-1549.1	Contig39	155500	158867	83%	Identities = 352/453 (77%), Positives = 402/453 (88%), Gaps = 1/453 (0%) sp P37350 YGDH_ECOLI_HYPOTHETICAL 51.0 KD PROTEIN IN BARA- SDAC INTERGENIC REGION pir G65081 hypothetical protein in sdaC 5'region - Escherichia coli (strain K-12) gb AAB40445.1 (U29581) TTG start; alternate gene name ygdH; ORF_o455 [Escherichia coli] gb AAC75837.1 (AE000363) orf, hypothetical protein [Escherichia coli] Identities = 139/219 (63%), Positives = 174/219 (78%)
SEQ ID n°645	Prot n°PL-155.1	Contig41	262107	262778	77%	sp P33196 YGH_B_ECOLI_HYPOTHETICAL 24.1 KD PROTEIN IN METC-SUFI INTERGENIC REGION pir G65087 hypothetical 24.1 kD protein in metC-sufi intergenic region - Escherichia coli (strain K-12) gb AAA69176.1 (U28377) ORF_o219; alternate name yghB [Escherichia coli] gb AAC76045.1 (AE000363) orf, hypothetical protein [Escherichia coli] Length = 219 "
SEQ ID n°646	Prot n°PL-1550.1	Contig39	156990	157838	76%	Identities = 203/283 (71%), Positives = 232/283 (81%), Gaps = 2/283 (0%) sp Q46920 YQCD_ECOLI_HYPOTHETICAL 32.6 KD PROTEIN IN SYD-SDAC INTERGENIC REGION pir J65061 hypothetical protein b2794 - Escherichia coli (strain K-12) gb AAB40444.1 (U29581) ORF_o282 [Escherichia coli] gb AAC75836.1 (AE000363) orf, hypothetical protein [Escherichia coli] Length = 282
SEQ ID n°647	Prot n°PL-1551.1	Contig39	159396	160166	68%	Identities = 178/262 (67%), Positives = 213/262 (80%), Gaps = 5/262 (1%) sp Q47417 YQCB_ERWCA_EXOENZYME REGULATION REGULON ORF1 pir S45107 hypothetical protein 1 - Erwinia carotovora emb CAA55982.1 (X79474) ORF1 [Erwinia carotovora] Length = 376
SEQ ID n°648	Prot n°PL-1552.1	Contig39	160658	161278	No Hits found	

TABLEAU I

SEQ ID n°649	Prot n°PL-1553.1	Contig39	162738	163562	89%	<p>Identities = 242/274 (88%), Positives = 258/274 (93%)</p> <p>sp P03948 DAPD_ECOLI 2,3,4,5-TETRAHYDROPYRIDINE-2-CARBOXYLATE N-SUCCINYLTRANSFERASE (TETRAHYDRODIPICOLINATE N-SUCCINYLTRANSFERASE) (THP SUCCINYLTRANSFERASE) (TETRAHYDRODIPICOLINATE SUCCINYLASE) pir XNECSD 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [EC 2.3.1.117] - Escherichia coli dbj BAA05610.1 (D26562) 'tetrahydropyridine N-succinyltransferase' [Escherichia coli] gb AAB08595.1 (U70214) tetrahydropyridine N-succinyltransferase [Escherichia coli] gb AAC73277.1 (AE000126) 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [Escherichia coli] Length = 274</p>
SEQ ID n°650	Prot n°PL-1554.1	Contig39	163734	166523	77%	<p>Identities = 605/881 (68%), Positives = 721/881 (81%), Gaps = 2/881 (0%)</p> <p>sp P27249 GLND_ECOLI [PROTEIN-PII] URIDYLTRANSFERASE (PII URIDYLTRANSFERASE) (URIDYL REMOVING ENZYME) (UTASE) pir G64740 uridylyltransferase (EC 2.7.7.59) - Escherichia coli gb AAB08596.1 (U70214) PII uridylyltransferase [Escherichia coli] gb AAC73278.1 (AE000126) protein PII, uridylyltransferase acts on regulator of <i>qlnA</i> [Escherichia coli] Length = 890</p>
SEQ ID n°651	Prot n°PL-1555.1	Contig39	166520	167317	83%	<p>Identities = 214/266 (80%), Positives = 242/266 (90%), Gaps = 2/266 (0%)</p> <p>sp P10882 AMPM_SAL.TY METHIONINE AMINOPEPTIDASE (MAP) (PEPTIDASE M) pir S12027 methionyl aminopeptidase (EC 3.4.11.18) - Salmonella typhimurium emb CAA39298.1 (X55778) peptidase M [Salmonella typhimurium] Length = 264</p>
SEQ ID n°652	Prot n°PL-1556.1	Contig39	167749	168474	92%	<p>Identities = 225/241 (93%), Positives = 234/241 (96%)</p> <p>sp P02351 RS2_ECOLI 30S RIBOSOMAL PROTEIN S2 pir JR3EC2 ribosomal protein S2 - Escherichia coli emb CAA23631.1 (V00343) ribosomal protein S2 [Escherichia coli] dbj BAA05613.1 (D26562) 'ribosomal protein S2' [Escherichia coli] gb AAB08598.1 (U70214) ribosomal protein S2 [Escherichia coli] gb AAC73280.1 (AE000126) 30S ribosomal subunit protein S2 [Escherichia coli] Length = 241</p>
SEQ ID n°653	Prot n°PL-1557.1	Contig39	168625	169476	82%	<p>Identities = 211/284 (74%), Positives = 252/284 (88%), Gaps = 2/284 (0%)</p> <p>sp P02997 EFTS_ECOLI ELONGATION FACTOR TS (EF-TS) pir JEFECS translation elongation factor EF-Ts - Escherichia coli emb CAA23632.1 (V00343) elongation factor Ts [Escherichia coli] dbj BAA05614.1 (D26562) 'elongation factor EF-Ts' [Escherichia coli] gb AAB08599.1 (U70214) elongation factor EF-Ts [Escherichia coli] gb AAC73281.1 (AE000126) protein chain elongation factor EF-Ts [Escherichia coli] dbj BAA77845.1 (D83536) Translation elongation factor TS [Escherichia coli] Length = 283</p>

TABLEAU I

SEQ ID n°654	Prot n°PL-1558.1	Contig39	169631	170359	85%	<p>Identities = 213/239 (89%), Positives = 230/239 (96%)</p> <p>sp P29484 PYRH_ECOLI URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) (SMBA PROTEIN) p I BA45269 uridine 5'-monophosphate kinase (EC 2.7.4.-) - Escherichia coli db JBA002598.1 (D13334) SmbA [Escherichia coli] db JBA005615.1 (D26562) 'mukB suppressor protein smbA' [Escherichia coli] gb AAB08600.1 (U70214) uridine 5'-monophosphate (UMP) kinase [Escherichia coli] gb AAC73282.1 (AE000126) uridylylate kinase [Escherichia coli] db JBA077846.1 (D83536) MukB suppressor protein. [Escherichia coli] Identities = 275/393 (69%), Positives = 322/393 (80%) sp P45568 DXR_ECOLI 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP REDUCTOISOMERASE) p I E64741 yaeM protein - Escherichia coli gb AAB08602.1 (U70214) hypothetical [Escherichia coli] gb AAC73284.1 (AE000126) putative ATP-binding component of a transport system [Escherichia coli] db JBA032426.1 (AB013300) 1-deoxy-D-xylulose 5-phosphate reductoisomerase [Escherichia coli] Length = 398</p>
SEQ ID n°655	Prot n°PL-1559.1	Contig39	171302	172498	77%	<p>Identities = 177/273 (64%), Positives = 220/273 (79%)</p> <p>sp Q46857 YQHE_ECOLI HYPOTHETICAL OXIDOREDUCTASE IN METC-SUFI INTERGENIC REGION Length = 275</p>
SEQ ID n°656	Prot n°PL-156.1	Contig41	263178	264056	74%	<p>Identities = 168/242 (69%), Positives = 203/242 (83%), Gaps = 4/242 (1%)</p> <p>sp Q47675 UPPS_ECOLI UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYL-CISTRANSFERASE) p I F64741 conserved hypothetical protein b0174 - Escherichia coli gb AAC73285.1 (AE000127) orf, hypothetical protein [Escherichia coli] Length = 253</p>
SEQ ID n°657	Prot n°PL-1560.1	Contig39	172713	173477	79%	<p>Identities = 148/245 (60%), Positives = 183/245 (74%)</p> <p>sp P08486 CDSA_ECOLI PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) (CDP-DG SYNTHETASE) p I SYECDG phosphatidate cytidylyltransferase (EC 2.7.41) - Escherichia coli gb AAA23545.1 (M11330) CDP-diglyceride synthetase [Escherichia coli] gb AAB08604.1 (U70214) phosphatidate cytidylyltransferase [Escherichia coli] gb AAC73286.1 (AE000127) CDP-diglyceride synthetase [Escherichia coli] db JBA077850.1 (D83536) Phosphatidate cytidylyltransferase (EC 2.7.41) [Escherichia coli]</p>
SEQ ID n°658	Prot n°PL-1561.1	Contig39	173487	174335	63%	

TABLEAU I

SEQ ID n°659	Prot n°PL-1562.1	Contig39	174364	175719	81%	<p>Identities = 303/450 (67%), Positives = 371/450 (82%), Gaps = 1/450 (0%) sp P37764 YAEI_ECOLI_HYPOTHETICAL 49.1 KD PROTEIN IN GDSA-HLPA INTERGENIC REGION pir H64741 yaeI protein - Escherichia coli gb AA080605.1 (U70214) hypothetical [Escherichia coli] gb AAC73287.1 (AE000127) orf, hypothetical protein [Escherichia coli] db BAA77851.1 (D83536) Hypothetical 49.1 kd protein in cdsA-hlpA intergenic region. [Escherichia coli] Length = 450</p>
SEQ ID n°660	Prot n°PL-1563.1	Contig39	175754	178147	96%	<p>Identities = 764/797 (95%), Positives = 777/797 (96%) emb CAB51929.1 (AJ236620) outer membrane antigen [Photobacterium luminescens] Length = 787</p>
SEQ ID n°661	Prot n°PL-1564.1	Contig39	178258	178755	77%	<p>Identities = 159/165 (96%), Positives = 161/165 (97%) emb CAB51930.1 (AJ236620) periplasmic protein [Photobacterium luminescens] Length = 165</p>
SEQ ID n°662	Prot n°PL-1565.1	Contig39	178759	179787	88%	<p>Identities = 278/340 (81%), Positives = 304/340 (88%) sp P32203 LPXD_YEREN UDP-3-O-[3-HYDROXYMYRISTOYL] GLUCOSAMINE N-ACYLTRANSFERASE (FIRA PROTEIN) (RIFAMPICIN RESISTANCE PROTEIN) pir S41752 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-) - Yersinia enterocolitica emb CAA80951.1 (Z25463) FIRA [Yersinia enterocolitica]</p>
SEQ ID n°663	Prot n°PL-1566.1	Contig39	180283	181035	No Hits found	<p>Identities = 213/267 (79%), Positives = 242/267 (89%), Gaps = 5/267 (1%) sp P72215 LPXA_PROMI ACYL-CARRIER-PROTEIN-UDP-N-ACETYLGLUCOSAMINE O-ACYLTRANSFERASE (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE) emb CAA70456.1 (Y09263) lpxA [Proteus mirabilis] Length = 267</p>
SEQ ID n°665	Prot n°PL-1568.1	Contig39	181214	182383	85%	<p>Identities = 310/377 (82%), Positives = 336/377 (88%) pir SYECLA lipid-A-disaccharide synthase (EC 2.4.1.182) - Escherichia coli gb AA080611.1 (U70214) lipid A disaccharide synthase [Escherichia coli] gb AAC73293.1 (AE000127) tetraacyldisaccharide-1-P; lipid A biosynthesis, penultimate step [Escherichia coli] Length = 382</p>
SEQ ID n°666	Prot n°PL-1569.1	Contig39	183015	186509	93%	<p>Identities = 996/1160 (85%), Positives = 1090/1160 (93%) sp P14567 DP3A_SALTY DNA POLYMERASE III, ALPHA CHAIN pir A45915 DNA-directed DNA polymerase (EC 2.7.7.7) III alpha chain - Salmonella typhimurium gb AA27057.1 (M28701) polymerase III polymerase subunit (dnaE) [Salmonella typhimurium] Length = 1160</p>
SEQ ID n°667	Prot n°PL-157.1	Contig41	264191	265612	79%	<p>Identities = 319/471 (67%), Positives = 381/471 (80%), Gaps = 2/471 (0%) sp P26848 SUFL_ECOLI_SUFU PROTEIN PRECURSOR pir G65088 sufl protein precursor - Escherichia coli gb AAA69185.1 (U28377) periplasmic protein [Escherichia coli] gb AAC76053.1 (AE000384) suppressor of ftsI [Escherichia coli] Length = 470</p>

TABLEAU I

SEQ ID n°668	Prot n°PL-1570.1	Contig39	186502	187482	92%	<p>Identities = 277/318 (87%), Positives = 304/318 (95%)</p> <p>sp P30867 ACCA_ECOLI ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT ALPHA pir A43452 acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase alpha chain - Escherichia coli gb AAA70370.1 (M96394) acetyl-CoA carboxylase [Escherichia coli] gb AAB08614.1 (U70214) acetyl-CoA carboxylase alpha subunit [Escherichia coli] dbj BAA08425.1 (D49445) AccA, alpha subunit of acetyl-CoA carboxylase [Escherichia coli] gb AAC73296.1 (AE000127) acetyl-CoA carboxylase, carboxyltransferase component, alpha subunit [Escherichia coli]</p> <p>Identities = 228/432 (52%), Positives = 289/432 (65%), Gaps = 4/432 (0%)</p> <p>sp P52097 MESJ_ECOLI PUTATIVE CELL CYCLE PROTEIN MESJ pir D64743 cell cycle protein mesJ - Escherichia coli emb CAA90751.1 (Z50870) similar to Acc.No. D26185 [Escherichia coli] dbj BAA08428.1 (D49445) YaeN [Escherichia coli] gb AAB08617.1 (U70214) hypothetical [Escherichia coli] gb AAC73299.1 (AE000128) cell cycle protein [Escherichia coli] dbj BAA77863.1 (D83536) Cell cycle protein MesJ. [Escherichia coli]</p> <p>Length = 432</p>
SEQ ID n°669	Prot n°PL-1571.1	Contig39	187821	189149	84%	<p>Identities = 88/210 (41%), Positives = 127/210 (59%), Gaps = 13/210 (6%)</p> <p>sp P40710 CUTF_ECOLI COPPER HOMEOSTASIS PROTEIN CUTF PRECURSOR (LIPROTEIN NLPE) pir H64743 copper homeostasis protein cutF precursor - Escherichia coli gb AAA86093.1 (U18345) NlpE precursor [Escherichia coli] gb AAA82972.1 (L38619) lipoprotein [Escherichia coli] dbj BAA08433.1 (D49445) NlpE, a lipoprotein [Escherichia coli] gb AAB08620.1 (U70214) lipoprotein NlpE [Escherichia coli] gb AAC73303.1 (AE000128) copper homeostasis protein (lipoprotein) [Escherichia coli] dbj BAA77868.1 (D83536) Copper homeostasis protein CutF precursor (lipoprotein NlpE). [Escherichia coli]</p> <p>Length = 236</p> <p>Identities = 469/570 (82%), Positives = 526/570 (92%)</p> <p>pir YPEC proline-tRNA ligase (EC 6.1.1.15) - Escherichia coli gb AAB08622.1 (U70214) proline-tRNA ligase [Escherichia coli] gb AAC73305.1 (AE000128) proline tRNA synthetase [Escherichia coli]</p> <p>Length = 572</p>
SEQ ID n°670	Prot n°PL-1572.1	Contig39	189771	190454	54%	
SEQ ID n°671	Prot n°PL-1573.1	Contig39	190556	192274	91%	<p>Identities = 152/234 (64%), Positives = 184/234 (77%)</p> <p>sp P28634 YAEB_ECOLI HYPOTHETICAL 26.4 KDA PROTEIN IN PROS-RCSF INTERGENIC REGION (ORF3) pir C64744 yaeB protein - Escherichia coli dbj BAA03656.1 (D15061) ORF235 [Escherichia coli] gb AAB08623.1 (U70214) hypothetical [Escherichia coli] gb AAC73306.1 (AE000128) orf, hypothetical protein [Escherichia coli] dbj BAA77871.1 (D83536) Hypothetical 26.4 kd protein in pros-rsf intergenic region (orf3). [Escherichia coli]</p>
SEQ ID n°672	Prot n°PL-1574.1	Contig39	192400	193107	75%	

TABLEAU I

SEQ ID n°673	Prot n°PL-1575.1	Contig39	193645	194460	94%	<p>Identities = 232/271 (85%), Positives = 258/271 (94%)</p> <p>sp P28635 YAEI_ECOLI PUTATIVE LIPOPROTEIN YAEI PRECURSOR pir E64744 probable lipoprotein yaeC - Escherichia coli dbj BAA03657.1 (D15061) ORF271 [Escherichia coli] gb AAB08625.1 (U70214) hypothetical [Escherichia coli] gb AAC73308.1 (AE000129) putative lipoprotein [Escherichia coli] dbj BAA77874.1 (D83536) Hypothetical 29.4 kd lipoprotein in rcsF-abc intergenic region precursor. [Escherichia coli] Length =</p>
SEQ ID n°674	Prot n°PL-1576.1	Contig39	194528	195179	92%	<p>Identities = 187/217 (86%), Positives = 206/217 (94%)</p> <p>sp P31547 YAEI_ECOLI HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN YAEI pir F64744 probable transport protein yaeE - Escherichia coli gb AAB08626.1 (U70214) hypothetical [Escherichia coli] gb AAC73309.1 (AE000129) putative transport system permease protein [Escherichia coli] dbj BAA77875.1 (D83536) Hypothetical 23.3 kd protein in rcsF-abc intergenic region. [Escherichia coli] Length =</p>
SEQ ID n°675	Prot n°PL-1577.1	Contig39	195172	196203	88%	<p>Identities = 265/343 (77%), Positives = 307/343 (89%) sp P30750 ABC_ECOLI ATP-BINDING PROTEIN ABC pir G64744 probable ABC-type transport protein abc - Escherichia coli gb AAB08627.1 (U70214) ATP-binding protein [Escherichia coli] gb AAC73310.1 (AE000129) ATP-binding component of a transporter [Escherichia coli] Length = 343</p>
SEQ ID n°676	Prot n°PL-1578.1	Contig39	196399	196965	72%	<p>Identities = 135/188 (71%), Positives = 160/188 (84%)</p> <p>sp P31546 YAEI_ECOLI HYPOTHETICAL 21.3 KD PROTEIN IN ABC-RRSH INTERGENIC REGION pir H64744 yaeD protein - Escherichia coli gb AAB08628.1 (U70214) hypothetical [Escherichia coli] gb AAC73311.1 (AE000129) putative phosphatase [Escherichia coli] dbj BAA77877.1 (D83536) Hypothetical 21.3 kd protein in abc-rmH intergenic region. [Escherichia coli] dbj BAA93568.1 (AB035926) phosphatase [Escherichia coli] Length = 256</p>
SEQ ID n°677	Prot n°PL-1579.1	Contig39	399087	399794	69%	<p>Identities = 147/225 (65%), Positives = 175/225 (77%), Gaps = 5/225 (2%)</p> <p>gb AAF93764.1 (AE004144) sugar fermentation stimulation protein [Vibrio cholerae] Length = 256</p>
SEQ ID n°678	Prot n°PL-158.1	Contig41	266017	266745	79%	<p>Identities = 163/241 (67%), Positives = 196/241 (80%), Gaps = 1/241 (0%)</p> <p>sp P26647 PLSC_ECOLI 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT) pir S20460 1-acylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51) - Escherichia coli gb AAA24397.1 (M63491) 1-acyl-glycerol-3-phosphate acyltransferase [Escherichia coli] gb AAA69186.1 (U28377) 1-acyl- glycerol-3-phosphate acyltransferase [Escherichia coli] gb AAC76054.1 (AE000384) 1-acyl-sn-glycerol-3-phosphate acyltransferase</p>

TABLEAU I

SEQ ID n°879	Prot n°PL-1580.1	Contig39	397423	398373	68%	<p>Identities = 187/294 (63%), Positives = 224/294 (75%)</p> <p>sp P27305 YADB_ECOLI HYPOTHETICAL 34.9 KD PROTEIN IN PCNB-DKSA INTERGENIC REGION pir H64737 glutamate--rRNA ligase homolog yadB - Escherichia coli (strain K-12) gb AAC73255.1 (AE000123) putative tRNA synthetase [Escherichia coli] Length = 308</p>
SEQ ID n°680	Prot n°PL-1581.1	Contig39	395630	397395	72%	<p>Identities = 343/513 (66%), Positives = 385/513 (74%), Gaps = 49/513 (9%)</p> <p>sp P13685 PCNB_ECOLI POLY(A) POLYMERASE (PAP) (PLASMID COPY NUMBER PROTEIN) Length = 472</p>
SEQ ID n°681	Prot n°PL-1582.1	Contig39	394447	395238	82%	<p>Identities = 182/264 (68%), Positives = 219/264 (82%), Gaps = 1/264 (0%)</p> <p>pir A47152 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) - Escherichia coli emb CAA46505.1 (X65538) 3-methyl-2-oxobutanoate hydroxymethyltransferase [Escherichia coli] Length = 264</p>
SEQ ID n°682	Prot n°PL-1583.1	Contig39	393566	394420	83%	<p>Identities = 189/282 (67%), Positives = 238/282 (84%)</p> <p>sp P31663 PANC_ECOLI PANTOATE--BETA-ALANINE LIGASE (PANTOTHENATE SYNTHETASE) (PANTOATE ACTIVATING ENZYME) pir E64736 pantoate--beta-alanine ligase (EC 6.3.2.1) - Escherichia coli gb AA24272.1 (L17086) pantothenate synthetase [Escherichia coli] gb AAC73244.1 (AE000122) pantothenate synthetase</p>
SEQ ID n°683	Prot n°PL-1584.1	Contig39	392269	393039	88%	<p>Identities = 197/256 (76%), Positives = 227/256 (87%)</p> <p>sp P36880 YADH_ECOLI HYPOTHETICAL 28.5 KD PROTEIN IN HPT-PAND INTERGENIC REGION pir H64735 probable ABC-2-type transport protein yadH - Escherichia coli gb AAC73239.1 (AE000122) orf, hypothetical protein [Escherichia coli] Length = 256</p>
SEQ ID n°684	Prot n°PL-1585.1	Contig39	391346	392257	88%	<p>Identities = 242/304 (79%), Positives = 268/304 (87%)</p> <p>sp P36879 YADG_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YADG pir S45204 probable ABC-type transport protein yagD - Escherichia coli db BAA05583.1 (D26562) 'ORF' [Escherichia coli] gb AAC73238.1 (AE000122) putative ATP-binding component of a transport system [Escherichia coli] Length = 308</p>
SEQ ID n°685	Prot n°PL-1586.1	Contig39	390505	391155	84%	<p>Identities = 156/215 (72%), Positives = 185/215 (85%)</p> <p>sp P36857 YADF_ECOLI HYPOTHETICAL 25.1 KD PROTEIN IN HPT-PAND INTERGENIC REGION pir F64735 yadF protein - Escherichia coli gb AAC73237.1 (AE000122) putative carbonic anhydrase (EC 4.2.1.1)</p>
SEQ ID n°686	Prot n°PL-1587.1	Contig39	381284	382450	55%	<p>Identities = 145/385 (37%), Positives = 223/385 (57%), Gaps = 8/385 (2%)</p> <p>gb AAF42125.1 (AE002528) hypothetical protein [Neisseria meningitidis MC58] Length = 384</p>
SEQ ID n°687	Prot n°PL-1588.1	Contig39	379827	380795	60%	<p>Identities = 188/314 (53%), Positives = 213/314 (67%), Gaps = 4/314 (1%)</p> <p>emb CAB84714.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis] emb CAB84719.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis] Length = 321</p>

TABLEAU I

SEQ ID n°688	Prot n°PL-1589.1	Contig39	378834	378857	45%	Identities = 89/217 (41%), Positives = 139/217 (64%) emb[CAC08936.1] (AX024121) unnamed protein product [Neisseria gonorrhoeae] Length = 229
SEQ ID n°689	Prot n°PL-159.1	Contig41	266768	268035	90%	Identities = 615/752 (81%), Positives = 682/752 (89%), Gaps = 5/752 (0%) gb/AAF80006.1 (AF227858.1) (AF227858) DNA topoisomerase IV subunit [Serratia marcescens] Length = 756
SEQ ID n°690	Prot n°PL-1590.1	Contig39	376835	378928	69%	Identities = 355/684 (51%), Positives = 490/684 (70%), Gaps = 3/684 (0%) gb/AAF61810.1 (AF129811) unknown [Moraxella catarrhalis] Length =
SEQ ID n°691	Prot n°PL-1591.1	Contig39	373798	374577	No Hits found	Identities = 337/519 (64%), Positives = 402/519 (76%), Gaps = 10/519 (1%) sp P36840 YACK_ECOLI_PROBABLE BLUE-COPPER PROTEIN YACK PRECURSOR pir C84735 probable copper-binding protein yack - Escherichia coli gb AAC73234.1 (AE000121) orf, hypothetical protein [Escherichia coli] Length = 516
SEQ ID n°693	Prot n°PL-1593.1	Contig39	370104	370973	81%	Identities = 219/283 (77%), Positives = 244/283 (85%) sp P09158 SPEE_ECOLI_SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE) (SPDSY) pir SYECSD spermidine synthase (EC 2.5.1.16) - Escherichia coli gb AAA24643.1 (J02804) spermidine synthase [Escherichia coli] dbj BAA05577.1 (D26562) 'spermidine synthase' [Escherichia coli] gb AAC73232.1 (AE000121) spermidine synthase = putrescine aminopropyltransferase [Escherichia coli] Length =
SEQ ID n°694	Prot n°PL-1594.1	Contig39	369271	370065	91%	Identities = 209/264 (79%), Positives = 244/264 (92%) sp P09159 DCAM_ECOLI_S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) pir DCECDM adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - Escherichia coli gb AAA24644.1 (J02804) S-adenosylmethionine decarboxylase [Escherichia coli] gb AAC73231.1 (AE000121) S-adenosylmethionine decarboxylase [Escherichia coli] dbj BAA05576.1 (D26562) 'adenosylmethionine decarboxylase proenzyme' [Escherichia coli] Length = 264
SEQ ID n°695	Prot n°PL-1595.1	Contig39	366609	368552	No Hits found	Identities = 205/286 (71%), Positives = 237/286 (82%) gb AAC44684.1 (U65015) putative aldolase [Vibrio furnissii] Length = 287
SEQ ID n°696	Prot n°PL-1596.1	Contig39	365748	366608	81%	Identities = 167/273 (61%), Positives = 218/273 (79%) gb AAC44681.1 (U65015) PTS permease for mannose subunit IIBMan [Vibrio furnissii] Length = 293
SEQ ID n°697	Prot n°PL-1597.1	Contig39	364388	365281	66%	Identities = 153/284 (57%), Positives = 201/284 (75%), Gaps = 10/284 (3%) gb AAC44680.1 (U65015) PTS permease for mannose subunit IIPMan [Vibrio furnissii] Length = 258
SEQ ID n°698	Prot n°PL-1598.1	Contig39	363601	364398	75%	

TABLEAU I

SEQ ID n°699	Prot n°PL-1599.1	Contig39	361895	363142	51%	Identities = 154/379 (40%), Positives = 214/379 (56%), Gaps = 28/379 (7%) sp P42907 AGAS_ECOLI PUTATIVE TAGATOSE-6-PHOSPHATE KETOSE/ALDOSE ISOMERASE pir D65103 agas protein - Escherichia coli (strain K-12) gb AAA57939.1 (U18997) ORF_o384 [Escherichia coli] gb AAC76170.1 (AE000395) putative tagatose-6-phosphate aldose/ketose isomerase [Escherichia coli] Length = 384
SEQ ID n°700	Prot n°PL-16.1	Contig41	28230	29297	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db BAB08239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°701	Prot n°PL-160.1	Contig41	269077	270972	92%	Identities = 568/631 (88%), Positives = 591/631 (93%), Gaps = 1/631 (0%) sp P20083 PARE_ECOLI TOPOISOMERASE IV SUBUNIT B pir D65090 topoisomerase IV subunit (EC 5.99.1.-) - Escherichia coli gb AAA69198.1 (U28377) topoisomerase IV subunit [Escherichia coli] gb AAC76066.1 (AE000385) DNA topoisomerase IV subunit B [Escherichia coli] Length = 630
SEQ ID n°702	Prot n°PL-1600.1	Contig39	360627	361922	65%	Identities = 241/424 (56%), Positives = 300/424 (69%), Gaps = 1/424 (0%) sp P42903 AGAZ_ECOLI PUTATIVE TAGATOSE 6-PHOSPHATE KINASE AGAZ pir H65102 probable tagatose 6-phosphate kinase agaz (EC 2.7.1.-) - Escherichia coli (strain K-12) gb AAA57935.1 (U18997) ORF_o426 [Escherichia coli] gb AAC76166.1 (AE000394) putative tagatose 6-phosphate kinase 2 [Escherichia coli] gb AAF81082.1 (AF228498) KbaZ [Escherichia coli] Length = 426
SEQ ID n°703	Prot n°PL-1601.1	Contig39	359818	360591	61%	Identities = 113/255 (44%), Positives = 163/255 (63%), Gaps = 2/255 (0%) sp P42902 AGAR_ECOLI PUTATIVE AGA OPERON TRANSCRIPTIONAL REPRESSOR pir G65102 probable transcription repressor of aga operon - Escherichia coli (strain K-12) gb AAA57834.1 (U18997) ORF_o269 [Escherichia coli] gb AAC76165.1 (AE000394) putative DEOR-type transcriptional regulator of aga operon [Escherichia coli] gb AAF81081.1 (AF228498) 1 (AF228498) Agar [Escherichia coli] Length = 269
SEQ ID n°704	Prot n°PL-1602.1	Contig39	358261	359418	69%	Identities = 205/386 (53%), Positives = 273/386 (70%), Gaps = 8/386 (2%) emb CAA63264.1 (X92508) ES-beta-lactamase [Klebsiella pneumoniae] Length = 382
SEQ ID n°705	Prot n°PL-1603.1	Contig39	356864	358180	20%	Identities = 57/205 (27%), Positives = 90/205 (43%), Gaps = 13/205 (6%) gb AAD10476.2 (U37262) phospholipase A1 [Serratia sp. MK1] Length = 320
SEQ ID n°706	Prot n°PL-1604.1	Contig39	353337	355589	41%	Identities = 207/576 (35%), Positives = 312/576 (53%), Gaps = 13/576 (2%) gb AAC32475.1 (AF044503) VgrG protein [Escherichia coli] Length =
SEQ ID n°707	Prot n°PL-1605.1	Contig39	351976	353378	No Hits found	

TABLEAU I

SEQ ID n°708	Prot n°PL-1606.1	Contig39	350814	351971	30%	Identities = 71/289 (24%), Positives = 119/289 (40%), Gaps = 15/289 (5%) gb AAG04210.1 AE004517_5 (AE004517) hypothetical protein [Pseudomonas aeruginosa] Length = 382
SEQ ID n°709	Prot n°PL-1607.1	Contig39	349236	350477	43%	Identities = 145/236 (61%), Positives = 180/236 (75%), Gaps = 3/236 (1%) sp P55220 VRP2_SALEN 65 KD VIRULENCE PROTEIN dbj BA003383.1 (D14490) SpvB [Salmonella enteritidis] Length = 591
SEQ ID n°710	Prot n°PL-1608.1	Contig39	346966	348366	No Hits found	Identities = 68/289 (23%), Positives = 123/289 (42%), Gaps = 15/289 (5%) gb AAG04210.1 AE004517_5 (AE004517) hypothetical protein [Pseudomonas aeruginosa] Length = 382
SEQ ID n°711	Prot n°PL-1609.1	Contig39	345804	348961	31%	Identities = 146/190 (76%), Positives = 166/190 (86%) sp P38653 YQIA_ECOLI HYPOTHETICAL 21.8 KD PROTEIN IN PARE-ICC INTERGENIC REGION (F193) pir E65090 hypothetical 15.2 kD protein in lcc 3'region - Escherichia coli (strain K-12) gb AA69199.1 (U28377) ORF_f193 [Escherichia coli] gb AAC76067.1 (AE000385) orf, hypothetical protein [Escherichia coli] Length = 193
SEQ ID n°713	Prot n°PL-1610.1	Contig39	344622	345803	31%	Identities = 66/289 (23%), Positives = 123/289 (42%), Gaps = 15/289 (5%) gb AAG04210.1 AE004517_5 (AE004517) hypothetical protein [Pseudomonas aeruginosa] Length = 362
SEQ ID n°714	Prot n°PL-1611.1	Contig39	341743	342375	72%	Identities = 122/207 (58%), Positives = 154/207 (73%), Gaps = 1/207 (0%) gb AAF96582.1 (AE004397) transcriptional regulator UhpA [Vibrio cholerae] Length = 208
SEQ ID n°715	Prot n°PL-1612.1	Contig39	340202	341791	62%	Identities = 221/511 (43%), Positives = 331/511 (64%), Gaps = 20/511 (3%) gb AAF96583.1 (AE004397) sensor protein UhpB [Vibrio cholerae] Length = 527
SEQ ID n°716	Prot n°PL-1613.1	Contig39	338788	340128	65%	Identities = 228/424 (53%), Positives = 301/424 (70%) gb AAF96584.1 (AE004397) regulatory protein UhpC [Vibrio cholerae] Length = 436
SEQ ID n°717	Prot n°PL-1614.1	Contig39	337740	338771	79%	Identities = 246/345 (71%), Positives = 285/345 (82%), Gaps = 8/345 (2%) gb AAF96585.1 (AE004398) iron(III) ABC transporter, periplasmic iron-compound-binding protein [Vibrio cholerae] Length = 344
SEQ ID n°718	Prot n°PL-1615.1	Contig39	335552	337753	78%	Identities = 488/679 (71%), Positives = 578/679 (84%) gb AAF96586.1 (AE004398) iron(III) ABC transporter, permease protein [Vibrio cholerae] Length = 700
SEQ ID n°719	Prot n°PL-1616.1	Contig39	334481	335536	87%	Identities = 282/347 (81%), Positives = 314/347 (90%), Gaps = 1/347 (0%) sp P37009 AFUC_ECOLI PUTATIVE FERRIC TRANSPORT ATP-BINDING PROTEIN AFUC Length = 348
SEQ ID n°720	Prot n°PL-1617.1	Contig39	328964	333412	36%	Identities = 412/857 (48%), Positives = 548/857 (63%), Gaps = 29/857 (3%) gb AAC38629.1 (AF047028) insecticidal toxin complex protein TccB [Photobacterium luminescens] Length = 1565
SEQ ID n°721	Prot n°PL-1618.2	Contig39	326003	328948		Unknown, similar to insecticidal toxins
SEQ ID n°722	Prot n°PL-1619.2	Contig39	323432	325741		

TABLEAU I

SEQ ID n°723	Prot n°PL-162.1	Contig41	271782	272821	74%	Identities = 174/279 (62%), Positives = 215/279 (76%), Gaps = 4/279 (1%) sp P36650 ICC_ECOLI ICC PROTEIN pir F65090 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) cpdA - Escherichia coli (strain K-12) dbj BAA03989.1 (D16557) lcc [Escherichia coli] gb AAC76068.1 (AE000385) regulator of lacZ [Escherichia coli] Length = 275
SEQ ID n°724	Prot n°PL-1620.1	Contig39	322114	323082	84%	Identities = 225/317 (70%), Positives = 276/317 (86%) pir T41325 probable serine-threonine dehydratase - fission yeast (Schizosaccharomyces pombe) pir T41287 probable serine/threonine dehydratase - fission yeast (Schizosaccharomyces pombe) emb CAA18316.1 (AL022245) putative serine/threonine dehydratase [Schizosaccharomyces pombe] emb CAA20920.1 (AL031603) putative serine-threonine dehydratase. [Schizosaccharomyces pombe] Length = 323
SEQ ID n°725	Prot n°PL-1621.1	Contig39	321315	321847	No Hits found	Identities = 210/398 (52%), Positives = 286/399 (71%), Gaps = 3/399 (0%) sp P55808 Y4OU RHISN HYPOTHETICAL PROTEIN Y4OU PRECURSOR gb AAB91807.1 (AE000089) Y4ou [Rhizobium sp. NGR234] Length = 399/413 (74%), Positives = 358/413 (85%) sp P22308 IMTR_ECOLI TRYPTOPHAN-SPECIFIC TRANSPORT PROTEIN (TRYPTOPHAN PERMEASE) pir A39187 tryptophan-specific permease - Escherichia coli gb AAA24182.1 (M59862) tryptophan-specific permease [Escherichia coli] gb AAA24183.1 (M58338) tryptophan-specific permease [Escherichia coli] gb AAA57984.1 (U18987) tryptophan-specific permease [Escherichia coli] gb AAC76195.1 (AE000397) tryptophan-specific transport protein [Escherichia coli] Length = 414
SEQ ID n°726	Prot n°PL-1622.1	Contig39	319755	320999	68%	Identities = 397/466 (85%), Positives = 429/466 (91%), Gaps = 4/466 (0%) sp Q59342 TNAA_ENTAE TRYPTOPHANASE (L-TRYPTOPHAN INDOLYLASE) (TNASE) dbj BAA03249.1 (D14297) tryptophanase [Enterobacter aerogenes] Length = 462
SEQ ID n°727	Prot n°PL-1623.1	Contig39	318163	319407	84%	Identities = 198/435 (45%), Positives = 282/435 (64%), Gaps = 4/435 (0%) emb CAB75255.1 (AL139075) putative integral membrane protein [Campylobacter jejuni] Length = 438
SEQ ID n°728	Prot n°PL-1624.1	Contig39	318652	318052	84%	Identities = 135/246 (54%), Positives = 171/246 (68%), Gaps = 11/246 (4%) sp P16250 HIS4_STRCO PHOSPHORIBOSYLFORMIMINO-6-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE pir JQ0641 N-(5'-phospho-D-riboseylformimino)-5-amino-1-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16) - Streptomyces coelicolor gb AAA26760.1 (M31628) isomerase (hisA) [Streptomyces coelicolor] emb CAB51442.1 (AL096884) phosphoribosylformimino-5-aminoimidazole carboxamide isomerase [Streptomyces coelicolor A3(2)] Length = 240
SEQ ID n°729	Prot n°PL-1625.1	Contig39	313938	315278	62%	
SEQ ID n°730	Prot n°PL-1626.1	Contig39	312251	313027	64%	
SEQ ID n°731	Prot n°PL-1627.1	Contig39	311046	312299	No Hits found	

TABLEAU I

SEQ ID n°732	Prot n°PL-1628.1	Contig39	310384	311049	65%	Identities = 103/220 (46%), Positives = 145/220 (65%), Gaps = 4/220 (1%) emb CAB8091.1 (AL355774) putative phosphatase [Streptomyces coelicolor A3(2)] Length = 223
SEQ ID n°733	Prot n°PL-1629.1	Contig39	308946	310205	56%	Identities = 149/425 (35%), Positives = 240/425 (56%), Gaps = 15/425 (3%) emb CAB84293.1 (AL162754) putative adenylosuccinate synthetase [Neisseria meningitidis] Length = 432
SEQ ID n°734	Prot n°PL-163.1	Contig41	272721	273362	78%	Identities = 149/208 (71%), Positives = 170/208 (81%) sp P36851 YQIE_ECOLI_HYPOTHETICAL_23.7_KD_PROTEIN_IN_ICC-TOLC_INTERGENIC_REGION_(F209) pir H65090 hypothetical protein b3034 - Escherichia coli (strain K-12) gb AAA69202.1 (U28377) ORF_209 [Escherichia coli] gb AAC76070.1 (AE000385) orf, hypothetical protein
SEQ ID n°735	Prot n°PL-1630.1	Contig39	307158	308354	No Hits found	Identities = 357/879 (40%), Positives = 499/879 (56%), Gaps = 58/879 (6%) sp P30130 FIMD_ECOLI_OUTER_MEMBRANE_USHER_PROTEIN_FIMD_PRECURSOR pir S56542 outer membrane usher protein fimD precursor - Escherichia coli gb AAA97213.1 (U14003) CG Site No. 18349 [Escherichia coli] gb AAC77273.1 (AE000502) outer membrane protein; export and assembly of type 1 fimbriae, interrupted [Escherichia coli] Length = 11/231 (30%), Positives = 11/231 (47%), Gaps = 33/231 (14%) emb CAB01713.1 (Z78535) type 1 fimbrial chaperone [Proteus mirabilis] Length = 225
SEQ ID n°737	Prot n°PL-1632.1	Contig39	303495	304382	37%	Identities = 74/238 (31%), Positives = 119/238 (49%), Gaps = 17/238 (7%) gb AAD26595.1 (AF012835) chaperone protein AafD [Escherichia coli] Length = 241
SEQ ID n°738	Prot n°PL-1633.1	Contig39	302745	303494	46%	Identities = 78/207 (37%), Positives = 122/207 (58%), Gaps = 11/207 (5%) pir S36632 molecular chaperone fimC - Salmonella typhi emb CAA52682.1 (X74602) fimC [Salmonella typhi] Length = 237
SEQ ID n°739	Prot n°PL-1634.1	Contig39	301411	302139	44%	
SEQ ID n°740	Prot n°PL-1635.1	Contig39	299265	300434	No Hits found	Identities = 357/878 (40%), Positives = 507/878 (57%), Gaps = 56/878 (6%) sp P30130 FIMD_ECOLI_OUTER_MEMBRANE_USHER_PROTEIN_FIMD_PRECURSOR pir S56542 outer membrane usher protein fimD precursor - Escherichia coli gb AAA97213.1 (U14003) CG Site No. 18349 [Escherichia coli] gb AAC77273.1 (AE000502) outer membrane protein; export and assembly of type 1 fimbriae, interrupted [Escherichia coli] Length = 61/188 (32%), Positives = 102/188 (53%), Gaps = 24/188 (12%) sp P46008 FOCC_ECOLI_CHAPERONE_PROTEIN_FOCC_PRECURSOR pir I41062 periplasmic chaperone focC protein - Escherichia coli emb CAA86604.1 (Z46635) focC [Escherichia coli] Length = 227
SEQ ID n°741	Prot n°PL-1636.1	Contig39	296488	299133	57%	
SEQ ID n°742	Prot n°PL-1637.1	Contig39	295585	296407	37%	

TABLEAU I

SEQ ID n°743	Prot n°PL-1639.1	Contig39	294842	295594	44%	Identities = 74/207 (35%), Positives = 111/207 (52%), Gaps = 10/207 (4%) sp P46008 FOCC_ECOLI_CHAPERONE_PROTEIN_FOCC_PRECURSOR pir J141002 periplasmic chaperone focC protein - Escherichia coli emb CAA86604.1 (Z46635) focC [Escherichia coli] Length = 227
SEQ ID n°744	Prot n°PL-164.1	Contig41	273722	275095	82%	Identities = 321/447 (71%), Positives = 383/447 (84%), Gaps = 4/447 (0%) emb CAA87138.1 (X98513) HAS ABC exporter outer membrane component [Seratia marcescens] Length = 500
SEQ ID n°745	Prot n°PL-1640.1	Contig39	293418	294254	41%	Identities = 79/211 (37%), Positives = 116/211 (54%), Gaps = 6/211 (2%) gb AAC45720.1 (AF022140) F17a-D [Escherichia coli] Length = 240
SEQ ID n°746	Prot n°PL-1641.1	Contig39	290841	291656	72%	Identities = 147/273 (53%), Positives = 186/273 (70%), Gaps = 5/273 (1%) emb CAB61439.1 (Z32686) mrpH [Proteus mirabilis] Length = 275
SEQ ID n°747	Prot n°PL-1642.1	Contig39	288565	289182	40%	Identities = 55/170 (32%), Positives = 83/170 (48%), Gaps = 20/170 (11%) sp P42185 PRSH_ECOLI_PRS_FIMBRIAL_MINOR_PLIN_PROTEIN PRECURSOR pir J525205 fimbrial protein prsH - Escherichia coli (strain 1442) emb CAA44092.1 (X62157) prsH [Escherichia coli] Length = 195
SEQ ID n°748	Prot n°PL-1643.1	Contig39	287815	288564	83%	Identities = 158/248 (63%), Positives = 210/249 (83%) emb CAA83636.1 (Z32686) mrpD [Proteus mirabilis] Length = 252
SEQ ID n°749	Prot n°PL-1644.1	Contig39	285175	287691	75%	Identities = 528/827 (63%), Positives = 663/827 (79%), Gaps = 6/827 (0%) emb CAA83635.1 (Z32686) mrpC [Proteus mirabilis] Length = 871
SEQ ID n°750	Prot n°PL-1645.1	Contig39	283945	284484	67%	Identities = 115/179 (64%), Positives = 141/179 (78%), Gaps = 4/179 (2%) sp Q03011 MRPA_PROMI_MAJOR_MRP_FIMBRIA_PROTEIN_PRECURSOR pir J40643 MRP_fimbriae, major fimbrial subunit - Proteus mirabilis emb CAA79244.1 (Z18753) MRP major fimbrial subunit polypeptide [Proteus mirabilis] emb CAA83633.1 (Z32686) mrpA [Proteus mirabilis] Length = 175
SEQ ID n°751	Prot n°PL-1646.1	Contig39	282689	283261	78%	Identities = 143/183 (78%), Positives = 165/183 (90%) emb CAB61438.1 (Z32686) MrpI [Proteus mirabilis] Length = 188
SEQ ID n°752	Prot n°PL-1647.1	Contig39	280816	281535	38%	Identities = 71/160 (44%), Positives = 92/160 (57%), Gaps = 4/160 (2%) emb CAB54047.1 (AJ245436) hypothetical protein, 21.8 kD [Pseudomonas putida] Length = 192
SEQ ID n°753	Prot n°PL-1648.1	Contig39	278564	279457	No Hits found	
SEQ ID n°754	Prot n°PL-1649.1	Contig39	277879	278589	No Hits found	
SEQ ID n°755	Prot n°PL-165.1	Contig41	276121	276873	75%	Identities = 163/233 (69%), Positives = 190/233 (80%), Gaps = 11/233 (4%) sp P24195 YGIB_ECOLI_HYPOTHETICAL_24.9_KD_PROTEIN_IN_TOLC-RIBB INTERGENIC_REGION (ORF) (0234) pir J522360 hypothetical protein D - Escherichia coli gb AAA71875.1 (M77129) ORF [Escherichia coli] gb AAA89205.1 (U28377) ORF_o234; alternate name ygiB; orf of M77129 [Escherichia coli] gb AAC76073.1 (AE000386) orf, hypothetical protein [Escherichia coli] Length = 234 "

TABLEAU I

SEQ ID n°756	Prot n°PL-1650.1	Contig39	276807	277895	38%	Identities = 85/304 (27%), Positives = 138/304 (44%), Gaps = 31/304 (10%) emb CAB11012.1 (Z98271) hypothetical protein MLCB1779.31 [Mycobacterium leprae] Length = 400	
SEQ ID n°757	Prot n°PL-1651.1	Contig39	275402	276820	34%	Identities = 85/393 (21%), Positives = 164/393 (41%), Gaps = 31/393 (7%) pir JH70158 conserved hypothetical integral membrane protein BB0473 - Lyme disease spirochete gb AAC66867.1 (AE001152) conserved hypothetical integral membrane protein [Borrelia burgdorferi] Length = 454	
SEQ ID n°758	Prot n°PL-1652.1	Contig39	273789	275397	46%	Identities = 154/520 (29%), Positives = 248/520 (47%), Gaps = 23/520 (4%) pir A69831 probable acid-CoA ligase (EC 6.2.1.-) vhl - Bacillus subtilis emb CAA74533.1 (Y14083) hypothetical protein [Bacillus subtilis] emb CAB12867.1 (Z99109) similar to long-chain fatty-acid-CoA ligase [Bacillus subtilis] Length = 513	
SEQ ID n°759	Prot n°PL-1653.1	Contig39	272729	273850	45%	Identities = 97/369 (26%), Positives = 170/369 (45%), Gaps = 35/369 (9%) gb AACG07782.1 (AE004853_5 (AE004853) probable RND efflux membrane fusion protein precursor [Pseudomonas aeruginosa] Length = 376	
SEQ ID n°760	Prot n°PL-1654.1	Contig39	269691	272732	56%	Identities = 355/1012 (35%), Positives = 590/1012 (58%), Gaps = 10/1012 (0%) gb AAF93340.1 (AE004106) multidrug resistance protein, putative [Vibrio cholerae] Length = 1036	
SEQ ID n°761	Prot n°PL-1655.1	Contig39	268747	269715	42%	Identities = 73/330 (22%), Positives = 137/330 (41%), Gaps = 32/330 (9%) spi P30790 FABH_RHOCA 3-OXOACYL-ACYL-CARRIER-PROTEIN SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) pir C41608 hypothetical protein 3 (hima 5' region) - Rhodobacter capsulatus gb AAA26127.1 (M84030) ORF3; putative [Rhodobacter capsulatus] Length = 324 "	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°762	Prot n°PL-1656.1	Contig39	267185	268753	50%	Identities = 169/509 (33%), Positives = 262/509 (51%), Gaps = 24/509 (4%) gb AAF94733.1 (AE004235) enterobactin synthetase component F-related protein [Vibrio cholerae] Length = 558	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°763	Prot n°PL-1657.1	Contig39	265886	266848	24%	Identities = 44/197 (22%), Positives = 80/197 (40%), Gaps = 45/197 (22%) pir S76481 hypothetical protein - Synechocystis sp. (strain PCC 6803) db BAA18610.1 (D90915) hypothetical protein [Synechocystis sp.] Length = 538	
SEQ ID n°764	Prot n°PL-1658.1	Contig39	264979	265941	No hits found	Identities = 63/263 (23%), Positives = 121/263 (45%), Gaps = 11/263 (4%) sp O67185 FABH_AQUAE 3-OXOACYL-ACYL-CARRIER-PROTEIN SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) pir F70394 3-oxoacyl-acyl-carrier-protein synthase III - Aquifex aeolicus gb AAC07144.1 (AE000723) 3-oxoacyl-acyl-carrier-protein synthase III [Aquifex aeolicus] Length = 309	
SEQ ID n°765	Prot n°PL-1659.1	Contig39	264035	264982	38%		

TABLEAU I

SEQ ID n°766	Prot n°PL-166.1	Contig41	276880	278040	88%	<p>Identities = 292/386 (75%), Positives = 345/386 (88%)</p> <p>sp P24198 YGC_ECOLI_HYPOTHETICAL 45.0 KD PROTEIN IN TOLC-RIBB INTERGENIC REGION (ORFA) (O386) pir S22361 hypothetical protein A - Escherichia coli gb AAAT1876.1 (M77129) ORFA [Escherichia coli] gb AAAG9206.1 (U28377) ORF_o386; alternate name ygiC; orfA of M77129 [Escherichia coli] gb AAC76074.1 (AE000385) putative synthetase/amidase [Escherichia coli] Length = 386 "</p>
SEQ ID n°767	Prot n°PL-1660.1	Contig39	262435	263697	47%	<p>Identities = 120/400 (30%), Positives = 200/400 (50%), Gaps = 18/400 (4%)</p> <p>sp Q67282 DCDA_AQUAE DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE) pir JC70404 diaminopimelate decarboxylase (EC 4.1.1.20) - Aquifex aeolicus gb AAC07208.1 (AE000728) diaminopimelate decarboxylase [Aquifex aeolicus] Length = 420</p>
SEQ ID n°768	Prot n°PL-1661.1	Contig39	260045	260809	39%	<p>Identities = 64/222 (28%), Positives = 100/222 (44%), Gaps = 31/222 (13%)</p> <p>sp Q46897 YGC_ECOLI_HYPOTHETICAL 22.3 KD PROTEIN IN IAP-CYSH INTERGENIC REGION pir H65056 hypothetical protein b2758 - Escherichia coli (strain K-12) gb AAA69266.1 (U29579) ORF_f199 [Escherichia coli] gb AAC75798.1 (AE000359) orf, hypothetical protein [Escherichia coli] Length = 199</p>
SEQ ID n°769	Prot n°PL-1662.1	Contig39	259273	260148	32%	<p>Identities = 70/167 (41%), Positives = 95/167 (55%), Gaps = 18/167 (10%)</p> <p>sp Q46898 YGC_ECOLI_HYPOTHETICAL 25.2 KDA PROTEIN IN IAP-CYSH INTERGENIC REGION PRECURSOR Length = 224</p>
SEQ ID n°770	Prot n°PL-1663.1	Contig39	258318	259391	45%	<p>Identities = 107/316 (33%), Positives = 163/316 (50%), Gaps = 34/316 (10%)</p> <p>sp Q46899 YGC_ECOLI_HYPOTHETICAL 40.0 KD PROTEIN IN IAP-CYSH INTERGENIC REGION pir B65057 hypothetical protein b2758 - Escherichia coli (strain K-12) gb AAA69266.1 (U29579) ORF_f363 [Escherichia coli] gb AAC75800.1 (AE000359) orf, hypothetical protein [Escherichia coli] Length = 363</p>
SEQ ID n°771	Prot n°PL-1664.1	Contig39	256130	257755	22%	<p>Identities = 73/296 (24%), Positives = 120/296 (39%), Gaps = 18/296 (5%)</p> <p>sp Q46901 YGC_ECOLI_HYPOTHETICAL 55.9 KDA PROTEIN IN IAP-CYSH INTERGENIC REGION pir D65057 hypothetical protein b2760 - Escherichia coli (strain K-12) gb AAA69270.1 (U29579) ORF_f502 [Escherichia coli] gb AAC75802.1 (AE000359) orf, hypothetical protein [Escherichia coli] Length = 502</p>
SEQ ID n°772	Prot n°PL-1665.1	Contig39	253419	256136	41%	<p>Identities = 244/823 (29%), Positives = 373/823 (44%), Gaps = 104/823 (12%)</p> <p>sp P38036 YGC_ECOLI_HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION pir E65057 hypothetical protein in cysH 3' region - Escherichia coli (strain K-12) gb AAA69271.1 (U29579) alternate gene name ygeB; ORF_f888 [Escherichia coli] gb AAC75803.1 (AE000359) orf, hypothetical protein [Escherichia coli] Length = 888 "</p>
SEQ ID n°773	Prot n°PL-1666.2	Contig39	251443	252897	No Hits found	
SEQ ID n°774	Prot n°PL-1667.1	Contig39	249267	250310		

TABLEAU I

SEQ ID n°775	Prot n°PL-1668.1	Contig39	246822	247979	47%	Identities = 128/309 (41%), Positives = 183/309 (58%), Gaps = 11/309 (3%) gb AAG05299.1 AE004617_3 (AE004617) probable transmembrane sensor [Pseudomonas aeruginosa] Length = 316
SEQ ID n°776	Prot n°PL-1668.1	Contig39	244132	246756	49%	Identities = 275/637 (29%), Positives = 433/937 (45%), Gaps = 144/937 (15%) gb AAG08282.1 AE004902_10 (AE004902) hypothetical protein [Pseudomonas aeruginosa] Length = 989
SEQ ID n°777	Prot n°PL-167.1	Contig41	278152	279219	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) dbj BAB08239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°778	Prot n°PL-1670.1	Contig39	242781	243794	72%	Identities = 198/329 (60%), Positives = 245/329 (74%) dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] Length = 345
SEQ ID n°779	Prot n°PL-1671.1	Contig39	241438	242580	27%	Identities = 72/271 (26%), Positives = 103/271 (37%), Gaps = 40/271 (14%) pir T37097 probable secreted neuraminidase - Streptomyces coelicolor emb CAB52948.1 (AL109950) putative secreted neuraminidase [Streptomyces coelicolor A3(2)] Length = 748
SEQ ID n°780	Prot n°PL-1672.1	Contig39	239785	240927	25%	Identities = 61/267 (22%), Positives = 96/267 (35%), Gaps = 62/267 (23%) pir T34699 hypothetical protein SC1C3.07 SC1C3.07 - Streptomyces coelicolor emb CAA19231.1 (AL023702) hypothetical protein SC1C3.07 [Streptomyces coelicolor A3(2)] Length = 373
SEQ ID n°781	Prot n°PL-1673.1	Contig39	238173	239309	29%	Identities = 75/291 (25%), Positives = 112/291 (37%), Gaps = 28/291 (9%) pir T37097 probable secreted neuraminidase - Streptomyces coelicolor emb CAB52948.1 (AL109950) putative secreted neuraminidase [Streptomyces coelicolor A3(2)] Length = 748
SEQ ID n°782	Prot n°PL-1674.1	Contig39	236598	237755	29%	Identities = 79/289 (27%), Positives = 114/289 (39%), Gaps = 22/289 (7%) pir T37097 probable secreted neuraminidase - Streptomyces coelicolor emb CAB52948.1 (AL109950) putative secreted neuraminidase [Streptomyces coelicolor A3(2)] Length = 748
SEQ ID n°783	Prot n°PL-1675.1	Contig39	234805	235968	31%	Identities = 82/336 (24%), Positives = 122/336 (35%), Gaps = 38/336 (11%) pir T37097 probable secreted neuraminidase - Streptomyces coelicolor emb CAB52948.1 (AL109950) putative secreted neuraminidase [Streptomyces coelicolor A3(2)] Length = 748
SEQ ID n°784	Prot n°PL-1676.1	Contig39	231618	232804	64%	Identities = 191/400 (47%), Positives = 284/400 (70%), Gaps = 1/400 (0%) sp O34884 YOAB_BACSU PUTATIVE TRANSPORTER YOAB pir ID69895 conserved hypothetical protein yoab - Bacillus subtilis gb AAB84444.1 (AF027868) putative transporter [Bacillus subtilis] emb CAB13747.1 (Z99114) similar to hypothetical proteins from B. subtilis [Bacillus subtilis] Length = 414
SEQ ID n°785	Prot n°PL-1677.1	Contig39	226314	228869	89%	Identities = 676/849 (79%), Positives = 762/849 (89%), Gaps = 2/849 (0%) emb CAB43497.1 (AJ006210) mismatch repair protein [Escherichia coli] Length = 853

TABLEAU I

SEQ ID n°786	Prot n°PL-1678.1	Contig39	225548	226309	83%	Identities = 187/248 (75%), Positives = 218/248 (87%) gb AAAF95058.1 (AE004266) IRNA-(MS2)IC[6A]-hydroxylase [Vibrio cholerae] Length = 487/53 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db JBA06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°787	Prot n°PL-1679.1	Contig39	224041	225108	21%	Identities = 161/266 (60%), Positives = 209/266 (78%), Gaps = 3/266 (1%) sp P24197 YGLD_ECOLI_HYPOTHETICAL 29.9 KD PROTEIN IN TOLC-RIBB INTERGENIC REGION (ORF) (F271) pir JE65091 yglD protein - Escherichia coli (strain K-12) gb AAA69207.1 (U28377) ORF_f271; alternate name yglD; orfC of M77129 [Escherichia coli] gb AAC76075.1 (AE000385) orf_hypothetical protein [Escherichia coli] Length = 271 "
SEQ ID n°788	Prot n°PL-168.1	Contig41	280375	281145	78%	Identities = 293/332 (88%), Positives = 320/332 (96%), Gaps = 1/332 (0%) gb AAF20816.1 (AF198628)_2 (AF198628) RpoS [Xenotaphus nematophilus] Length = 331
SEQ ID n°789	Prot n°PL-1680.1	Contig39	222030	223028	95%	Identities = 202/381 (53%), Positives = 245/381 (64%), Gaps = 54/381 (14%) emb CAA06881.1 (AJ006131) nlpD [Salmonella dublin] Length = 377
SEQ ID n°790	Prot n°PL-1681.1	Contig39	220983	221978	70%	Identities = 151/208 (72%), Positives = 177/208 (84%) sp P24206 PMT_ECOLI_PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) pir JH0242 protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) type II - Escherichia coli gb AA24302.1 (M83493) L-isoaspartyl protein carboxyl methyltransferase [Escherichia coli] gb AAA69253.1 (U29579) L-isoaspartyl protein carboxyl methyltransferase type II [Escherichia coli] gb AAC75785.1 (AE000358) L-isoaspartate protein carboxylmethyltransferase type II
SEQ ID n°791	Prot n°PL-1682.1	Contig39	220205	220831	83%	Identities = 180/246 (73%), Positives = 204/246 (82%) gb AAA69254.1 (U29579) alternate name ygcC; ORF1 of L07942, has different start to frameshift in L07942; ORF_f255 [Escherichia coli] Length = 255 "
SEQ ID n°792	Prot n°PL-1683.1	Contig39	219447	220211	72%	Identities = 203/333 (60%), Positives = 250/333 (74%) sp Q57261 YGB0_ECOLI 39.1 KDA PROTEIN IN SURE-CYSC INTERGENIC REGION pir J169731 hypothetical protein b2745 - Escherichia coli gb AAA69255.1 (U29579) was ORF_f292 and ORF_f255 before splice; ORF_f349 [Escherichia coli] gb AAA79838.1 (L07942) ORF1 [Escherichia coli] gb AAC75787.1 (AE000358) putative hydrogenase subunit
SEQ ID n°793	Prot n°PL-1684.1	Contig39	218417	219469	71%	

TABLEAU I

SEQ ID n°794	Prot n°PL-1685.1	Contig39	217198	217929	69%	<p>Identities = 144/233 (61%), Positives = 174/233 (73%), Gaps = 11/233 (4%) sp Q46893 YGBP_ECOLI_HYPOTHETICAL_25.7_KDA_PROTEIN_IN_SURE-CYSC_INTERGENIC_REGION_pir JG65055_hypothetical_protein_b2747_Escherichia_coli_strain_K-12_gb AA69257.1 (U29579) ORF_7236 [Escherichia coli] gb AAC75789.1 (AE000358) orf, hypothetical protein [Escherichia coli] dbj BAA90761.1 (AB037143) 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Escherichia coli] gb AAF43207.1 AF230736_1 (AF230736) 4-diphosphocytidylyl-2C-methyl-D-erythritol synthase [Escherichia coli] Length = 236 Identities = 141/196 (71%), Positives = 168/198 (84%) sp P23846 CYSC_ECOLI_ADENYLYLSULFATE_KINASE (APS_KINASE) (ADENOSINE-5'-PHOSPHOSULFATE_KINASE) (ATP_ADENOSINE-5'-PHOSPHOSULFATE_3'-PHOSPHOTRANSFERASE) pir B69056 adenylsulfate kinase (EC 2.7.1.25) precursor - Escherichia coli gb AA23303.1 (M86936) adenylsulfate 3'-phosphotransferase [Escherichia coli] gb AA69260.1 (U29579) adenosine 5-phosphosulfate kinase [Escherichia coli] gb AAC75792.1 (AE000358) adenosine 5-phosphosulfate Identities = 337/474 (71%), Positives = 401/474 (84%) sp P23845 CYSN_ECOLI_SULFATE_ADENYLYLTRANSFERASE_SUBUNIT_1 (SULFATE_ADENYLYLTRANSFERASE) (SAT) (ATP-SULFURYLASE LARGE SUBUNIT) pir JN0327_sulfate_adenylyltransferase (EC 2.7.7.4) large chain - Escherichia coli gb AA23646.1 (M74586) ATP sulfurylase [Escherichia coli] gb AA69261.1 (U29579) ATP sulfurylase (ATP:sulfate adenyltransferase) subunit [Escherichia coli] gb AAC75793.1 (AE000358) ATP-sulfurylase (ATP:sulfate adenyltransferase), subunit 1, probably a GTPase [Escherichia coli] Length = 475 Identities = 266/302 (88%), Positives = 284/302 (93%) pir D65056_sulfate_adenylyltransferase (EC 2.7.7.4) small chain - Escherichia coli gb AA69262.1 (U29579) ATP sulfurylase (ATP:sulfate adenyltransferase) [Escherichia coli] gb AAC75794.1 (AE000358) ATP-sulfurylase (ATP:sulfate adenyltransferase), subunit 2 [Escherichia coli] Length = 302 Identities = 276/468 (58%), Positives = 350/468 (73%), Gaps = 4/468 (0%) sp P57001 CYSG_NEIMA_SIROHEME_SYNTHASE [INCLUDES: UROPORPHYRIN-III C-METHYLTRANSFERASE (UROGEN III METHYLASE) (SUMT) (UROPORPHYRINOGEN III METHYLASE) (UROM); PRECORRIN-2 OXIDASE; FERROCHELATASE 1] emb CAB84613.1 (AL162765) sirohaem synthase [Neisseria meningitidis]</p>
SEQ ID n°795	Prot n°PL-1686.1	Contig39	216093	216725	73%	
SEQ ID n°796	Prot n°PL-1687.1	Contig39	214718	216091	80%	
SEQ ID n°797	Prot n°PL-1688.1	Contig39	213729	214637	92%	
SEQ ID n°798	Prot n°PL-1689.1	Contig39	212307	213719	72%	

TABLEAU I

SEQ ID n°799	Prot n°PL-169.1	Contig41	281355	282008	87%	<p>Identities = 173/217 (79%), Positives = 195/217 (89%)</p> <p>sp P24199 RIBB_ECOLI_3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE (DHBP SYNTHASE) pir S22384 3,4-dihydroxy-2-butanone 4-phosphate synthase - Escherichia coli emb CAA47252.1 (X66720) 3,4-dihydroxy-2-butanone 4-phosphate synthase [Escherichia coli] gb AA71879.1 (M77129) luxH gene product [Escherichia coli] gb AAA69208.1 (U28377) 3,4-dihydroxy-2-butanone 4-phosphate synthase [Escherichia coli] gb AAC76077.1 (AE000386) 3,4 dihydroxy-2- Identities = 185/243 (76%), Positives = 211/243 (86%)</p>
SEQ ID n°800	Prot n°PL-1690.1	Contig39	210571	211305	78%	<p>sp P17853 CYSH_SALTY PHOSPHOADENOSINE PHOSPHOSULFATE REDUCTASE (PAPS REDUCTASE, THIOREDOXIN DEPENDENT) (PADOPS REDUCTASE) (3'-PHOSPHOADENYLYLSULFATE REDUCTASE) (PAPS SULFOTRANSFERASE) pir C34354 3'-phosphoadenosine 5'-phosphosulfate reductase (EC 1.8.99.4) - Salmonella typhimurium gb AAA27048.1 (M23007) 3'-phosphoadenosine-5'-phosphosulfate sulfotransferase [Salmonella typhimurium] Length = Identities = 455/571 (79%), Positives = 512/571 (88%), Gaps = 1/571 (0%)</p>
SEQ ID n°801	Prot n°PL-1692.1	Contig39	208844	210574	87%	<p>pir I RDCEGH sulfite reductase (NADPH) (EC 1.8.1.2) hemoprotein - Escherichia coli gb AAA69273.1 (U29579) sulfite reductase (NADPH) hemoprotein alpha subunit [Escherichia coli] gb AAC75805.1 (AE000360) sulfite reductase, alpha subunit [Escherichia coli] Length =</p>
SEQ ID n°802	Prot n°PL-1693.1	Contig39	207042	208844	81%	<p>Identities = 416/602 (69%), Positives = 491/602 (81%), Gaps = 5/602 (0%)</p> <p>sp P38038 CYSJ_ECOLI_SULFITE REDUCTASE [NADPH] FLAVOPROTEIN ALPHA-COMPONENT (SIR-FP) pir B34231 sulfite reductase (NADPH) (EC 1.8.1.2) - Escherichia coli gb AAA23650.1 (M23008) NADPH-sulfite reductase flavoprotein component [Escherichia coli] Length =</p>
SEQ ID n°803	Prot n°PL-1694.1	Contig39	205697	206368	80%	<p>Identities = 163/223 (73%), Positives = 193/223 (86%)</p> <p>sp P55139 YGCF_ECOLI_HYPOTHETICAL 25.0 KD PROTEIN IN CYSJ-ENO INTERGENIC REGION (F223) pir E65059 hypothetical protein b2777 - Escherichia coli (strain K-12) gb AAA69287.1 (U29580) ORF_f223 [Escherichia coli] gb AAC75818.1 (AE000361) orf, hypothetical protein</p>
SEQ ID n°804	Prot n°PL-1695.1	Contig39	204141	205526	82%	<p>Identities = 325/449 (72%), Positives = 381/449 (84%), Gaps = 1/449 (0%)</p> <p>gb AAB86967.1 (AF032970) Inducible histidine transporter [Pseudomonas putida] Length = 467</p>
SEQ ID n°805	Prot n°PL-1696.1	Contig39	203083	203865	76%	<p>Identities = 167/258 (64%), Positives = 204/258 (78%), Gaps = 2/258 (0%)</p> <p>pir C64745 yafD protein - Escherichia coli gb AAC73314.1 (AE000130) orf, hypothetical protein [Escherichia coli] Length = 266</p>
SEQ ID n°806	Prot n°PL-1697.1	Contig35	242432	243070	No Hits found	
SEQ ID n°807	Prot n°PL-1698.1	Contig35	240420	241613	33%	<p>Identities = 76/223 (34%), Positives = 132/223 (59%), Gaps = 3/223 (1%)</p> <p>gb AAF98876.1 (AF173869) putative site-specific recombinase XerD [Staphylococcus aureus] Length = 295</p>

TABLEAU I

SEQ ID n°808	Prot n°PL-1699.1	Contig35	237104	240496	16%	Identities = 105/406 (25%), Positives = 190/406 (45%), Gaps = 50/406 (12%) sp P47762 PRIM_LISMO DNA PRIMASE gb AAC43305.1 (U13165) DNA primase [Listeria monocytogenes] prf 2104269B DNA primase [Listeria monocytogenes] Length = 626
SEQ ID n°809	Prot n°PL-17.1	Contig41	30900	32078	54%	Identities = 146/380 (38%), Positives = 217/380 (56%), Gaps = 2/380 (0%) sp Q08432 PATB_BACSU PUTATIVE AMINOTRANSFERASE B pir S32934 aminotransferase patB - Bacillus subtilis emb CAB07910.1 (Z93933) aminotransferase [Bacillus subtilis] emb CAB07924.1 (Z93934) aminotransferase [Bacillus subtilis] gb AAB61979.1 (U63302) patB [Bacillus subtilis] emb CAB15133.1 (Z99120) aminotransferase [Bacillus subtilis] Length = 387
SEQ ID n°810	Prot n°PL-170.1	Contig41	282838	283500	62%	Identities = 103/204 (50%), Positives = 141/204 (68%), Gaps = 3/204 (1%) gb AAF42718.1 AF226570_1 (AF226570) putative lipoprotein GNA1162 [Neisseria meningitidis] Length = 215
SEQ ID n°811	Prot n°PL-1700.1	Contig35	233454	234065	No Hits found	
SEQ ID n°812	Prot n°PL-1701.1	Contig35	230601	231341	No Hits found	
SEQ ID n°813	Prot n°PL-1702.1	Contig35	229959	230600	No Hits found	
SEQ ID n°814	Prot n°PL-1703.1	Contig35	226992	235844	37%	Identities = 72/2338 (30%), Positives = 1120/2338 (47%), Gaps = 237/2338 (10%) gb AAF42109.1 (AE002526) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58] Length = 2514
SEQ ID n°815	Prot n°PL-1704.1	Contig35	225318	226982	56%	Identities = 239/546 (43%), Positives = 323/546 (58%), Gaps = 26/546 (4%) gb AAF65347.1 AE004082_2 (AE004082) outer membrane hemolysin activator protein [Xylella fastidiosa] Length = 597
SEQ ID n°816	Prot n°PL-1705.1	Contig35	222949	223929	36%	Identities = 66/294 (22%), Positives = 120/294 (40%), Gaps = 51/294 (17%) gb AAD17308.1 (AF121418) unknown [Francisella tularensis subsp. novicida] Length = 292
SEQ ID n°817	Prot n°PL-1706.1	Contig35	218821	220803	19%	Identities = 85/292 (28%), Positives = 130/292 (44%), Gaps = 36/292 (12%) dbj BAB16219.1 (AP002086) similar to ardC gene in pSa(lncW plasmid) [Agrobacterium rhizogenes] Length = 309
SEQ ID n°818	Prot n°PL-1707.1	Contig35	217810	218820	No Hits found	
SEQ ID n°819	Prot n°PL-1708.1	Contig35	216085	217005	47%	Identities = 109/314 (34%), Positives = 167/314 (52%), Gaps = 16/314 (5%) dbj BAA75117.1 (AB021078) yccB [Plasmid Collib-Pg] gnl PID1038851 yccB Length = 308
SEQ ID n°820	Prot n°PL-1709.1	Contig35	215215	215943	No Hits found	
SEQ ID n°821	Prot n°PL-171.1	Contig41	283878	284549	84%	Identities = 155/222 (69%), Positives = 190/222 (84%), Gaps = 1/222 (0%) gb AAG03435.1 AE004444_4 (AE004444) hypothetical protein [Pseudomonas aeruginosa] Length = 228
SEQ ID n°822	Prot n°PL-1710.1	Contig35	213299	214831	22%	Identities = 70/228 (30%), Positives = 115/228 (49%), Gaps = 7/228 (3%) gb AAF64562.1 AE003998_4 (AE003998) hypothetical protein [Xylella fastidiosa] Length = 616

Unknown, similar to
toxins

TABLEAU 1

SEQ ID n°823	Prot n°PL-1711.1	Contig35	212203	213219	47%	Identities = 113/305 (37%), Positives = 162/305 (53%), Gaps = 8/305 (2%) gb AAAG02084.1 AF285416_2 (AF285416) XerC [Pseudomonas aeruginosa] Length = 427
SEQ ID n°824	Prot n°PL-1712.2	Contig35	210507	211580		Identities = 256/344 (74%), Positives = 284/344 (82%) sp P17802 MUTY_ECOLI A/G-SPECIFIC ADENINE GLYCOSYLASE pir J338535 A/G-specific adenine glycosylase (EC 3.2.2.-) - Escherichia coli emb CAA36624.1 X52391 adenine glycosylase (AA 1-350) [Escherichia coli] gb AAA72957.1 U28377 A/G-specific adenine glycosylase [Escherichia coli] gb AAA69128.1 U28377 CG Site No. 18130; alternate name mlcA [Escherichia coli] gb AAC75998.1 AE000378 adenine glycosylase; G.C → T.A transversions [Escherichia coli] Length = 350 "
SEQ ID n°825	Prot n°PL-1713.1	Contig35	209100	210140	80%	Identities = 182/239 (76%), Positives = 208/239 (88%) sp P32049 YGGH_ECOLI HYPOTHETICAL 27.3 KD PROTEIN IN ANSB- MUTY INTERGENIC REGION (F239) pir JG65081 hypothetical 27.3 kD protein in muty 5' region - Escherichia coli (strain K-12) gb AAA69127.1 (U28377) ORF_239; alternate name yggH; orf of M59471 [Escherichia coli] gb AAC75997.1 AE000378 orf, hypothetical protein [Escherichia coli]
SEQ ID n°826	Prot n°PL-1714.1	Contig35	208011	208730	82%	Identities = 211/308 (68%), Positives = 254/308 (81%) sp P77470 YNEH_ECOLI HYPOTHETICAL 33.5 KD PROTEIN IN UXAB- MARR INTERGENIC REGION pir JG64906 glutaminase homolog yneh - Escherichia coli db BAA15206.1 D90785 Glutaminase, kidney isoform precursor (EC 3.5.1.2) (GLS). [Escherichia coli] db BAA15214.1 (D90796) Glutaminase, kidney isoform precursor (EC 3.5.1.2) (GLS). [Escherichia coli] gb AAC74597.1 AE000250 putative glutaminase
SEQ ID n°827	Prot n°PL-1715.1	Contig35	206679	207605	79%	Identities = 116/241 (48%), Positives = 175/241 (72%), Gaps = 3/241 (1%) sp P46143 YGGN_ECOLI HYPOTHETICAL 26.4 KD PROTEIN IN GSHB- ANSB INTERGENIC REGION (F239) pir JG65081 hypothetical protein in ansB 5' region - Escherichia coli (strain K-12) gb AAA69125.1 U28377 ORF_239; was ORF_1191 and ORF_1194 before splice [Escherichia coli] gb AAC75995.1 AE000378 orf, hypothetical protein [Escherichia coli]
SEQ ID n°828	Prot n°PL-1716.1	Contig35	205909	206631	66%	Identities = 110/285 (38%), Positives = 168/285 (58%), Gaps = 9/285 (3%) pir JG69763 probable ferrichrome ABC transporter ycdQ - Bacillus subtilis db JBA09015.1 D50453 ferric anguibactin-binding protein precursor FaB of V. anguillarum [Bacillus subtilis] emb CAB12191.1 Z99106 similar to ferrichrome ABC transporter (binding protein) [Bacillus subtilis] Length = 317
SEQ ID n°829	Prot n°PL-1717.1	Contig35	204841	205815	51%	
SEQ ID n°830	Prot n°PL-1718.1	Contig35	203491	204156	No Hits found	

TABLEAU I

SEQ ID n°831	Prot n°PL-1719.1	Contig35	201743	202873	86%	<p>Identities = 302/376 (80%), Positives = 330/376 (87%)</p> <p>sp P52062 YGGW_ECOLI HYPOTHETICAL 42.6 KDA PROTEIN IN GSHB-ANSB INTERGENIC REGION pir B65081 hypothetical protein b2955 - Escherichia coli (strain K-12) gb AAA69122.1 (U28377) ORF_o378 [Escherichia coli] gb AAC75992.1 (AE000378) putative oxidase [Escherichia coli] Length = 378</p>
SEQ ID n°832	Prot n°PL-172.1	Contig41	285139	286563	87%	<p>Identities = 383/475 (80%), Positives = 421/475 (88%)</p> <p>sp P76558 RFAE_ECOLI ADP-HEPTOSE SYNTHASE pir B65093 ADP-heptose synthase homolog - Escherichia coli (strain K-12) gb AAC76088.1 (AE000387) putative kinase [Escherichia coli] Length = 477</p>
SEQ ID n°833	Prot n°PL-1720.1	Contig35	199742	200563	71%	<p>Identities = 161/273 (58%), Positives = 213/273 (77%), Gaps = 12/73 (0%)</p> <p>gb AAF93633.1 (AE004132) pyrroline-5-carboxylate reductase [Vibrio cholerae] Length = 272</p>
SEQ ID n°834	Prot n°PL-1721.1	Contig35	199021	199716	77%	<p>Identities = 160/231 (69%), Positives = 182/231 (78%), Gaps = 2/231 (0%)</p> <p>sp P52054 YGGG_ECOLI HYPOTHETICAL 25.8 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION pir F65080 hypothetical protein b2951 - Escherichia coli (strain K-12) gb AAA69118.1 (U28377) ORF_o234 [Escherichia coli] gb AAC75988.1 (AE000378) orf, hypothetical protein [Escherichia coli] Length = 234</p>
SEQ ID n°835	Prot n°PL-1722.1	Contig35	197962	198999	69%	<p>Identities = 184/331 (55%), Positives = 241/331 (72%), Gaps = 5/331 (1%)</p> <p>sp P52052 YGGG_ECOLI HYPOTHETICAL 36.0 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION Length = 326</p>
SEQ ID n°836	Prot n°PL-1723.1	Contig35	196924	197487	69%	<p>Identities = 126/187 (67%), Positives = 158/187 (84%)</p> <p>sp P52049 YQGE_ECOLI 20.7 KDA PROTEIN IN GSHB-ANSB INTERGENIC REGION Length = 187</p>
SEQ ID n°837	Prot n°PL-1724.1	Contig35	195864	196814	88%	<p>Identities = 251/317 (79%), Positives = 282/317 (88%), Gaps = 1/317 (0%)</p> <p>sp P04425 GSHB_ECOLI GLUTATHIONE SYNTHETASE (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) (GSHASE) pir SYECGS glutathione synthase (EC 6.3.2.3) - Escherichia coli pdb 1GSA Structure Of Glutathione Synthase Complexed With Adp And Glutathione pdb 1GSH Structure Of Escherichia Coli Glutathione Synthetase At Ph 7.5 pdb 2GLT Structure Of Escherichia Coli Glutathione Synthetase At Ph 6.0. emb CAA25826.1 (X01666) GSH-II [Escherichia coli] gb AAA69114.1 (U28377) glutathione synthetase [Escherichia coli] gb AAC75984.1 (AE000377) glutathione synthetase [Escherichia coli] Length = 316</p>
SEQ ID n°838	Prot n°PL-1725.1	Contig35	195087	195854	74%	<p>Identities = 198/249 (78%), Positives = 218/249 (88%)</p> <p>pir A65080 hypothetical protein in endA-gshB intergenic region - Escherichia coli (strain K-12) gb AAA69113.1 (U28377) ORF_o252 [Escherichia coli] gb AAC75983.1 (AE000377) orf, hypothetical protein [Escherichia coli] Length = 252</p>

TABLEAU I

SEQ ID n°839	Prot n°PL-1726.1	Contig35	194186	194860	49%	Identities = 77/166 (46%), Positives = 111/166 (66%), Gaps = 1/166 (0%) sp O88964 LEP4_AERSA TYPE 4 PREPILIN-LIKE PROTEINS LEADER PEPTIDE PROCESSING ENZYME [INCLUDES: LEADER PEPTIDASE (PREPILIN PEPTIDASE); N-METHYLTRANSFERASE] gb AAC23569.1 (AF059249) type IV prepilin peptidase TapD [Aeromonas salmonicida] Length = 291 "
SEQ ID n°840	Prot n°PL-1727.1	Contig35	193486	194137	55%	Identities = 97/206 (47%), Positives = 124/206 (60%), Gaps = 3/206 (1%) gb AAG03448.1 AE004445_9 (AE004445) hypothetical protein [Pseudomonas aeruginosa] Length = 234
SEQ ID n°841	Prot n°PL-1728.1	Contig35	192400	193464	57%	Identities = 159/284 (55%), Positives = 204/284 (70%) gb AAG03447.1 AE004445_8 (AE004445) hypothetical protein [Pseudomonas aeruginosa] Length = 295
SEQ ID n°842	Prot n°PL-1729.1	Contig35	191560	192477	70%	Identities = 165/297 (55%), Positives = 216/297 (72%) gb AAG03446.1 AE004445_7 (AE004445) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 308
SEQ ID n°843	Prot n°PL-173.1	Contig41	286651	289521	77%	Identities = 630/957 (65%), Positives = 740/957 (76%), Gaps = 11/957 (1%) sp P30870 GLNE_ECOLI GLUTAMATE-AMMONIA-LIGASE ADENYLYLTRANSFERASE (GLUTAMINE-SYNTHETASE ADENYLYLTRANSFERASE) (ATASE) pif C65093 [glutamate-ammonia-ligase] adenylyltransferase (EC 2.7.7.42) - Escherichia coli gb AAC76089.1 (AE000387) adenylylating enzyme for glutamine synthetase [Escherichia coli] Length = 946
SEQ ID n°844	Prot n°PL-1730.1	Contig35	190642	191577	76%	Identities = 198/296 (66%), Positives = 243/296 (81%), Gaps = 4/296 (1%) sp P03030 LYSR_ECOLI TRANSCRIPTIONAL ACTIVATOR PROTEIN LYSR pif IRGECK regulatory protein lysR - Escherichia coli gb AAA83862.1 (J01614) activatory protein [Escherichia coli] gb AAC75878.1 (AE000367) positive regulator for lys [Escherichia coli] Length = 311
SEQ ID n°845	Prot n°PL-1731.1	Contig35	189218	190594	74%	Identities = 290/408 (71%), Positives = 344/408 (84%) sp P00861 DCDA_ECOLI DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE) pif DCEDC diaminopimelate decarboxylase (EC 4.1.1.20) - Escherichia coli gb AAA83861.1 (J01614) diaminopimelate decarboxylase [Escherichia coli] gb AAB40485.1 (U29581) diaminopimelate decarboxylase [Escherichia coli] gb AAC75877.1 (AE000367) diaminopimelate decarboxylase [Escherichia coli] Length = 420
SEQ ID n°846	Prot n°PL-1732.1	Contig35	186710	189145	87%	Identities = 631/815 (77%), Positives = 718/815 (87%), Gaps = 5/815 (0%) db BAA77891.1 (D83536) Acyl-CoA dehydrogenase (EC 1.3.99.-) [Escherichia coli] Length = 840
SEQ ID n°847	Prot n°PL-1733.1	Contig35	185869	186450	89%	Identities = 171/192 (89%), Positives = 182/192 (94%) gb AAB08644.1 (U70214) hypothetical [Escherichia coli] Length = 198

TABLEAU I

SEQ ID n°848	Prot n°PL-1734.1	Contig35	184952	185719	83%	<p>Identities = 194/255 (76%), Positives = 222/255 (86%)</p> <p>sp Q47147 YAFJ_ECOLI HYPOTHETICAL 28.6 KD PROTEIN IN GMHA-DINJ INTERGENIC REGION pir H64746 yafJ protein - Escherichia coli dbj BAA07585.1 (D38582) YafJ [Escherichia coli] gb AAB08645.1 (U70214) hypothetical [Escherichia coli] gb AAC73327.1 (AE000131) putative amidotransferase [Escherichia coli] dbj BAA77893.1 (D83536) Hypothetical protein H11037 [Escherichia coli] Length = 255</p>
SEQ ID n°849	Prot n°PL-1735.1	Contig35	184238	184981	63%	<p>Identities = 127/249 (51%), Positives = 166/249 (66%), Gaps = 5/249 (2%)</p> <p>sp Q47148 YAFK_ECOLI HYPOTHETICAL 28.0 KD PROTEIN IN GMHA-DINJ INTERGENIC REGION PRECURSOR pir A84747 probable membrane protein yafK - Escherichia coli dbj BAA07586.1 (D38582) YafK [Escherichia coli] gb AAB08646.1 (U70214) hypothetical [Escherichia coli] gb AAC73328.1 (AE000131) orf, hypothetical protein [Escherichia coli] dbj BAA77894.1 (D83536) Hypothetical 28.0 kd protein in gmha-dinJ intergenic region precursor. [Escherichia coli] Length = 246</p>
SEQ ID n°860	Prot n°PL-1736.1	Contig35	182475	183818	77%	<p>Identities = 294/447 (65%), Positives = 353/447 (78%) emb CAB84035.1 (AL162754) putative Na(+)-translocating NADH-ubiquinone reductase subunit A [Neisseria meningitidis] Length = 447</p>
SEQ ID n°851	Prot n°PL-1737.1	Contig35	181232	182470	86%	<p>Identities = 315/411 (76%), Positives = 363/411 (87%) dbj BAA22911.1 (AB008030) Nqr2 subunit of Na-translocating NADH-quinone reductase complex [Vibrio alginolyticus] Length = 414</p>
SEQ ID n°852	Prot n°PL-1738.1	Contig35	180442	181239	67%	<p>Identities = 139/256 (54%), Positives = 186/256 (72%), Gaps = 5/256 (1%)</p> <p>pir S65528 Na+-translocating NADH-ubiquinone oxidoreductase (EC 1.-.-.-) gamma chain - Vibrio alginolyticus dbj BAA22912.1 (AB008030) Nqr3 subunit of Na-translocating NADH-quinone reductase complex gamma-subunit [Vibrio alginolyticus] prf J211280A Na-translocating NADH quinone reductase [Vibrio alginolyticus] Length = 256</p>
SEQ ID n°853	Prot n°PL-1739.1	Contig35	179820	180449	87%	<p>Identities = 159/210 (75%), Positives = 185/210 (87%)</p> <p>gb AAD29965.1 AF117331_4 (AF117331) NqrD [Vibrio cholerae] gb AAF85436.1 (AE004300) NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrD [Vibrio cholerae] Length = 210</p>
SEQ ID n°854	Prot n°PL-174.1	Contig41	289555	290493	53%	<p>Identities = 139/319 (43%), Positives = 186/319 (57%), Gaps = 10/319 (3%)</p> <p>sp P30871 YGIF_ECOLI HYPOTHETICAL 48.4 KD PROTEIN IN GLNE-CCA INTERGENIC REGION (ORFXE) pir S37754 ygfF protein - Escherichia coli emb CAA79891.1 (Z21844) open reading frame upstream glnE [Escherichia coli] gb AAC76090.1 (AE000387) orf, hypothetical protein [Escherichia coli] Length = 433</p>

TABLEAU I

SEQ ID n°855	Prot n°PL-1740.1	Contig35	177973	179199	89%	Identities = 323/408 (79%), Positives = 371/408 (90%) pir[D64052 Na ⁺ -translocating NADH-ubiquinone oxidoreductase (EC 1.-.-.-) beta chain - Haemophilus influenzae (strain Rd KW20) gb AAC21841.1 (U32702) Nqr6 subunit of Na-translocating NADH-quinone reductase complex beta-subunit (nqr6) [Haemophilus influenzae Rd] Length = 411
SEQ ID n°856	Prot n°PL-1741.1	Contig35	176865	177893	72%	Identities = 199/339 (58%), Positives = 251/339 (73%), Gaps = 4/339 (1%) gb AAF98433.1 (AE004300) thiamin biosynthesis lipoprotein ApBE [Vibrio cholerae] Length = 367
SEQ ID n°857	Prot n°PL-1742.1	Contig35	175127	175931	No Hits found	
SEQ ID n°858	Prot n°PL-1743.2	Contig35	172656	173672		
SEQ ID n°859	Prot n°PL-1744.2	Contig35	170608	171399	50%	Identities = 125/305 (40%), Positives = 166/305 (53%) gb AAG05692.1 AE004658.4 (AE004656) hypothetical protein [Pseudomonas aeruginosa] Length = 362
SEQ ID n°860	Prot n°PL-1745.2	Contig35	168845	170629	47%	Identities = 182/556 (32%), Positives = 283/556 (50%), Gaps = 17/556 (3%) gb AAD04758.1 (U95370) lichenysin synthetase B; LicB [Bacillus licheniformis] Length = 3588
SEQ ID n°861	Prot n°PL-1746.1	Contig35	165045	168860	26%	Identities = 223/686 (32%), Positives = 338/686 (48%), Gaps = 71/686 (10%) emb CA836627.1 (AL035480) putative polyketide synthase [Mycobacterium leprae] Length = 1540
SEQ ID n°862	Prot n°PL-1747.1	Contig35	160033	165069	42%	Identities = 445/1527 (29%), Positives = 706/1527 (46%), Gaps = 169/1527 (11%) gb AAG05790.1 AE004667_1 (AE004667) probable non-ribosomal peptide synthetase [Pseudomonas aeruginosa] Length = 5149
SEQ ID n°863	Prot n°PL-1748.1	Contig35	158277	160046	48%	Identities = 170/557 (30%), Positives = 287/557 (51%), Gaps = 25/557 (4%) pir S74455 ABC-type transport protein sir1488 - Synecocystis sp. (strain PCC 6803) dbj BAA16607.1 (D90899) ABC transporter [Synecocystis sp.] Length = 605
SEQ ID n°864	Prot n°PL-1749.1	Contig35	156634	158292	50%	Identities = 162/587 (27%), Positives = 282/587 (47%), Gaps = 65/587 (11%) pir S74481 ABC transporter sir1494 - Synecocystis sp. (strain PCC 6803) dbj BAA16613.1 (D90899) ABC transporter [Synecocystis sp.] Length = 613
SEQ ID n°865	Prot n°PL-175.1	Contig41	290755	291375	78%	Identities = 126/206 (61%), Positives = 167/206 (80%) sp P39202 YJGIM_ECOLI_HYPOTHETICAL_23.1_KD_PROTEIN_IN_GLNE-CCA INTERGENIC REGION PRECURSOR pir JE65093 hypothetical protein in gene-cca intergenic region - Escherichia coli (strain K-12) (fragment) gb AA89135.1 (U28379) alternate name yglM; ORF_0206 [Escherichia coli] gb AAC78091.1 (AE000387) orf, hypothetical protein [Escherichia coli]

TABLEAU I

SEQ ID n°866	Prot n°PL-1750.1	Contig35	155697	156488	46%	Identities = 76/241 (31%), Positives = 122/241 (50%), Gaps = 18/241 (7%) pir T17413 thioesterase II (EC 3.1.2.-) - Streptomyces venezuelae gb AAC69333.1 (AF079138) thioesterase II PkAV [Streptomyces venezuelae] Length = 281	
SEQ ID n°867	Prot n°PL-1751.1	Contig35	154174	155808	26%	Identities = 88/313 (28%), Positives = 145/313 (46%), Gaps = 27/313 (8%) sp P39641 YWFE_BACSU HYPOTHETICAL 52.3 KD PROTEIN IN ROCC- PTA INTERGENIC REGION pir S39738 ywfe protein - Bacillus subtilis emb CAA51639.1 (X73124) ipa-83d [Bacillus subtilis] emb CAB15798.1 (Z99123) alternate gene name: ipa-83d [Bacillus subtilis] Length = 472	
SEQ ID n°868	Prot n°PL-1752.1	Contig35	152942	154150	58%	Identities = 163/335 (41%), Positives = 245/335 (61%), Gaps = 1/335 (0%) gb AAF67502.1 (AF170880) Novl [Streptomyces spheroides] Length = 407	
SEQ ID n°869	Prot n°PL-1753.1	Contig35	149750	152935	47%	Identities = 311/1035 (30%), Positives = 500/1035 (48%), Gaps = 95/1035 (9%) pir T17468 peptide-synthetase - Amycolatopsis mediterranei (fragment) emb CAA66454.1 (X97860) peptide-synthetase [Amycolatopsis mediterranei] Length = 1324	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°870	Prot n°PL-1754.1	Contig35	147916	148920	84%	Identities = 238/334 (70%), Positives = 286/334 (84%) pir T08494 probable transposase - Enterobacter aerogenes plasmid R751 gb AAB03489.1 (U60777) transposase [Plasmid R751] gb AAC64438.1 (U67194) TnpA [Enterobacter aerogenes] Length = 334	
SEQ ID n°871	Prot n°PL-1755.1	Contig35	145599	146603	84%	Identities = 236/334 (70%), Positives = 286/334 (84%) pir T08494 probable transposase - Enterobacter aerogenes plasmid R751 gb AAB03489.1 (U60777) transposase [Plasmid R751] gb AAC64438.1 (U67194) TnpA [Enterobacter aerogenes] Length = 334	
SEQ ID n°872	Prot n°PL-1756.1	Contig35	144015	145331	61%	Identities = 205/418 (49%), Positives = 277/418 (66%), Gaps = 8/418 (1%) pir S77027 hypothetical protein sir0801 - Synecocystis sp. (strain PCC 6803) db BAA10719.1 (D64005) hypothetical protein [Synecocystis sp.] Length = 416	
SEQ ID n°873	Prot n°PL-1757.1	Contig35	142594	143703	41%	Identities = 107/278 (38%), Positives = 153/278 (54%), Gaps = 2/278 (0%) sp Q55946 Y787_SYNY3 HYPOTHETICAL 34.7 KD PROTEIN SLL0787 pir S77022 hypothetical protein sir0787 - Synecocystis sp. (strain PCC 6803) db BAA10714.1 (D64005) hypothetical protein [Synecocystis sp.] Length = 322	
SEQ ID n°874	Prot n°PL-1758.1	Contig35	141005	142075	67%	Identities = 201/356 (56%), Positives = 259/356 (72%), Gaps = 2/356 (0%) pir S77024 hypothetical protein sir0785 - Synecocystis sp. (strain PCC 6803) db BAA10716.1 (D64005) hypothetical protein [Synecocystis sp.] Length = 362	
SEQ ID n°875	Prot n°PL-1759.1	Contig35	139947	140954	65%	Identities = 189/302 (62%), Positives = 230/302 (75%), Gaps = 1/302 (0%) pir S77025 nitrilase (EC 3.5.5.1) - Synecocystis sp. (strain PCC 6803) db BAA10717.1 (D64005) nitrilase [Synecocystis sp.] Length = 346	

TABLEAU I

SEQ ID n°876	Prot n°PL-176.1	Contig41	291391	292641	81%	<p>Identities = 293/406 (72%), Positives = 338/406 (83%) sp P06961 CCA_ECOLI TRNA NUCLEOTIDYLTRANSFERASE (TRNA ADENYLYLTRANSFERASE) (TRNA CCA-PYROPHOSPHORYLASE) (CCA-ADDING ENZYME) pir JIRNECTA tRNA adenylyltransferase (EC 2.7.7.25) - Escherichia coli gb AA23541.1 (M12788) tRNA nucleotidyltransferase [Escherichia coli] gb AAA89136.1 (U28379) CG Site No. 933 [Escherichia coli] gb AAC76092.1 (AE00387) tRNA nucleotidyl transferase [Escherichia coli] Length = 160/368 (43%), Positives = 239/368 (64%), Gaps = 4/368 (1%) dbj BAA16380.1 (D90878) FORMATE HYDROGENLYASE TRANSCRIPTIONAL ACTIVATOR. [Escherichia coli] Length = 116/278 (41%), Positives = 165/278 (59%), Gaps = 13/278 (4%) gb AAG08178.1 (AE004892) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 311</p> <p>Identities = 73/207 (35%), Positives = 121/207 (58%), Gaps = 8/207 (3%) gb AAF13668.1 (AF188935) pXO2-63 [Bacillus anthracis] Length = 205</p> <p>Identities = 369/695 (53%), Positives = 486/695 (69%), Gaps = 10/695 (1%) sp P44523 HXC1_HAEIN HEME-HEME-HEMOPEXIN UTILIZATION PROTEIN C PRECURSOR pir J864049 outer membrane protein hxcC homolog - Haemophilus influenzae (strain Rd KW20) gb AAC21789.1 (U32696) hemin receptor (hemR) [Haemophilus influenzae Rd] Length = 744</p> <p>Identities = 250/349 (71%), Positives = 294/349 (83%) sp Q47155 DINP_ECOLI DNA-DAMAGE-INDUCIBLE PROTEIN P pir JH64747 DNA-damage-inducible protein dinP - Escherichia coli dbj BAA07593.1 (D38582) DinP [Escherichia coli] gb AAB08651.1 (U70214) DinP [Escherichia coli] gb AAC73335.1 (AE000131) damage-inducible protein P; putative tRNA synthetase [Escherichia coli] dbj BAA77901.1 (D83536) DNA-damage-inducible protein p. [Escherichia coli] Length = 351</p>
SEQ ID n°877	Prot n°PL-1760.1	Contig35	137226	139160	37%	Identities = 311/367 (84%), Positives = 337/367 (91%) sp P17856 PROB_SERMA GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK) pir JIKISEEM glutamate 5-kinase (EC 2.7.2.11) - Serratia marcescens emb CAA37254.1 (X53086) gamma-glutamyl kinase [Serratia marcescens] Length = 367
SEQ ID n°878	Prot n°PL-1761.1	Contig35	136163	137059	55%	
SEQ ID n°879	Prot n°PL-1762.1	Contig35	134374	135012	50%	
SEQ ID n°880	Prot n°PL-1763.1	Contig35	131442	133802	61%	
SEQ ID n°881	Prot n°PL-1764.1	Contig35	130186	131241	83%	
SEQ ID n°882	Prot n°PL-1765.2	Contig35	128690	130150		
SEQ ID n°883	Prot n°PL-1766.2	Contig35	126742	127989		
SEQ ID n°884	Prot n°PL-1767.1	Contig35	125438	126544	89%	

TABLEAU I

SEQ ID n°885	Prot n°PL-1768.1	Contig35	124175	125428	87%	<p>sp P17857 PROA_SERMA GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE) pir JRDSEEM glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41) - Serratia marcescens emb CAA37255.1 (X53086) gamma-glutamyl phosphate reductase [Serratia marcescens] db BAA14365.1 (D90351) gamma-glutamyl phosphate reductase [Serratia marcescens] Length = 379/618 (61%), Positives = 481/618 (77%) sp P31119 AAS_ECOLI AAS BIFUNCTIONAL PROTEIN [INCLUDES: 2-ACYLGLYCEROPHOSPHOETHANOLAMINE ACYLTRANSFERASE (2-ACYL-GPE ACYLTRANSFERASE); ACYL-ACYL CARRIER PROTEIN SYNTHETASE (ACYL-ACP SYNTHETASE)] pir E65066 2-acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase - Escherichia coli (strain K-12) gb AAB40483.1 (U29581) 2-acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase [Escherichia coli] gb AAC75875.1 (AE000367) 2-acylglycerophospho-ethanolamine acyltransferase; acyl-acyl-carrier protein synthetase [Escherichia coli] Length = 719 "</p>
SEQ ID n°886	Prot n°PL-1769.1	Contig35	121331	123250	74%	<p>Identities = 220/272 (80%), Positives = 246/272 (89%), Gaps = 1/272 (0%) sp P31054 BACA_ECOLI BACITRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) pir JG65093 bacitracin resistance protein bacA - Escherichia coli gb AAA89137.1 (U28378) CG Site No. 29739 [Escherichia coli] gb AAC76093.1 (AE000387) bacitracin resistance; possibly phosphorylates undecaprenol [Escherichia coli] Length = 273 "</p>
SEQ ID n°887	Prot n°PL-177.1	Contig41	292706	293524	82%	<p>Identities = 266/385 (69%), Positives = 317/385 (82%) sp P39196 YGED_ECOLI HYPOTHETICAL 41.7 KD PROTEIN IN MUTH-AAS INTERGENIC REGION pir JG65066 hypothetical protein in muth-aas intergenic region - Escherichia coli (strain K-12) gb AAB40482.1 (U29581) ORF_f397 [Escherichia coli] gb AAC75874.1 (AE000367) putative resistance proteins [Escherichia coli] Length = 397</p>
SEQ ID n°888	Prot n°PL-1770.1	Contig35	120122	121330	78%	<p>Identities = 109/165 (66%), Positives = 129/165 (78%), Gaps = 3/165 (1%) sp P51967 YGAD_ENTAG HYPOTHETICAL 17.2 KD PROTEIN 1 IN RECA 5 REGION pir JG31480 hypothetical protein 1 - Enterobacter agglomerans gb AAA91765.1 (L03291) unnamed protein [Pantoea agglomerans] Length = 164</p>
SEQ ID n°889	Prot n°PL-1772.1	Contig35	118364	119431	94%	<p>Identities = 329/359 (91%), Positives = 346/359 (95%), Gaps = 5/359 (1%) sp P98185 RECA_XENBV RECA PROTEIN gb AAD12585.1 (U87924) RecA [Xenorhabdus bovienii] Length = 358</p>

TABLEAU I

SEQ ID n°891	Prot n°PL-1773.1	Contig35	115343	117973	87%	<p>Identities = 691/877 (78%), Positives = 778/877 (87%), Gaps = 1/877 (0%) sp P00957 SYA_ECOLI ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS) pir SYECAT alarine-TRNA ligase (EC 6.1.1.7) - Escherichia coli gb AAC75739.1 (AE000353) alanyl-HRNA synthetase [Escherichia coli] dbj BAA16559.1 (D90892) ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE-TRNA LIGASE) (ALARS) [Escherichia coli] Identities = 342/514 (66%), Positives = 413/514 (79%), Gaps = 1/514 (0%)</p>
SEQ ID n°892	Prot n°PL-1774.1	Contig35	112139	113698	76%	<p>sp O88838 GSH1_SALTY GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) gb AAC09345.1 (AF055352) gamma-glutamylcysteine synthetase [Salmonella typhimurium] Identities = 308/428 (71%), Positives = 382/428 (88%)</p>
SEQ ID n°893	Prot n°PL-1775.1	Contig35	110080	111372	86%	<p>sp P37908 YFJD_ECOLI HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION Length = 428</p>
SEQ ID n°894	Prot n°PL-1776.1	Contig35	109207	110040	80%	<p>Identities = 175/262 (66%), Positives = 223/262 (84%), Gaps = 1/262 (0%) gb AAD31437.1 AF130857_1 (AF130857) CorE [Salmonella typhimurium] Length = 288</p>
SEQ ID n°895	Prot n°PL-1777.1	Contig35	107703	109064	92%	<p>Identities = 397/453 (87%), Positives = 425/453 (93%) sp P07019 SR54_ECOLI SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) (P48) pir E65039 signal recognition particle protein - Escherichia coli gb AAC75659.1 (AE000347) GTP-binding export factor binds to signal sequence, GTP and RNA [Escherichia coli] Identities = 220/244 (90%), Positives = 237/244 (96%)</p>
SEQ ID n°896	Prot n°PL-1778.1	Contig35	105959	106711	92%	<p>sp P36244 TRMD_SERMA TRNA (GUANINE-N1)-METHYLTRANSFERASE (M1G-METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE) gb AAA50783.1 (L23334) m1G-methyltransferase [Serratia marcescens] Length = 255</p>
SEQ ID n°897	Prot n°PL-1779.1	Contig35	104231	105037	62%	<p>Identities = 131/268 (48%), Positives = 170/268 (62%), Gaps = 6/268 (2%) gb AAF83690.1 (AE004138) beta-ketoadipate enol-lactone hydrolase, putative [Vibrio cholerae] Length = 270</p>
SEQ ID n°898	Prot n°PL-178.1	Contig41	294158	294814	78%	<p>Identities = 161/207 (80%), Positives = 179/207 (88%) sp P31056 YGIH_ECOLI HYPOTHETICAL 22.2 KD PROTEIN IN BACA-TTDA INTERGENIC REGION (O205) pir A65094 ygiH protein - Escherichia coli (strain K-12) gb AAA89139.1 (U28378) alternate name ygiH; ORF_o205 [Escherichia coli] gb AAC76095.1 (AE000387) orf, hypothetical protein</p>
SEQ ID n°899	Prot n°PL-1780.2	Contig35	102596	103690		

TABLEAU I

SEQ ID n°900	Prot n°PL-1781.1	Contig35	101469	102590	81%	<p>sp Q02287 TYRA_ERWHE_T-PROTEIN [INCLUDES: CHORISMATE MUTASE (CM); PREPHENATE DEHYDROGENASE (PDH)] pir IS29934 chorismate mutase (EC 5.4.99.5) T / prephenate dehydrogenase (EC 1.3.1.12) - Erwinia herbicola emb CAA42950.1 (X60420) chorismate mutase [Erwinia herbicola] Length = 373 "</p> <p>Identities = 268/372 (72%), Positives = 318/372 (85%)</p>
SEQ ID n°901	Prot n°PL-1782.1	Contig35	97496	98653	78%	<p>sp P07022 PHEA_ECOLI_P-PROTEIN [INCLUDES: CHORISMATE MUTASE (CM); PREPHENATE DEHYDRATASE (PDT)] pir KMECPW chorismate mutase (EC 5.4.99.5) P / prephenate dehydratase (EC 4.2.1.51) - Escherichia coli gb AA24330.1 (M10431) chorismate mutase/prephenate dehydratase [Escherichia coli] gb AAC75648.1 (AE000346) chorismate mutase-P and prephenate dehydratase [Escherichia coli] dbj BAA16484.1 (D90888) chorismate mutase (EC 5.4.99.5) P / prephenate dehydratase (EC 4.2.1.51) [Escherichia coli]</p> <p>Identities = 264/383 (68%), Positives = 325/383 (83%)</p>
SEQ ID n°902	Prot n°PL-1783.1	Contig35	95845	96576	76%	<p>sp P77146 YFIO_ECOLI_HYPOTHETICAL 27.8 KD LIPOPROTEIN IN RLUD-PHEL INTERGENIC REGION PRECURSOR pir F65037 hypothetical protein b2595 - Escherichia coli (strain K-12) gb AAC75644.1 (AE000346) orf, hypothetical protein [Escherichia coli] dbj BAA16480.1 (D90887) similar to [SwissProt Accession Number P44553] [Escherichia coli] Length</p> <p>Identities = 267/313 (85%), Positives = 291/313 (92%)</p>
SEQ ID n°903	Prot n°PL-1784.1	Contig35	94729	95706	88%	<p>gb AAF78066.1 AF263561_1 (AF263561) 23S rRNA pseudouridine synthase [secondary endosymbiont of Glycaspis brimblecombei] Length = 314</p> <p>Identities = 267/313 (85%), Positives = 291/313 (92%)</p>
SEQ ID n°904	Prot n°PL-1785.1	Contig35	93997	94728	72%	<p>sp P33644 YFIH_ECOLI_HYPOTHETICAL 26.3 KD PROTEIN IN SFHB-CLPB INTERGENIC REGION pir D65037 hypothetical 26.3 kD protein in clpB 5' region - Escherichia coli (strain K-12) gb AAC75642.1 (AE000346) orf, hypothetical protein [Escherichia coli] dbj BAA16477.1 (D90887) similar to [SwissProt Accession Number P33644] [Escherichia coli] Length</p> <p>Identities = 156/243 (64%), Positives = 177/243 (72%)</p>
SEQ ID n°905	Prot n°PL-1786.1	Contig35	91290	93863	91%	<p>sp P03815 CLPB_ECOLI_CLPB PROTEIN (HEAT SHOCK PROTEIN F84.1) pir D35905 endopeptidase Clp ATP-binding chain B - Escherichia coli gb AAC75641.1 (AE000345) heat shock protein [Escherichia coli] dbj BAA16476.1 (D90887) CLPB PROTEIN (HEAT SHOCK PROTEIN F84.1).</p> <p>Identities = 734/857 (85%), Positives = 803/857 (93%)</p>
SEQ ID n°906	Prot n°PL-1787.1	Contig33	17492	18631	20%	<p>emb CAA70510.1 (Y09330) ferulic acid esterase A [Aspergillus niger] Length = 281</p> <p>Identities = 42/161 (26%), Positives = 76/161 (47%), Gaps = 28/161 (17%)</p>
SEQ ID n°907	Prot n°PL-1788.1	Contig33	19217	20344	No Hits found	

TABLEAU I

SEQ ID n°908	Prot n°PL-1789.1	Contig33	20652	21845	18%	Identities = 47/144 (32%), Positives = 72/144 (49%), Gaps = 17/144 (11%) gb AAB07724.1 (U55887) pomoea nll Pr47p Length = 402
SEQ ID n°909	Prot n°PL-179.1	Contig41	294873	295886	88%	Identities = 292/335 (87%), Positives = 309/335 (92%) pir QECR6 O-sialoglycoprotein endopeptidase (EC 3.4.24.57) - Escherichia coli gb AAB89144.1 (U28379) ORF_337 [Escherichia coli] gb AAC76100.1 (AE00388) putative O-sialoglycoprotein endopeptidase [Escherichia coli] Length = 337
SEQ ID n°910	Prot n°PL-1780.1	Contig33	22251	23372	No Hits found	
SEQ ID n°911	Prot n°PL-1791.1	Contig33	23681	24739	64%	Identities = 160/350 (45%), Positives = 239/350 (67%), Gaps = 9/350 (2%) emb CAA40809.1 (X57583) mcbB [Escherichia coli] Length = 350
SEQ ID n°912	Prot n°PL-1792.1	Contig33	24712	25911	43%	Identities = 101/402 (25%), Positives = 175/402 (43%), Gaps = 34/402 (8%) pir E64665 tetracycline resistance protein tetA(P) homolog - Helicobacter pylori (strain 26895) gb AAD08210.1 (AE00622) tetracycline resistance protein tetA(P), putative [Helicobacter pylori 26895] Length = 388
SEQ ID n°913	Prot n°PL-1793.1	Contig33	26668	27601	91%	Identities = 255/311 (81%), Positives = 287/311 (91%) sp P33371 YOHL ECOLI HYPOTHETICAL 35.2 KD PROTEIN IN PBPG-CDD INTERGENIC REGION pir C64982 hypothetical 35.2 kD protein in pbpg-cdd intergenic region - Escherichia coli (strain K-12) gb AAA60503.1 (U00007) yohI [Escherichia coli] gb AAC75201.1 (AE000303) putative regulator protein [Escherichia coli] pir J2014253AN yohI gene [Escherichia coli] Identities = 336/423 (79%), Positives = 367/423 (86%), Gaps = 1/423 (0%) sp P25888 RHLE ECOLI PUTATIVE ATP-DEPENDENT RNA HELICASE RHLE pir E64816 probable ATP-dependent RNA helicase rhle - Escherichia coli gb AAA53653.1 (L02123) ATP-dependent RNA helicase [Escherichia coli] dbj BAA35463.1 (D90717) Putative ATP-dependent RNA helicase RHLE [Escherichia coli] gb AAC73884.1 (AE000182) putative ATP-dependent RNA helicase [Escherichia coli] dbj BAA35457.1 (D90716) Putative ATP-dependent RNA helicase Rhle [Escherichia coli] Identities = 105/229 (45%), Positives = 150/229 (64%), Gaps = 3/229 (1%) pir D64816 probable transcription regulator ybhH - Escherichia coli gb AAC73883.1 (AE000181) putative transcriptional regulator [Escherichia coli] Length = 227
SEQ ID n°914	Prot n°PL-1794.1	Contig33	27605	28909	84%	
SEQ ID n°915	Prot n°PL-1795.1	Contig33	29187	29879	63%	Identities = 197/320 (61%), Positives = 256/320 (79%), Gaps = 2/320 (0%) pir C64816 hypothetical protein b0795 precursor - Escherichia coli gb AAC73882.1 (AE000181) putative membrane protein [Escherichia coli] dbj BAA35455.1 (D90716) Hypothetical protein f355 [Escherichia coli] dbj BAA35461.1 (D90717) Hypothetical protein f355 [Escherichia coli] Length = 332
SEQ ID n°916	Prot n°PL-1796.1	Contig33	29896	30888	75%	
SEQ ID n°917	Prot n°PL-1797.1	Contig33	30898	32637	82%	Identities = 417/573 (72%), Positives = 482/573 (83%) sp P75776 YBHF ECOLI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBHF Length = 578

TABLEAU I

SEQ ID n°918	Prot n°PL-1798.1	Contig33	32622	33794	80%	<p>Identities = 264/371 (71%), Positives = 315/371 (84%)</p> <p>sp P75775 YBHS_ECOLI_HYPOTHETICAL_42.1_KDA_PROTEIN_IN_MOAE-RHLE_INTERGENIC_REGION pir A04816 ybhS protein - Escherichia coli gb AAC73880.1 (AE000181) orf, hypothetical protein [Escherichia coli] dbj BAA35453.1 (D90716) Hypothetical protein F648 [Escherichia coli]</p>
SEQ ID n°919	Prot n°PL-1799.1	Contig33	33807	34913	86%	<p>Identities = 277/367 (75%), Positives = 323/367 (87%)</p> <p>sp P75774 YBHR_ECOLI_HYPOTHETICAL_41.6_KDA_PROTEIN_IN_MOAE-RHLE_INTERGENIC_REGION pir H64815 ybhR protein - Escherichia coli gb AAC73879.1 (AE000181) orf, hypothetical protein [Escherichia coli]</p>
SEQ ID n°920	Prot n°PL-18.1	Contig41	32065	33519	67%	<p>Identities = 256/457 (56%), Positives = 333/457 (72%), Gaps = 5/457 (1%)</p> <p>sp Q57007 YB07_HAEIN_HYPOTHETICAL_NA+/H+_ANTIporter_HI1107 pir H64182 Na+/H+-exchanging protein homolog - Haemophilus influenzae (strain Rd KW20) gb AAC22762.1 (U32790) Na+/H+ antiporter (nhaC) [Haemophilus influenzae Rd] Length = 468</p>
SEQ ID n°921	Prot n°PL-180.1	Contig41	296517	298262	81%	<p>Identities = 428/581 (73%), Positives = 494/581 (84%)</p> <p>sp P02923 PRIM_ECOLI_DNA_PRIMASE_pir RYEC2_DNA_primase_(EC_2.7.7.-) - Escherichia coli gb AA24600.1 (J01687) DNA primase [Escherichia coli] gb AAA89146.1 (U28379) CG Site No. 847; alternate gene name dnaP, parB [Escherichia coli] emb CAA23531.1 (V00274) DNA primase [Escherichia coli] gb AAC76102.1 (AE000388) DNA biosynthesis; DNA primase [Escherichia coli] Length = 581 "</p>
SEQ ID n°922	Prot n°PL-1800.1	Contig33	35200	36396	40%	<p>Identities = 91/324 (28%), Positives = 161/324 (49%), Gaps = 7/324 (2%)</p> <p>pir S44207 hypothetical protein 337 - Coxiella burnetii Length = 338</p>
SEQ ID n°923	Prot n°PL-1801.2	Contig33	36462	37811		
SEQ ID n°924	Prot n°PL-1802.1	Contig33	38521	39231	80%	<p>Identities = 168/236 (71%), Positives = 193/236 (81%), Gaps = 2/236 (0%)</p> <p>sp P75768 YBHL_ECOLI_HYPOTHETICAL_25.9_KDA_PROTEIN_IN_MOAE-RHLE_INTERGENIC_REGION pir B64815 ybhL protein - Escherichia coli gb AAC73873.1 (AE000181) orf, hypothetical protein [Escherichia coli] dbj BAA35444.1 (D90716) Hypothetical protein, 23.5K [Escherichia coli] Length = 234</p>
SEQ ID n°925	Prot n°PL-1803.1	Contig33	40631	41614	79%	<p>Identities = 233/329 (70%), Positives = 270/329 (81%), Gaps = 2/329 (0%)</p> <p>sp P30745 MOAA_ECOLI_MOLYBDENUM_COFACTOR_BIOSYNTHESIS_PROTEIN_A_pir S31879 molybdenum cofactor biosynthesis protein A - Escherichia coli emb CAA49861.1 (X70420) moaA [Escherichia coli] dbj BAA35439.1 (D90716) Molybdenum cofactor biosynthesis protein A. [Escherichia coli] gb AAC73868.1 (AE000181) molybdopterine biosynthesis, protein A [Escherichia coli] Length = 329</p>

TABLEAU I

SEQ ID n°926	Prot n°PL-1804.1	Contig33	42023	42931	83%	<p>Identities = 233/302 (77%), Positives = 285/302 (87%)</p> <p>sp P75767 YBHK_ECOLI_HYPOTHETICAL_32.8_KDA_PROTEIN_IN_UVRB-MOAA_INTERGENIC_REGION_pir D64814_ybhK_protein_Escherichia_coli_gb AAC73867.1 (AE000180) putative structural protein [Escherichia coli] dbj BAA35438.1 (D90716) Hypothetical protein 1 [Escherichia coli]</p>
SEQ ID n°927	Prot n°PL-1805.1	Contig33	43756	44769	72%	<p>Identities = 198/329 (60%), Positives = 245/329 (74%) dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] Length = 345</p>
SEQ ID n°928	Prot n°PL-1806.1	Contig33	45466	46677	30%	<p>Identities = 72/289 (24%), Positives = 125/289 (42%), Gaps = 15/289 (5%)</p> <p>gb AAG04210.1 (AE004517_5) (AE004517) hypothetical protein [Pseudomonas aeruginosa] Length = 362</p>
SEQ ID n°929	Prot n°PL-1807.1	Contig33	46649	47992	27%	<p>Identities = 68/290 (23%), Positives = 123/290 (41%), Gaps = 17/290 (5%)</p> <p>gb AAG04210.1 (AE004517_5) (AE004517) hypothetical protein [Pseudomonas aeruginosa] Length = 362</p>
SEQ ID n°930	Prot n°PL-1808.1	Contig33	47809	49209	No Hits found	
SEQ ID n°931	Prot n°PL-1809.1	Contig33	49170	51284	41%	<p>Identities = 204/576 (35%), Positives = 313/576 (53%), Gaps = 13/576 (2%)</p> <p>gb AAC32475.1 (AF044503) VgrG protein [Escherichia coli] Length = 567/615 (92%), Positives = 585/615 (94%), Gaps = 1/615 (0%)</p>
SEQ ID n°932	Prot n°PL-181.1	Contig41	298412	300277	80%	<p>sp P07336 RPSD_SALTY_RNA_POLYMERASE_SIGMA_FACTOR_RPOD (SIGMA-70) pir RNEBST_transcription_initiation_factor_sigma_70_Salmonella_typhimurium_gb AA27242.1 (M14427) rpoD protein [Salmonella typhimurium] Length = 615</p>
SEQ ID n°933	Prot n°PL-1811.1	Contig33	51934	53943	90%	<p>Identities = 570/671 (84%), Positives = 614/671 (90%), Gaps = 4/671 (0%)</p> <p>sp P07025 UVRB_ECOLI_EXCINUCLEASE_ABC_SUBUNIT_B_pir BVCECUB_excinuclease_ABC_chain_B_Escherichia_coli_emb CAA27357.1 (X03722) uvrB gene product (AA 1 - 673) [Escherichia coli] gb AAC73866.1 (AE000180) DNA repair; excision nuclease subunit B [Escherichia coli] Length</p>
SEQ ID n°934	Prot n°PL-1812.1	Contig33	55608	56231	No Hits found	
SEQ ID n°935	Prot n°PL-1813.1	Contig33	56232	57125	39%	<p>Identities = 62/232 (26%), Positives = 119/232 (50%), Gaps = 22/232 (9%)</p> <p>pir A72517_hypothetical_protein_APE2110_Aeropyrum_pernix_strain_K1_dbj BAA81121.1 (AP000063) 247aa long hypothetical protein [Aeropyrum pernix] Length = 247</p>
SEQ ID n°936	Prot n°PL-1814.1	Contig33	57442	58122	76%	<p>Identities = 148/225 (65%), Positives = 175/225 (77%), Gaps = 1/225 (0%)</p> <p>sp P13000 BIOD_ECOLI_DETHIOBIOTIN_SYNTHETASE (DETHIOBIOTIN SYNTHASE) (DTB SYNTHETASE) (DTBS) pir SYECDDB_dethiobiotin_synthase (EC 6.3.3.3) - Escherichia coli_gb AAC73865.1 (AE000180) dethiobiotin synthetase [Escherichia coli] Length = 225</p>
SEQ ID n°937	Prot n°PL-1815.1	Contig33	58115	58862	69%	<p>Identities = 143/255 (56%), Positives = 181/255 (70%)</p> <p>sp P36571 BIOC_SERMA_BIOTIN_SYNTHESIS_PROTEIN_BIOC_dbj BAA04287.1 (D17468) the product of bioC [Serratia marcescens]</p>

TABLEAU I

SEQ ID n°946	Prot n°PL-1824.1	Contig33	67802	68300	85%	<p>Identities = 177/227 (77%), Positives = 205/227 (89%)</p> <p>sp P09834 MODB_ECOLI_MOLYBDENUM_TRANSPORT_SYSTEM PERMEASE PROTEIN MODB gb AAB00836.1 (L34009) hydrophobic membrane-bound protein [Escherichia coli] gb AAB60172.1 (U27192) ModB [Escherichia coli] gb AAB08894.1 (U07867) part of a molybdenum periplasmic binding protein dependent transport system [Escherichia coli] prf J2204295C modB gene [Escherichia coli] Length = 229</p>
SEQ ID n°947	Prot n°PL-1825.1	Contig33	68437	69207	72%	<p>Identities = 156/254 (61%), Positives = 191/254 (74%), Gaps = 1/254 (0%)</p> <p>sp P37323 MODA_ECOLI_MOLYBDATE-BINDING_PERIPLASMIC_PROTEIN_PRECURSOR pir JC64812 molybdate-binding periplasmic protein precursor - Escherichia coli gb AAB00835.1 (L34009) periplasmic molybdate-binding protein [Escherichia coli] gb AAB60171.1 (U27192) ModA [Escherichia coli] gb AAB06893.1 (U07867) part of a molybdenum periplasmic binding protein dependent transport system [Escherichia coli] dbj BAA35427.1 (D90715) Molybdate-binding periplasmic protein precursor. [Escherichia coli] gb AAC73850.1 (AE000179) molybdate-binding periplasmic protein; permease [Escherichia coli] Length = 257</p>
SEQ ID n°948	Prot n°PL-1826.1	Contig33	69898	70689	72%	<p>Identities = 178/264 (67%), Positives = 209/264 (78%), Gaps = 3/264 (1%)</p> <p>pdb 1B9N A Chain A, Regulator From Escherichia Coli pdb 1B9N B Chain B, Regulator From Escherichia Coli Length = 265</p> <p>Identities = 335/489 (68%), Positives = 393/489 (79%)</p>
SEQ ID n°949	Prot n°PL-1827.1	Contig33	70866	72341	79%	<p>sp P31060 MODF_ECOLI_PUTATIVE_MOLYBDENUM_TRANSPORT_ATP-BINDING_PROTEIN_MODF (PHOTOREPAIR PROTEIN PHRA) pir JC6038 probable molybdenum transport protein modF - Escherichia coli gb AAB60176.1 (U27192) ModF [Escherichia coli] gb AAB06891.1 (U07867) ORF6 [Escherichia coli] gb AAC73847.1 (AE000178) ATP-binding component of molybdate transport system [Escherichia coli] dbj BAA35422.1 (D90714) Putative molybdenum transport ATP-binding protein ModF (photorepair protein Phra). [Escherichia coli] prf J2204295A modF gene [Escherichia coli] Length = 490</p>
SEQ ID n°950	Prot n°PL-1828.1	Contig33	72751	73572	65%	<p>Identities = 153/285 (57%), Positives = 184/265 (68%)</p> <p>gb AAG08517.1 AE004926_7 (AE004926) hypothetical protein [Pseudomonas aeruginosa] Length = 272</p>
SEQ ID n°951	Prot n°PL-1829.1	Contig33	73732	74484	90%	<p>Identities = 209/250 (83%), Positives = 229/250 (91%)</p> <p>sp P31217 PMG1_ECOLI_PHOSPHOGLYCERATE_MUTASE_1 (PHOSPHOGLYCEROMUTASE 1) (PGAM 1) (BPG-DEPENDENT PGAM 1) pir JC64811 phosphoglycerate mutase (EC 5.4.2.1) - Escherichia coli gb AAC73842.1 (AE000178) phosphoglyceromutase 1 [Escherichia coli] dbj BAA35417.1 (D90714) phosphoglycerate mutase 1 (EC 5.4.2.1) (phosphoglyceromutase 1) (pgam 1) (bpg-dependent pgam 1).</p>

TABLEAU I

SEQ ID n°952	Prot n°PL-183.1	Contig41	303737	304786	52%	<p>Identities = 117/311 (37%), Positives = 183/311 (58%), Gaps = 16/311 (5%) ref NP_043508.1 orf35 sp P51739 YO35_BPHP1_HYPOTHETICAL 58.7 KD PROTEIN IN LYS 3'REGION (ORF35) pir S69543 hypothetical protein 35- phage HP1 gb AAB09222.1 (U24159) orf35 [Bacteriophage HP1] Length = 533</p>
SEQ ID n°953	Prot n°PL-1830.1	Contig33	74581	75633	90%	<p>Identities = 292/350 (83%), Positives = 320/350 (91%) sp P00886 AROG_ECOLI PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, PHE-SENSITIVE (PHOSPHO-2-KETO-3- DEOXYHEPTONATE ALDOLASE) (DAHP SYNTHETASE) (3-DEOXY-D- ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE) pir ADECHF 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) (Phe-sensitive) - Escherichia coli pdb 1QR7 D Chain D, Crystal Structure Of Phenylalanine-Regulated 3-Deoxy-D- Arabino-Heptulosonate-7- Phosphate Synthase From Escherichia Coli Complexed With Pb2+ And Pep pdb 1QR7 A Chain A, Crystal Structure Of Phenylalanine-Regulated 3- Deoxy-D- Arabino-Heptulosonate-7-Phosphate Synthase From Escherichia Coli Complexed With Pb2+ And Pep pdb 1QR7 B Chain B, Crystal Structure Of Phenylalanine-Regulated 3-Deoxy-D- Arabino- Heptulosonate-7-Phosphate Synthase From Escherichia Coli Identities = 167/239 (69%), Positives = 193/239 (79%)</p>
SEQ ID n°954	Prot n°PL-1831.1	Contig33	76025	76750	79%	<p>sp P31215 PNUC_ECOLI PNUC PROTEIN pir G84810 pnuC protein - Escherichia coli dbj BAA35413.1 (D90714) PnuC protein . [Escherichia coli] gb AAC73838.1 (AE000177) required for NIMN transport [Escherichia coli] Length = 239</p>
SEQ ID n°955	Prot n°PL-1832.1	Contig33	76927	77957	82%	<p>Identities = 273/346 (78%), Positives = 311/346 (88%) sp P11459 NADA_ECOLI QUINOLINATE SYNTHETASE A pir SYECQA quinolinate synthetase A - Escherichia coli dbj BAA35409.1 (D90713) Quinolinate synthetase A. [Escherichia coli] dbj BAA35412.1 (D90714) Quinolinate synthetase A. [Escherichia coli] gb AAC73837.1 (AE000177) quinolinate synthetase, A protein [Escherichia coli] Length = 347</p>
SEQ ID n°956	Prot n°PL-1833.1	Contig33	78975	79745	43%	<p>Identities = 63/186 (33%), Positives = 113/186 (59%), Gaps = 4/186 (2%) emb CAB88835.1 (AL353832) putative ABC-transport protein, ATP-binding component. [Streptomyces coelicolor A3(2)] Length = 354</p>
SEQ ID n°957	Prot n°PL-1834.1	Contig33	80581	81375	32%	<p>Identities = 52/205 (25%), Positives = 88/205 (41%), Gaps = 22/205 (10%) pir H75377 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb AAAF11145.1 AE002002_3 (AE002002) conserved hypothetical protein [Deinococcus radiodurans] Length = 262</p>
SEQ ID n°958	Prot n°PL-1835.1	Contig33	81533	82399	32%	<p>Identities = 78/161 (47%), Positives = 95/161 (58%), Gaps = 26/161 (16%) pir S16687 Sc/SN protein - Escherichia coli plasmid p15B emb CAA44050.1 (X62121) DNA Inversion product [Escherichia coli] Length = 762</p>

TABLEAU I

SEQ ID n°959	Prot n°PL-1836.1	Contig33	82768	83691	32%	Identities = 84/154 (54%), Positives = 100/154 (64%), Gaps = 8/154 (5%) pir S18690 Sc/SvQ protein - Escherichia coli plasmid p15B emb CAA44053.1 (X62121) DNA inversion product [Escherichia coli] Length = 748
SEQ ID n°960	Prot n°PL-1837.1	Contig33	85234	85229	31%	Identities = 81/152 (53%), Positives = 104/152 (68%), Gaps = 8/152 (5%) pir S18690 Sc/SvQ protein - Escherichia coli plasmid p15B emb CAA44053.1 (X62121) DNA inversion product [Escherichia coli] Length = 748
SEQ ID n°961	Prot n°PL-1838.1	Contig33	86928	87791	49%	Identities = 69/278 (24%), Positives = 142/278 (50%), Gaps = 13/278 (4%) pir S25259 streptomycin resistance protein - Bacteroides spp. transposon Tn4551 gb AA27459.1 (M72415) streptomycin adenyltransferase [Transposon Tn4551] Length = 287
SEQ ID n°962	Prot n°PL-1839.1	Contig33	89475	90251	79%	Identities = 158/267 (59%), Positives = 207/267 (77%), Gaps = 13/267 (4%) spiP45955 YBGF_ECOLI HYPOTHETICAL 28.2 KDA PROTEIN IN PAL-LYST INTERGENIC REGION PRECURSOR pir E64810 ybgF protein precursor - Escherichia coli gb AAC73836.1 (AE000177) orf, hypothetical protein [Escherichia coli] dbj BAA35408.1 (D90713) hypothetical 28.2 kd protein in pal-lysT intergenic region. [Escherichia coli] Length =
SEQ ID n°963	Prot n°PL-184.1	Contig41	304787	305755	26%	Identities = 52/187 (27%), Positives = 84/187 (44%), Gaps = 18/187 (10%) gb AAD02882.1 (AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana] Length = 348
SEQ ID n°964	Prot n°PL-1840.1	Contig33	90804	92096	86%	Identities = 340/431 (78%), Positives = 386/431 (88%) pir JVO058 tolB protein - Escherichia coli gb AAA24684.1 (M28232) tolB [Escherichia coli] dbj BAA35406.1 (D90713) TolB protein [Escherichia coli] Length = 431
SEQ ID n°965	Prot n°PL-1841.1	Contig33	92563	93186	44%	Identities = 60/171 (35%), Positives = 92/171 (53%), Gaps = 5/171 (2%) dbj BAA87453.1 (AB029393) streptococcal hemagglutinin [Streptococcus gordonii] Length = 2178
SEQ ID n°966	Prot n°PL-1842.1	Contig33	92310	93380	72%	Identities = 223/425 (52%), Positives = 264/425 (61%), Gaps = 74/425 (17%) spiP19934 TOLA_ECOLI TOLA PROTEIN pir JVO057 tolA protein - Escherichia coli gb AAA24683.1 (M28232) tolA [Escherichia coli] dbj BAA35405.1 (D90713) TolA protein. [Escherichia coli] gb AAC73833.1 (AE000177) membrane spanning protein, required for outer membrane integrity [Escherichia coli] Length = 421
SEQ ID n°967	Prot n°PL-1843.1	Contig33	93866	94561	90%	Identities = 199/222 (89%), Positives = 212/222 (94%) spiP05828 TOLQ_ECOLI TOLQ PROTEIN pir BVECTQ biopolymer transport protein tolQ - Escherichia coli gb AAA83919.1 (M16489) ORF 2; putative [Escherichia coli] dbj BAA35403.1 (D90713) TolQ protein. [Escherichia coli] gb AAC73831.1 (AE000177) inner membrane protein, membrane-spanning, maintains integrity of cell envelope; tolerance to group A colicins [Escherichia coli] Length = 230

TABLEAU I

SEQ ID n°968	Prot n°PL-1844.1	Contig33	95508	96647	83%	<p>Identities = 288/379 (75%), Positives = 325/379 (84%)</p> <p>sp P11027 CYDB_ECOLI CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (CYTOCHROME BD-I OXIDASE SUBUNIT II) pir B28940 cytochrome d ubiquinol oxidase (EC 1.10.3.-) chain II - Escherichia coli gb AAA18805.1 J03939 cytochrome oxidase d subunit II [Escherichia coli] dbj BAA35400.1 D90713 Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-) [Escherichia coli] gb AAC73828.1 AE000176 cytochrome d terminal oxidase polypeptide subunit II [Escherichia coli] Length = 1039</p> <p>Identities = 439/522 (84%), Positives = 484/522 (92%) gb AAA18804.1 J03939 cytochrome oxidase d subunit I [Escherichia coli] Length = 522</p> <p>Identities = 69/183 (37%), Positives = 102/183 (55%)</p> <p>gb AAG07569.1 AE004834.9 AE004834 hypothetical protein [Pseudomonas aeruginosa] Length = 212</p> <p>Identities = 91/297 (30%), Positives = 148/297 (49%), Gaps = 11/297 (3%)</p> <p>sp Q9ZHEJ HIS8_BUCAP HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (IMIDAZOLE ACETOL-PHOSPHATE TRANSAMINASE) gb AAC97356.1 AF067228 histidinophosphate aminotransferase [Buchnera aphidicola] Length = 355</p> <p>Identities = 75/377 (19%), Positives = 152/377 (39%), Gaps = 23/377 (6%)</p> <p>pir H72265 hypothetical protein TM1336 - Thermotoga maritima (strain MSB8) gb AAD36408.1 AE001788.3 AE001788 permease, putative [Thermotoga maritima] Length = 390</p> <p>Identities = 96/378 (25%), Positives = 164/378 (42%), Gaps = 27/378 (7%)</p> <p>emb CAB67718.1 AJ271405 putative carbamoyl-phosphate-synthetase [Streptomyces rochei] Length = 410</p> <p>Identities = 124/296 (41%), Positives = 181/296 (60%), Gaps = 2/296 (0%)</p> <p>sp P75828 YBJX_ECOLI HYPOTHETICAL 38.4 KDA PROTEIN IN AQPZ-CSPD INTERGENIC REGION pir E84826 ybX protein - Escherichia coli gb AAC73984.1 AE000189 putative enzyme [Escherichia coli] dbj BAA35585.1 D90725 VirK protein [Escherichia coli] Length = 330</p> <p>Identities = 67/249 (26%), Positives = 116/249 (45%), Gaps = 9/249 (3%)</p> <p>emb CAB82560.1 AL356812 putative carboxylase. [Streptomyces coelicolor A3(2)] Length = 405</p> <p>Identities = 62/237 (26%), Positives = 100/237 (42%), Gaps = 37/237 (15%)</p> <p>emb CAC11881.1 AL445085 conserved hypothetical protein [Thermoplasma acidophilum] Length = 220</p> <p>Identities = 107/272 (39%), Positives = 165/272 (60%), Gaps = 11/272 (4%)</p> <p>sp O67733 ILVE_AQUAE PROBABLE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (BCAT) pir C70463 branched-chain amino acid aminotransferase - Aquifex aeolicus gb AAC07697.1 AE000762 branched-chain amino acid aminotransferase [Aquifex aeolicus] Length = 1039</p>
SEQ ID n°969	Prot n°PL-1845.1	Contig33	96662	98230	91%	
SEQ ID n°970	Prot n°PL-1846.1	Contig33	100604	101242	46%	
SEQ ID n°971	Prot n°PL-1847.1	Contig33	101731	102837	40%	
SEQ ID n°972	Prot n°PL-1848.1	Contig33	102879	104069	38%	
SEQ ID n°973	Prot n°PL-1849.1	Contig33	104127	106595	19%	
SEQ ID n°974	Prot n°PL-185.1	Contig41	306980	307915	58%	
SEQ ID n°975	Prot n°PL-1850.1	Contig33	106589	107881	26%	
SEQ ID n°976	Prot n°PL-1851.1	Contig33	107882	108646	39%	
SEQ ID n°977	Prot n°PL-1852.1	Contig33	108664	109464	61%	

TABLEAU I

SEQ ID n°978	Prot n°PL-1853.1	Contig33	109608	111239	38%	Identities = 120/420 (28%), Positives = 188/420 (46%), Gaps = 25/420 (5%) dbj BAA82878.1 (AB024335) 3-(3-hydroxyphenyl)propionate hydroxylase [Comamonas testosteroni] Length = 589
SEQ ID n°979	Prot n°PL-1854.1	Contig33	111240	112541	No Hits found	Identities = 107/362 (29%), Positives = 181/362 (49%), Gaps = 11/362 (3%) sp P42533 YCBU_BACSU HYPOTHETICAL 40.8 KD PROTEIN IN PCP-LMRB INTERGENIC REGION PRECURSOR (ORF21) pir E69754 nifs protein homolog ycbU - Bacillus subtilis dbj BAA22227.1 (AB000617) YcbU [Bacillus subtilis] emb CAB12060.1 (Z99105) similar to Nifs protein homolog [Bacillus subtilis] Length = 370
SEQ ID n°980	Prot n°PL-1855.1	Contig33	112575	113738	46%	Identities = 68/265 (25%), Positives = 102/265 (37%), Gaps = 54/265 (20%) pir T36536 probable oxidoreductase - Streptomyces coelicolor emb CAB42033.1 (AL049754) putative oxidoreductase [Streptomyces coelicolor A3(2)] Length = 271
SEQ ID n°981	Prot n°PL-1856.1	Contig33	113723	114436	42%	Identities = 267/288 (92%), Positives = 278/288 (95%) sp P07459 SUCCD_ECOLI SUCCINYL-COA SYNTHETASE ALPHA CHAIN (SCS-ALPHA) pir SYECSC succinate-CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain - Escherichia coli gb AAA23900.1 (J01619) succinyl-CoA synthetase alpha-subunit [Escherichia coli] dbj BAA35395.1 (D90711) Succinate-CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain. [Escherichia coli] gb AAC73823.1 (AE000176) succinyl-CoA synthetase, alpha subunit [Escherichia coli] Length = 289
SEQ ID n°982	Prot n°PL-1857.1	Contig33	115168	116043	91%	Identities = 352/388 (90%), Positives = 363/388 (92%) sp P07480 SUCC_ECOLI SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS BETA) pir SYECSCB succinate-CoA ligase (ADP-forming) (EC 6.2.1.5) beta chain - Escherichia coli pdb 1SCUJB Chain B, Succinyl-CoA Synthetase (Succinate-CoA Ligase) (Adp-Forming) (E.C.6.2.1.5) pdb 1SCUJE Chain E, Succinyl-CoA Synthetase (Succinate-CoA Ligase) (Adp-Forming) (E.C.6.2.1.5) pdb 2SCUJB Chain B, A Detailed Description Of The Structure Of Succinyl-CoA Synthetase From Escherichia Coli Structure Of Succinyl-CoA Synthetase From Escherichia Coli Structure Of Succinyl-CoA Synthetase From Escherichia Coli gb AAA23889.1 (J01619) succinyl-CoA synthetase beta-subunit [Escherichia coli] dbj BAA35394.1 (D90711) Succinate-CoA ligase (ADP-forming) (EC 6.2.1.5) beta chain. [Escherichia coli] gb AAC73822.1 (AE000176) succinyl-CoA synthetase, beta subunit [Escherichia coli] Length = 388
SEQ ID n°983	Prot n°PL-1858.1	Contig33	116046	117212	92%	Identities = 85/185 (45%), Positives = 117/185 (62%), Gaps = 3/185 (1%) gb AAC03422.1 (U81516) unknown [Mycococcus xanthus] Length = 216
SEQ ID n°984	Prot n°PL-186.1	Contig41	307969	308568	54%	

TABLEAU I

SEQ ID n°985	Prot n°PL-1860.1	Contig33	117379	118599	87%	<p>Identities = 328/407 (80%), Positives = 362/407 (88%), Gaps = 3/407 (0%)</p> <p>sp P07016 ODO2_ECOLI DIHYDROLIPOAMIDE SUCCINYLTTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (E2) pir JXUECD dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - Escherichia coli emb CAA25284.1 (X00664) E20 component [Escherichia coli] gb AA23898.1 (J01619) dihydrolipoamide succinyltransferase [Escherichia coli] dbj BAA35393.1 (D90711) Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61). [Escherichia coli] gb AAC73821.1 (AE000175) 2-oxoglutarate dehydrogenase (dihydrolipoamylsuccinyltransferase E2 component) [Escherichia coli]</p>
SEQ ID n°986	Prot n°PL-1861.1	Contig33	118614	121421	90%	<p>Identities = 780/935 (83%), Positives = 849/935 (90%), Gaps = 2/935 (0%)</p> <p>sp P07015 ODO1_ECOLI 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE) pir DEECOG oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - Escherichia coli dbj BAA35392.1 (D90711) Oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) [Escherichia coli] gb AAC73820.1 (AE000175) 2-oxoglutarate dehydrogenase (decarboxylase component) [Escherichia coli] Length = 933</p>
SEQ ID n°987	Prot n°PL-1862.1	Contig33	121688	122404	95%	<p>Identities = 215/238 (90%), Positives = 228/238 (95%)</p> <p>sp P07014 DHSB_ECOLI SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN pir DEECSE succinate dehydrogenase (EC 1.3.99.1) Iron-sulfur protein - Escherichia coli emb CAA25534.1 (X01070) succinate dehydrogenase iron-sulphur protein subunit [Escherichia coli] gb AA23896.1 (J01619) succinate dehydrogenase small subunit [Escherichia coli] dbj BAA35391.1 (D90711) Succinate dehydrogenase (EC 1.3.99.1) Iron-sulfur protein [Escherichia coli] gb AAC73818.1 (AE000175) succinate dehydrogenase, iron sulfur protein [Escherichia coli] Identities = 535/588 (90%), Positives = 566/588 (95%)</p>
SEQ ID n°988	Prot n°PL-1863.1	Contig33	122441	124207	96%	<p>sp P10444 DHSA_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT pir DEECSE succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Escherichia coli dbj BAA35390.1 (D90711) Succinate dehydrogenase (EC 1.3.99.1) flavoprotein [Escherichia coli] gb AAC73817.1 (AE000175) succinate dehydrogenase, flavoprotein subunit Identities = 368/427 (83%), Positives = 394/427 (91%)</p>
SEQ ID n°989	Prot n°PL-1864.1	Contig33	125808	127091	86%	<p>Identities = 368/427 (83%), Positives = 394/427 (91%)</p> <p>pir YKEC citrate (si)-synthase (EC 4.1.3.7) - Escherichia coli dbj BAA35387.1 (D90711) Citrate synthase (EC 4.1.3.7) [Escherichia coli] gb AAC73814.1 (AE000175) citrate synthase [Escherichia coli] Length = 427</p>

TABLEAU I

SEQ ID n°990	Prot n°PL-1865.1	Contig33	127444	128187	75%	<p>Identities = 175/246 (71%), Positives = 197/246 (79%)</p> <p>sp P75743 YBGL_ECOLI HYPOTHETICAL 26.9 KDA PROTEIN IN PHRB-NEI INTERGENIC REGION pir E64806 ybgI protein - Escherichia coli</p> <p>gb AAC73804.1 (AE000174) orf, hypothetical protein [Escherichia coli]</p> <p>dbj BAA35374.1 (D90710) Hypothetical protein H10105 [Escherichia coli]</p> <p>Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%)</p> <p>dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188</p>
SEQ ID n°991	Prot n°PL-1866.1	Contig33	129449	130516	21%	<p>Identities = 387/562 (68%), Positives = 469/562 (82%), Gaps = 7/562 (1%)</p> <p>sp P03959 ATKA_ECOLI POTASSIUM-TRANSPORTING ATPASE A CHAIN (ATP PHOSPHOHYDROLASE [POTASSIUM-TRANSPORTING] A CHAIN) pir PWECAR H+/K+-exchanging ATPase (EC 3.6.1.36) chain A - Escherichia coli gb AAB96335.1 (K02670) kdpA [Escherichia coli]</p> <p>dbj BAA35356.1 (D90709) Potassium-transporting ATPase (EC 3.6.1.36), a chain (ATP phosphohydrolase (potassium-transporting), A chain), [Escherichia coli] gb AAC73792.1 (AE000173) ATPase of high-affinity potassium transport system, A chain [Escherichia coli] Length =</p> <p>Identities = 548/684 (80%), Positives = 611/684 (89%), Gaps = 9/684 (0%)</p> <p>gb AAB96336.1 (K02670) kdpB [Escherichia coli] Length = 682</p>
SEQ ID n°992	Prot n°PL-1867.1	Contig33	131017	132723	82%	<p>Identities = 467/670 (69%), Positives = 543/670 (80%)</p> <p>sp P42593 FADH_ECOLI 2,4-DIENOYL-COA REDUCTASE [NADPH] (2,4-DIENOYL COENZYME A REDUCTASE) pir F65096 probable NADH-dependent flavin oxidoreductase (EC 1.-.-.-) - Escherichia coli (strain K-12) gb AAA57882.1 (U18997) ORF_0672 [Escherichia coli] gb AAC76116.1 (AE000390) putative NADPH dehydrogenase [Escherichia coli]</p> <p>gb AAB82738.1 (U83405) 2,4-dienoyl-CoA reductase [Escherichia coli]</p> <p>Identities = 582/892 (65%), Positives = 707/892 (79%), Gaps = 10/892 (1%)</p> <p>sp P21865 KDPD_ECOLI SENSOR PROTEIN KDPD pir B42372 sensor protein kdpD (EC 2.7.3.-) - Escherichia coli gb AAA24041.1 (M36066) transmembrane protein (kdpD) [Escherichia coli] dbj BAA35352.1 (D90709) Regulatory protein KdpD. [Escherichia coli] gb AAC73789.1 (AE000173) sensor for high-affinity potassium transport system [Escherichia coli] Length = 894</p>
SEQ ID n°995	Prot n°PL-1870.1	Contig33	135406	138105	77%	<p>Identities = 165/221 (74%), Positives = 190/221 (85%)</p> <p>sp P21866 KDPE_ECOLI KDP OPERON TRANSCRIPTIONAL REGULATORY PROTEIN KDPE pir E64804 transcription regulator kdpE - Escherichia coli</p> <p>gb AAC73788.1 (AE000173) regulator of kdp operon (transcriptional effector) [Escherichia coli] Length = 225</p>
SEQ ID n°997	Prot n°PL-1872.1	Contig33	139060	140601	No Hits found	
SEQ ID n°998	Prot n°PL-1873.1	Contig33	141025	141852	59%	<p>Identities = 109/265 (41%), Positives = 184/265 (61%) gb AAF93311.1 (AE004104) conserved hypothetical protein [Vibrio cholerae] Length =</p>

TABLEAU I

SEQ ID n°999	Prot n°PL-1874.1	Contig33	141860	142546	27%	Identities = 42/123 (34%), Positives = 64/123 (51%), Gaps = 2/123 (1%) pir A75275 methionyl-tRNA formyltransferase - Deinococcus radiodurans (strain R1) gb AAAF1976.1 AE002073.6 (AE002073) methionyl-tRNA formyltransferase [Deinococcus radiodurans] Length = 318
SEQ ID n°1000	Prot n°PL-1875.1	Contig33	142531	144387	55%	Identities = 198/607 (32%), Positives = 345/607 (56%), Gaps = 27/607 (4%) gb AAC05838.1 (AF052516) hemolysin erythrocyte lysis protein 2 [Prevotella intermedia] Length = 606
SEQ ID n°1001	Prot n°PL-1876.1	Contig33	144624	145829	18%	Identities = 38/157 (24%), Positives = 74/157 (46%), Gaps = 17/157 (10%) pir E71622 probable membrane associated protein PF80125c - malaria parasite (Plasmodium falciparum) gb AAC71815.1 (AE001374) predicted membrane associated protein [Plasmodium falciparum] Length = 1308
SEQ ID n°1002	Prot n°PL-1877.1	Contig33	146174	147421	65%	Identities = 132/379 (34%), Positives = 229/379 (59%), Gaps = 6/379 (1%) gb AAF98868.1 (AE004423) conserved hypothetical protein [Vibrio cholerae] Length = 434
SEQ ID n°1003	Prot n°PL-1878.1	Contig33	148658	150298	84%	Identities = 419/539 (77%), Positives = 475/539 (87%) sp P36938 PGMU_ECOLI PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM) pir G64803 phosphoglucomutase (EC 5.4.2.2) - Escherichia coli gb AAA57067.1 (U08369) phosphoglucomutase [Escherichia coli] dbj BAA35337.1 (D90707) Phosphoglucomutase (EC 5.4.2.2) (glucose phosphomutase) (pgm). [Escherichia coli] dbj BAA35345.1 (D90708) Phosphoglucomutase (EC 5.4.2.2) (glucose phosphomutase) (pgm). [Escherichia coli] gb AAC73782.1 (AE000172) phosphoglucomutase [Escherichia coli] Length = 546
SEQ ID n°1004	Prot n°PL-1879.1	Contig33	151671	152636	76%	Identities = 212/320 (66%), Positives = 249/320 (77%) sp P46880 HXKG_ECOLI GLUCOKINASE (GLUCOSE KINASE) pir A65013 glucokinase (EC 2.7.1.2) - Escherichia coli (strain K-12) gb AAC75447.1 (AE000327) glucokinase [Escherichia coli] dbj BAA16258.1 (D90868) GLUCOKINASE (EC 2.7.1.2). [Escherichia coli] dbj BAA16261.1 (D90869) GLUCOKINASE (EC 2.7.1.2). [Escherichia coli] Length = 321
SEQ ID n°1005	Prot n°PL-188.1	Contig41	311103	312350	83%	Identities = 287/405 (73%), Positives = 352/405 (86%) sp P42602 YGJU_ECOLI HYPOTHETICAL SYMPORTER YGJU pir F65097 hypothetical 43.5 kD protein in ebgC-exuT intergenic region - Escherichia coli (strain K-12) gb AAA57891.1 (U18997) ORF_0414; Geneplot suggests frameshift near start but none found [Escherichia coli] gb AAC76124.1 (AE000391) putative transport protein [Escherichia coli]

TABLEAU I

SEQ ID n°1006	Prot n°PL-1880.1	Contig33	155630	157048	89%	<p>Identities = 396/469 (84%), Positives = 429/469 (91%) spiP04805[SYE_ECOLI GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE-TRNA LIGASE) (GLURS) pir SYECET glutamate-TRNA ligase (EC 6.1.1.17) - Escherichia coli emb CAA45391.1 (X63976) glutamyl-TRNA synthetase [Escherichia coli] gb AA065715.1 (M13687) glutamyl-TRNA synthetase [Escherichia coli] gb AAC75457.1 (AE000328) glutamate tRNA synthetase, catalytic subunit [Escherichia coli] dbj BAA16272.1 (D90869) glutamate-TRNA ligase (EC 6.1.1.17) [Escherichia coli] Length = 471</p> <p>Identities = 310/400 (77%), Positives = 352/400 (87%), Gaps = 6/400 (1%) spiP33031 NUPC_ECOLI NUCLEOSIDE PERMEASE NUPC (NUCLEOSIDE-TRANSPORT SYSTEM PROTEIN NUPC) pir F65013 nucleoside transport protein nupC - Escherichia coli gb AAC75452.1 (AE000327) permease of transport system for 3 nucleosides [Escherichia coli] dbj BAA16263.1 (D90869) NUCLEOSIDE PERMEASE NUPC (NUCLEOSIDE-TRANSPORT SYSTEM PROTEIN NUPC) [Escherichia coli] Length = 400</p> <p>Identities = 522/671 (77%), Positives = 595/671 (87%), Gaps = 1/671 (0%) spiP15042 DNLI_ECOLI DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [NAD+]) pir LQEC6 DNA ligase (NAD+) (EC 6.5.1.2) - Escherichia coli gb AAA24070.1 (M24278) DNA ligase (EC 6.5.1.2) [Escherichia coli] gb AAC75464.1 (AE000328) DNA ligase [Escherichia coli] Identities = 159/322 (49%), Positives = 199/322 (61%), Gaps = 27/322 (8%) spiP77173 ZIPA_ECOLI CELL DIVISION PROTEIN ZIPA gb AAB42081.1 (U74850) ZipA [Escherichia coli] Length = 328</p> <p>Identities = 169/249 (67%), Positives = 209/249 (83%), Gaps = 2/249 (0%) spiP12610 CYSZ_ECOLI CYSZ PROTEIN pir BVECCZ probable sulfate transport protein CysZ - Escherichia coli (strain K-12) gb AAC75466.1 (AE000329) required for sulfate transport [Escherichia coli] Length = 253</p> <p>Identities = 255/318 (80%), Positives = 287/318 (90%), Gaps = 1/318 (0%) pdb 1OAS A Chain A, O-Acetylserine Sulfhydrylase From Salmonella Typhimurium pdb 1OAS B Chain B, O-Acetylserine Sulfhydrylase From Salmonella Typhimurium Length = 322</p> <p>Identities = 454/575 (78%), Positives = 507/575 (87%) spiP12654 PT1_SALTY PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I) pir WQEBPI phosphotransferase system enzyme I (EC 2.7.3.9) - Salmonella typhimurium gb AA27060.1 (M76176) enzyme I [Salmonella typhimurium] Length = 575</p>
SEQ ID n°1007	Prot n°PL-1881.1	Contig33	158024	159208	85%	
SEQ ID n°1008	Prot n°PL-1882.1	Contig33	159569	161587	88%	
SEQ ID n°1009	Prot n°PL-1883.1	Contig33	161649	162560	64%	
SEQ ID n°1010	Prot n°PL-1884.1	Contig33	162781	163551	72%	
SEQ ID n°1011	Prot n°PL-1885.1	Contig33	163666	164619	89%	
SEQ ID n°1012	Prot n°PL-1886.1	Contig33	165815	167342	87%	
SEQ ID n°1013	Prot n°PL-1887.1	Contig38	532469	533764	50%	<p>Identities = 147/396 (37%), Positives = 216/396 (54%), Gaps = 11/396 (2%) gb AAC31494.1 (AF071034) L0015 [Escherichia coli] Length = 512</p>

TABLEAU I

SEQ ID n°1014	Prot n°PL-1888.1	Contig38	529546	530676	56%	<p>Identities = 135/354 (38%), Positives = 214/354 (60%), Gaps = 13/354 (3%) gb AAA96312.1 (U50906) outer membrane adherence protein-associated protein [Escherichia coli] Length = 547</p>
SEQ ID n°1015	Prot n°PL-1889.1	Contig38	527949	528815	89%	<p>Identities = 239/288 (82%), Positives = 259/288 (89%), Gaps = 1/288 (0%) sp P32705 YJCG_ECOLI_HYPOTHETICAL_59.2_KD_PROTEIN_IN_SOXR-ACS_INTERGENIC_REGION (F549) pir B65215 hypothetical 59.2 kD protein in soxr-acs intergenic region - Escherichia coli (strain K-12) gb AAC43161.1 (U00006) similar to Salmonella proline permease [Escherichia coli] gb AAC77037.1 (AE000480) putative transport protein [Escherichia coli] Length = 549</p>
SEQ ID n°1016	Prot n°PL-189.1	Contig41	312767	313729	77%	<p>Identities = 228/312 (73%), Positives = 264/312 (84%) sp P42601 YGJT_ECOLI_HYPOTHETICAL_35.8_KDA_PROTEIN_IN_EBGC-UXAA_INTERGENIC_REGION pir E65097 hypothetical 35.8 kD protein in ebGC-exuI intergenic region - Escherichia coli (strain K-12) gb AAA57890.1 (U18997) ORF_0321 [Escherichia coli] gb AAC76123.1 (AE000391) putative transport protein [Escherichia coli] Length = 321</p>
SEQ ID n°1017	Prot n°PL-1890.1	Contig38	527166	527948	84%	<p>Identities = 199/254 (78%), Positives = 223/254 (87%) gb AAG06622.1 (AE004746_6 (AE004746) probable sodium:solute symporter [Pseudomonas aeruginosa] Length = 551</p>
SEQ ID n°1018	Prot n°PL-1891.1	Contig38	524838	526793	90%	<p>Identities = 529/650 (81%), Positives = 591/650 (90%) sp P27550 ACSA_ECOLI_ACETYL-COENZYME_A_SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME) pir D65215 acetate-CoA ligase (EC 6.2.1.1) - Escherichia coli gb AAC43163.1 (U00006) acetyl-CoA synthetase [Escherichia coli] gb AAC77039.1 (AE000480) acetyl-CoA synthetase [Escherichia coli] Length = 652</p>
SEQ ID n°1019	Prot n°PL-1892.1	Contig38	523838	524464	81%	<p>Identities = 174/205 (84%), Positives = 192/205 (92%) sp P53655 SODM_YEREN_SUPEROXIDE_DISMUTASE [MN] emb CAA65586.1 (X96852) soda [Yersinia enterocolitica] Length = 207</p>
SEQ ID n°1020	Prot n°PL-1893.1	Contig38	523048	523719	77%	<p>Identities = 145/222 (65%), Positives = 174/222 (78%) sp P32157 YIIM_ECOLI_HYPOTHETICAL_26.6_KD_PROTEIN_IN_KDGT-CPXA_INTERGENIC_REGION (O234) pir S40854 hypothetical 26.6k protein (kdgt-cpxa intergenic region) - Escherichia coli gb AAB03043.1 (L19201) ORF_0234 [Escherichia coli] gb AAC76892.1 (AE000466) orf, hypothetical protein [Escherichia coli] Length = 234</p>
SEQ ID n°1021	Prot n°PL-1894.1	Contig38	522073	522705	54%	<p>Identities = 80/182 (43%), Positives = 114/182 (61%), Gaps = 3/182 (1%) sp P45215 YE59_HAEIN_PROBABLE_RNA_POLYMERASE_SIGMA_FACTOR_H11459 - pir G64124 transcription initiation factor sigma homolog H11459 - Haemophilus influenzae (strain Rd KW20) gb AAC23107.1 (U32824) sigma factor, putative [Haemophilus influenzae Rd] Length = 194</p>
SEQ ID n°1022	Prot n°PL-1895.1	Contig38	520594	521388	No Hits found	

TABLEAU I

SEQ ID n°1023	Prot n°PL-1896.1	Contig38	519801	520670	48%	Identities = 104/304 (34%), Positives = 163/304 (50%), Gaps = 30/304 (9%) sp P44268 YG00_HAEIN HYPOTHETICAL PROTEIN HI1600 pir IH64037 hypothetical protein HI1600 - Haemophilus influenzae (strain Rd KW20) gb AAC23259.1 (U32834) H. influenzae predicted coding region HI1600 [Haemophilus influenzae Rd] Length = 317
SEQ ID n°1024	Prot n°PL-1897.1	Contig38	517665	518723	83%	Identities = 271/332 (81%), Positives = 294/332 (87%) pir YWEC tryptophan- tRNA ligase (EC 6.1.1.2) - Escherichia coli gb AAA58181.1 (U18997) CG site No. 67 [Escherichia coli] gb AAC76409.1 (AE000414) tryptophan tRNA synthetase [Escherichia coli] Length = 334
SEQ ID n°1025	Prot n°PL-1898.1	Contig38	516977	517681	59%	Identities = 134/244 (54%), Positives = 169/244 (68%), Gaps = 17/244 (6%) sp P32662 GPH_ECOLI PHOSPHOGLYCULATE PHOSPHATASE (PGP) pir IS5288 gph protein - Escherichia coli emb CAA79864.1 (Z19601) ORF for 27kD protein. [Escherichia coli] gb AAA58182.1 (U18997) 27 kD protein in ECDAOPRA [Escherichia coli] gb AAC76410.1 (AE000414) phosphoglycolate phosphatase [Escherichia coli] Length = 252
SEQ ID n°1026	Prot n°PL-1899.1	Contig38	516295	516987	83%	Identities = 187/224 (83%), Positives = 207/224 (91%) sp P32661 RPE_ECOLI RIBULOSE-PHOSPHATE 3-EPIMERASE (PENTOSE-5-PHOSPHATE 3- EPIMERASE) (PPE) (R5P3E) pir E65133 ribulose-phosphate 3- epimerase (EC 5.1.3.1) - Escherichia coli gb AAA58183.1 (U18997) 24 kD protein [Escherichia coli] gb AAC76411.1 (AE000414) D-ribulose-5- phosphate 3-epimerase [Escherichia coli] Length = 225
SEQ ID n°1027	Prot n°PL-19.1	Contig41	33677	34678	60%	Identities = 133/329 (40%), Positives = 203/329 (61%) gb AAF95481.1 (AE004303) transcriptional regulator, LacI family [Vibrio cholerae] Length = 335
SEQ ID n°1028	Prot n°PL-190.1	Contig41	314381	315052	85%	Identities = 152/215 (70%), Positives = 193/215 (89%) sp P42614 YQJA_ECOLI HYPOTHETICAL 24.8 KDA PROTEIN IN EXUR- TDCC INTERGENIC REGION pir ID65098 hypothetical protein b3095 - Escherichia coli (strain K-12) gb AAA57899.1 (U18997) ORF_o220 [Escherichia coli] gb AAC76130.1 (AE000391) orf, hypothetical protein Identities = 203/270 (75%), Positives = 238/270 (87%)
SEQ ID n°1029	Prot n°PL-1900.1	Contig38	515434	516246	86%	sp P45454 DMA_SERMA DNA ADENINE METHYLASE (DEOXYADENOSYL- METHYLTRANSFERASE) pir IS47099 site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) dam - Serratia marcescens emb CAA55177.1 (X78412) Deoxyadenosyl-methyltransferase [Serratia marcescens] Length = 189/372 (50%), Gaps = 76/372 (20%)
SEQ ID n°1030	Prot n°PL-1901.1	Contig38	514324	515349	55%	Identities = 123/372 (33%), Positives = 189/372 (50%), Gaps = 76/372 (20%) pir Q4ECAD damX protein (aroB-dam intergenic region) - Escherichia coli gb AAA58185.1 (U18997) damX [Escherichia coli] gb AAC76413.1 (AE000414) putative membrane protein; interferes with cell division [Escherichia coli] Length = 428 "

TABLEAU I

SEQ ID n°1031	Prot n°PL-1902.1	Contig38	513030	514130	85%	<p>Identities = 269/360 (74%), Positives = 318/360 (87%), Gaps = 1/360 (0%)</p> <p>sp P07639 AROB_ECOLI_3-DEHYDROQUINATE SYNTHASE pir SYECQ_3-dehydroquinolate synthase (EC 4.6.1.3) - Escherichia coli emb CAA27485.1 (X03867) 3-dehydroquinolate synthase (aa 1-362) [Escherichia coli] emb CAA79666.1 (Z19801) ORF, aroB, Millar G., Coggins J.R.; FEBS Lett. 200;11-17(1986) [Escherichia coli] gb AAA58186.1 (U18997) 3-dehydroquinolate synthase [Escherichia coli] gb AAC76414.1 (AE000414) 3-dehydroquinolate synthase [Escherichia coli] Length = 362 "</p>
SEQ ID n°1032	Prot n°PL-1903.1	Contig38	511015	512091	53%	<p>Identities = 142/300 (47%), Positives = 192/300 (63%), Gaps = 6/300 (2%)</p> <p>sp P34749 HOFQ_ECOLI PROTEIN TRANSPORT PROTEIN HOFQ-PRERUSOR pir B65134 protein transport protein hofq precursor - Escherichia coli (strain K-12) gb AAA58188.1 (U18997) hofQ [Escherichia coli] gb AAC76416.1 (AE000414) putative transport portein [Escherichia coli] Length = 412</p>
SEQ ID n°1033	Prot n°PL-1904.1	Contig38	509133	509978	40%	<p>Identities = 66/269 (24%), Positives = 114/269 (41%), Gaps = 22/269 (8%)</p> <p>sp P45753 YRFD_ECOLI HYPOTHETICAL 30.0 KD PROTEIN IN HOFQ-MRCA INTERGENIC REGION (F268) pir F65134 hypothetical 30.0 kD protein in hofQ-mrca intergenic region - Escherichia coli (strain K-12) gb AAA58192.1 (U18997) ORF_f268; gtt start, overlaps next gene [Escherichia coli] gb AAC76420.1 (AE000414) orf, hypothetical protein [Escherichia coli] Length = 268 "</p>
SEQ ID n°1034	Prot n°PL-1905.1	Contig38	506500	509028	85%	<p>Identities = 637/856 (74%), Positives = 733/856 (85%), Gaps = 10/856 (1%)</p> <p>pir ZPECPA penicillin-binding protein 1A - Escherichia coli gb AAA58193.1 (U18997) CG Site No.484; alternate name ponA [Escherichia coli] gb AAC76421.1 (AE000415) peptidoglycan synthetase; penicillin-binding protein 1A [Escherichia coli] Length = 858 "</p>
SEQ ID n°1035	Prot n°PL-1906.1	Contig38	505908	508456	73%	<p>Identities = 126/176 (71%), Positives = 151/176 (85%)</p> <p>sp P45798 YRFE_ECOLI HYPOTHETICAL 21.2 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION (F186) pir H65134 hypothetical 21.2 kD protein in mrca-pcka intergenic region - Escherichia coli (strain K-12) gb AAA58194.1 (U18997) ORF_f186 [Escherichia coli] gb AAC76422.1 (AE000415) orf, hypothetical protein [Escherichia coli] Length = 186</p>
SEQ ID n°1036	Prot n°PL-1907.1	Contig38	503298	505431	68%	<p>Identities = 361/707 (51%), Positives = 490/707 (69%), Gaps = 1/7707 (2%)</p> <p>gb AAC28926.1 (U66822) UmoB [Proteus mirabilis] Length = 702</p>
SEQ ID n°1037	Prot n°PL-1908.1	Contig38	501920	502792	79%	<p>Identities = 194/284 (68%), Positives = 234/284 (82%), Gaps = 1/284 (0%)</p> <p>pir D65135 hypothetical 32.8 kD protein in mrca-pcka intergenic region - Escherichia coli (strain K-12) gb AAA58198.1 (U18997) ORF_o294 [Escherichia coli] gb AAC76426.1 (AE000415) orf, hypothetical protein [Escherichia coli] Length = 294</p>
SEQ ID n°1038	Prot n°PL-1909.1	Contig38	500061	501680	90%	<p>Identities = 467/535 (87%), Positives = 495/535 (92%) pdb 1AYL Phosphoenolpyruvate Carboxykinase Length = 541</p>

TABLEAU I

SEQ ID n°1039	Prot n°PL-191.1	Contig41	317494	318390	86%	<p>Identities = 256/296 (86%), Positives = 279/295 (93%)</p> <p>sp P42823 YHAJ_ECOLI_HYPOTHETICAL_TRANSCRIPTIONAL_REGULATOR_IN_EXUR-TDCC_INTERGENIC_REGION_pir F65099_hypothetical_transcription_regulator_exuR-tdcC_intergenic_region_-Escherichia_coli_(strain_K-12)_gb AAA57909.1 (U18997)ORF_2298[Escherichia_coli]gb AAC76140.1 (AE000392)putative_transcriptional_regulator_LYSR-type[Escherichia_coli]Length = 298</p>
SEQ ID n°1040	Prot n°PL-1910.1	Contig38	499318	500013	86%	<p>Identities = 173/231 (74%), Positives = 203/231 (88%), Gaps = 2/231 (0%)</p> <p>sp P46882 YHHW_ECOLI_PROTEIN_YHHW_pir B65140_hypothetical_26.3_kD_protein_in_gntR-ggt_intergenic_region_-Escherichia_coli_(strain_K-12)_gb AAA58237.1 (U18997)ORF_2231[Escherichia_coli]gb AAC76464.1 (AE000420)orf_hypothetical_protein[Escherichia_coli]Length = 231</p>
SEQ ID n°1041	Prot n°PL-1911.1	Contig38	497263	498642	27%	<p>Identities = 67/248 (27%), Positives = 127/248 (51%), Gaps = 6/248 (2%)</p> <p>sp P23222 FIXL_BRAJA_SENSOR_PROTEIN_FIXL_pir S13330_fixL_protein_-Bradyrhizobium_japonicum_emb CAA40143.1 (X56808)ttg_start_codon[Bradyrhizobium_japonicum]emb CAA06276.1 (AJ005001)FixL_protein[Bradyrhizobium_japonicum]Length = 505</p>
SEQ ID n°1042	Prot n°PL-1912.1	Contig38	496637	497263	59%	<p>Identities = 81/205 (39%), Positives = 128/205 (60%), Gaps = 4/205 (1%)</p> <p>gb AAD12185.1 (U57900)utilizing_regulatory_protein_tutB_[Thaueria_aromatica]Length = 218</p>
SEQ ID n°1043	Prot n°PL-1913.1	Contig38	492059	495343	77%	<p>Identities = 718/1092 (65%), Positives = 844/1092 (76%), Gaps = 23/1092 (2%)</p> <p>gb AAA25124.1 (M16187)pullulanase_precursor[Klebsiella_aerogenes]Length = 1102</p>
SEQ ID n°1044	Prot n°PL-1914.1	Contig38	490244	491761	42%	<p>Identities = 117/444 (26%), Positives = 213/444 (47%), Gaps = 28/444 (6%)</p> <p>gb AAF85518.1 AE004079_9(AE004079)hypothetical_protein[Xylella_fastidiosae]Length = 510</p>
SEQ ID n°1045	Prot n°PL-1915.1	Contig38	489299	490195	No Hits found	
SEQ ID n°1046	Prot n°PL-1916.1	Contig38	485880	489345	44%	<p>Identities = 276/1109 (24%), Positives = 508/1109 (44%), Gaps = 81/1109 (7%)</p> <p>gb AAF85519.1 AE004080_1(AE004080)hypothetical_protein[Xylella_fastidiosae]Length = 1144</p>
SEQ ID n°1047	Prot n°PL-1917.1	Contig38	484697	485902	44%	<p>Identities = 102/396 (25%), Positives = 179/396 (44%), Gaps = 34/396 (8%)</p> <p>gb AAF85520.1 AE004080_2(AE004080)hypothetical_protein[Xylella_fastidiosae]Length = 401</p>
SEQ ID n°1048	Prot n°PL-1918.1	Contig38	483753	484655	72%	<p>Identities = 172/288 (60%), Positives = 219/288 (76%), Gaps = 2/288 (0%)</p> <p>gb AAG05442.1 AE004632_1(AE004632)transcriptional_regulator_CynR[Pseudomonas_aeruginosa]Length = 295</p>
SEQ ID n°1049	Prot n°PL-1919.1	Contig38	482749	483408	73%	<p>Identities = 144/210 (68%), Positives = 176/210 (83%)</p> <p>sp P17582 CYNT_ECOLI_CARBOANIC_ANHYDRASE_pir QRECTC_carbonate_dehydratase(EC_4.2.1.1)-Escherichia_coli_gb AAB18063.1 (U73857)cyanoate_anhydrase[Escherichia_coli]gb AAC73442.1 (AE000141)carbonic_anhydrase[Escherichia_coli]Length = 219</p>

TABLEAU I

SEQ ID n°1050	Prot n°PL-192.1	Contig41	318501	319202	70%	<p>Identities = 139/231 (60%), Positives = 178/231 (78%)</p> <p>sp P42624 YHAK_ECOLI_HYPOTHETICAL_25.9_KD_PROTEIN_IN_EXUR-TDCC_INTERGENIC_REGION (0233) pir G65099 hypothetical 25.9 kD protein in exuR-tdcC intergenic region - Escherichia coli (strain K-12) gb AA57910.1 (U18997) ORF_0233 [Escherichia coli] gb AAC76141.1 (AE000392) orf, hypothetical protein [Escherichia coli] Length = 233</p> <p>Identities = 45/199 (22%), Positives = 50/199 (44%), Gaps = 15/199 (7%)</p> <p>pir S76458 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj BAA18585.1 (D90915) hypothetical protein [Synechocystis sp.] Length = 231</p>
SEQ ID n°1051	Prot n°PL-1920.1	Contig38	481190	482095	29%	<p>Identities = 93/300 (31%), Positives = 159/300 (53%), Gaps = 5/300 (1%)</p> <p>emb CAB92560.1 (AL356812) putative carboxylase. [Streptomyces coelicolor A3(2)] Length = 405</p>
SEQ ID n°1052	Prot n°PL-1921.1	Contig38	478451	477688	39%	<p>Identities = 192/389 (49%), Positives = 276/389 (70%), Gaps = 1/389 (0%)</p> <p>gb AAG04601.1 AE004551_5 (AE004551) probable MFS transporter [Pseudomonas aeruginosa] Length = 409</p>
SEQ ID n°1053	Prot n°PL-1922.1	Contig38	475215	476426	66%	<p>Identities = 295/394 (74%), Positives = 341/394 (85%)</p> <p>sp P37631 YHIN_ECOLI_HYPOTHETICAL_43.8_KD_PROTEIN_IN_RHSB-PIT_INTERGENIC_REGION pir G65146 hypothetical 43.8 kD protein in rhsB-pit intergenic region - Escherichia coli (strain K-12) gb AAC76517.1 (AE000425) orf, hypothetical protein [Escherichia coli] Length = 400</p>
SEQ ID n°1054	Prot n°PL-1923.1	Contig38	473750	474934	80%	<p>Identities = 349/500 (69%), Positives = 426/500 (84%), Gaps = 5/500 (1%)</p> <p>sp P37308 PITA_ECOLI_LOW-AFFINITY_INORGANIC_PHOSPHATE_TRANSPORTER_1 pir S47713 pita protein - Escherichia coli gb AAB18469.1 (U00039) CG Site No. 385 [Escherichia coli] gb AAC76518.1 (AE000425) low affinity phosphate transport [Escherichia coli] Length = 499</p>
SEQ ID n°1055	Prot n°PL-1924.1	Contig38	471990	473480	82%	<p>Identities = 373/447 (83%), Positives = 412/447 (91%), Gaps = 1/447 (0%)</p> <p>sp P14657 DHE4_UNKP_NADP-SPECIFIC_GUTAMATE_DEHYDROGENASE (NADP-GDH) pir S06938 glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - unidentified bacterium emb CAA34434.1 (X16399) glutamate dehydrogenase (AA 1-446) [unidentified bacterium] Length = 446</p>
SEQ ID n°1056	Prot n°PL-1925.1	Contig38	469099	470442	91%	<p>Identities = 193/245 (78%), Positives = 212/245 (85%)</p> <p>pir S47717 hypothetical protein f285 - Escherichia coli gb AAB18473.1 (U00039) gfg start, alternate starts possible [Escherichia coli] Length = 285</p>
SEQ ID n°1057	Prot n°PL-1926.1	Contig38	468318	469061	84%	<p>Identities = 495/680 (72%), Positives = 589/680 (85%)</p> <p>sp P27298 OPDA_ECOLI_OLIGOPEPTIDASE_A pir S47718 oligopeptidase A (EC 3.4.24.-) - Escherichia coli gb AAB18474.1 (U00039) CG Site No. 18031 [Escherichia coli] gb AAC76523.1 (AE000426) oligopeptidase A [Escherichia coli] Length = 680</p>
SEQ ID n°1058	Prot n°PL-1927.1	Contig38	466269	468311	81%	

TABLEAU I

SEQ ID n°1059	Prot n°PL-1928.1	Contig38	484562	465785	88%	gb AAD54663.1 AF097520_1 (AF097520) Sal integrase [Shigella flexneri] Length = 403
SEQ ID n°1060	Prot n°PL-1929.1	Contig38	461248	484541	No Hits found	
SEQ ID n°1061	Prot n°PL-1930.1	Contig38	459443	461089	28%	Identities = 86/394 (21%), Positives = 153/394 (40%), Gaps = 68/394 (16%) gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae] Length = 552
SEQ ID n°1062	Prot n°PL-1931.1	Contig38	458454	457584	60%	Identities = 165/365 (45%), Positives = 235/365 (64%), Gaps = 6/365 (1%) spiP28912 YHHI_ECOLI_H REPEAT-ASSOCIATED PROTEIN IN RHSP-PIT INTERGENIC REGION (ORF-H) pti S47703 H repeat-associated protein-like protein b3484 - Escherichia coli gb AAC61885.1 (L02370) H repeat-associated protein [Escherichia coli] gb AAB18459.1 (U00039) alternate gene name yhhI [Escherichia coli] gb AAC76509.1 (AE000424) putative receptor [Escherichia coli] Length = 378
SEQ ID n°1063	Prot n°PL-1932.1	Contig38	455672	458460	No Hits found	
SEQ ID n°1064	Prot n°PL-1933.1	Contig38	453383	454429	28%	Identities = 91/105 (86%), Positives = 100/105 (94%) gb AAD16951.1 (AF106566) putative ATP binding protein SugR [Salmonella typhimurium] Length = 519
SEQ ID n°1065	Prot n°PL-1934.1	Contig38	452258	453384	57%	Identities = 207/215 (96%), Positives = 211/215 (97%) gb AAD16952.1 (AF106566) RhuM [Salmonella typhimurium] Length = 215
SEQ ID n°1066	Prot n°PL-1935.1	Contig38	450721	451593	56%	Identities = 118/241 (48%), Positives = 163/241 (66%) gb AAC38247.1 (AF003947) PcaR [Rhodococcus opacus] Length = 265
SEQ ID n°1067	Prot n°PL-1936.1	Contig38	449157	450149	No Hits found	
SEQ ID n°1068	Prot n°PL-1937.1	Contig38	447668	449164	82%	Identities = 232/478 (48%), Positives = 310/478 (64%), Gaps = 7/478 (1%) dbj BAB04258.1 (AP001508) NADP-dependent aldehyde dehydrogenase [Bacillus halodurans] Length = 498
SEQ ID n°1069	Prot n°PL-1938.1	Contig38	446783	447646	80%	Identities = 188/283 (66%), Positives = 237/283 (83%) gb AAG03615.1 AE004460_8 (AE004460) probable CoA transferase, subunit A [Pseudomonas aeruginosa] Length = 283
SEQ ID n°1070	Prot n°PL-1939.1	Contig38	446007	446786	68%	Identities = 165/258 (63%), Positives = 201/258 (76%) gb AAG03616.1 AE004460_9 (AE004460) probable CoA transferase, subunit B [Pseudomonas aeruginosa] Length = 260
SEQ ID n°1071	Prot n°PL-194.1	Contig41	319698	320564	84%	Identities = 228/285 (80%), Positives = 251/285 (88%), Gaps = 1/285 (0%) spiP45528 YRAL_ECOLI_HYPOTHETICAL 31.3 KD PROTEIN IN AGAI-MTR INTERGENIC REGION (F286) pti F65104 hypothetical 31.3 KD protein in agai-mtr intergenic region - Escherichia coli (strain K-12) gb AAA57949.1 (U18997) ORF 1286 [Escherichia coli] gb AAC76180.1 (AE000395) orf. hypothetical protein [Escherichia coli] Length = 286

TABLEAU I

SEQ ID n°1072	Prot n°PL-1940.1	Contig38	444946	448010	67%	Identities = 189/353 (53%), Positives = 247/353 (69%), Gaps = 2/353 (0%) sp Q45072 TFE_BURCE MALEYLACETATE REDUCTASE pir 40177 maleylacetate reductase (EC 1.3.1.32) - Pseudomonas cepacia gb AAC4333.1 (U19883) maleylacetate reductase [Burkholderia cepacia] Length = 352
SEQ ID n°1073	Prot n°PL-1941.1	Contig38	443677	444888	77%	Identities = 284/402 (70%), Positives = 328/402 (80%), Gaps = 2/402 (0%) gb AAG12159.1 (AY007371) beta-ketoadipyl CoA thiolase [Burkholderia pseudomallei] Length = 400
SEQ ID n°1074	Prot n°PL-1943.1	Contig38	441624	442232	No Hits found	Identities = 84/347 (24%), Positives = 157/347 (45%), Gaps = 49/347 (14%) emb CAB65693.1 (AL136058) putative helicase [Streptomyces coelicolor A3(2)] Length = 945
SEQ ID n°1075	Prot n°PL-1944.1	Contig38	439226	441148	24%	
SEQ ID n°1076	Prot n°PL-1945.2	Contig41	872719	873375		Identities = 123/249 (49%), Positives = 181/249 (72%), Gaps = 2/249 (0%) pir 40452 ABC-type transport system probable ATP binding subunit - Bacillus subtilis emb CAA54726.1 (X77636) putative ATP binding subunit [Bacillus subtilis] Length = 247
SEQ ID n°1077	Prot n°PL-1946.1	Contig41	873353	874117	70%	Identities = 124/233 (53%), Positives = 169/233 (72%), Gaps = 1/233 (0%) (AP001507) amino acid ABC transporter (amino acid-binding protein) [Bacillus halodurans] Length = 275
SEQ ID n°1078	Prot n°PL-1947.1	Contig41	874205	874978	61%	Identities = 445/671 (66%), Positives = 529/671 (78%), Gaps = 14/671 (2%) gb AAC38630.1 (AF047028) insecticidal toxin complex protein TccC [Photobacterium luminescens] Length = 1043
SEQ ID n°1079	Prot n°PL-1948.1	Contig41	875335	878145	56%	Identities = 239/333 (71%), Positives = 291/333 (86%) sp P04391 OTC1_ECOLI ORNITHINE CARBAMOYLTRANSFERASE CHAIN I (OTCSE-1) pir OWECI ornithine carbamoyltransferase (EC 2.1.3.3) chain I - Escherichia coli gb AAA97150.1 (U14003) ornithine carbamoyltransferase [Escherichia coli] gb AAC77211.1 (AE000496) ornithine carbamoyltransferase 1 [Escherichia coli] Length = 334
SEQ ID n°1080	Prot n°PL-1949.1	Contig41	878832	879848	84%	Identities = 267/546 (48%), Positives = 360/546 (65%), Gaps = 18/546 (3%) sp P45464 YRAM_ECOLI HYPOTHETICAL 72.8 KD PROTEIN IN AGAI-MTR INTERGENIC REGION (O678) pir G65104 hypothetical 72.8 kD protein in agai-mtr intergenic region - Escherichia coli (strain K-12) gb AAA57950.1 (U18997) ORF_0678 [Escherichia coli] gb AAC76181.1 (AE000396) putative glycosylase [Escherichia coli] Length = 878
SEQ ID n°1081	Prot n°PL-195.1	Contig41	320526	322370	58%	Identities = 255/308 (82%), Positives = 282/308 (90%) gb AAF01338.1 AF190426.2 (AF190426) aspartate transcarbamylase catalytic subunit [Erwinia herbicola] Length = 311
SEQ ID n°1082	Prot n°PL-1950.1	Contig41	880155	881078	91%	Identities = 206/489 (42%), Positives = 269/489 (54%), Gaps = 47/489 (9%) pdb 1F3 A Chain A, Crystal Structure Of Tns Transposase Complexed With Transposon End Dna Length = 481
SEQ ID n°1083	Prot n°PL-1951.1	Contig41	882228	883610	57%	

TABLEAU I

SEQ ID n°1084	Prot n°PL-1952.1	Contig41	883802	884605	No Hits found	49%	Identities = 74/261 (28%), Positives = 133/261 (50%), Gaps = 7/261 (2%) gb AAF93838.1 (AE004153) conserved hypothetical protein [Vibrio cholerae] Length = 264
SEQ ID n°1085	Prot n°PL-1953.1	Contig41	885013	886665	1097634		Identities = 273/306 (89%), Positives = 291/306 (94%) pdb 1A3G A Chain A, Branched-Chain Amino Acid Aminotransferase From Escherichia Coli
SEQ ID n°1086	Prot n°PL-1954.2	Contig41	1095988	1095988			
SEQ ID n°1087	Prot n°PL-1955.1	Contig41	1094784	1095710		92%	Identities = 539/616 (87%), Positives = 577/616 (93%) pdb 1A3G B Chain B, Branched-Chain Amino Acid Aminotransferase From Escherichia Coli pdb 1A3G C Chain C, Branched-Chain Amino Acid Aminotransferase From Escherichia Coli Length = 308
SEQ ID n°1088	Prot n°PL-1956.1	Contig41	1092741	1094591		84%	Identities = 391/487 (80%), Positives = 438/487 (89%), Gaps = 2/487 (0%) sp P05791 ILVD_ECOLI DIHYDROXY-ACID DEHYDRATASE (DAD) pir J04822 DWECD dihydroxy-acid dehydratase (EC 4.2.1.9) - Escherichia coli gb AAB59053.1 (M10313) dihydroxyacid dehydratase [Escherichia coli] emb CAA28576.1 (X04890) dihydroxy acid [Escherichia coli] pir 1312306A gene livGMEDA cluster [Escherichia coli] Length = 616
SEQ ID n°1089	Prot n°PL-1957.1	Contig41	1091246	1092736		87%	Identities = 391/487 (80%), Positives = 438/487 (89%), Gaps = 2/487 (0%) gb AAF33479.1 (AF233324) S. typhimurium threonine deaminase (LVA) (SP:P20506); contains similarity to Pfam families PF00291 (Pyridoxal-phosphate dependent enzyme, score=467.9, E=8.4e-137, N=1) and PF00685 (C-terminal domain of Threonine dehydratase, score=329.2, E=> Length = 514 "
SEQ ID n°1090	Prot n°PL-1958.1	Contig41	1089480	1090997		78%	Identities = 335/500 (67%), Positives = 412/500 (82%) sp P27304 EMR_B_ECOLI MULTIDRUG RESISTANCE PROTEIN B pir J065048 multidrug resistance protein B - Escherichia coli gb AAC75733.1 (AE000353) multidrug resistance; probably membrane translocase [Escherichia coli] dbj BAA16548.1 (D90891) multidrug resistant protein emrB [Escherichia coli] dbj BAA16553.1 (D90892) multidrug resistant protein emrB [Escherichia coli] Length = 512 "
SEQ ID n°1091	Prot n°PL-1959.1	Contig41	1088300	1089472		72%	Identities = 209/383 (54%), Positives = 292/383 (75%), Gaps = 1/383 (0%) pir J01344 multidrug resistant protein emrA - Escherichia coli gb AAA23724.1 (M86657) multidrug resistance; putative [Escherichia coli]
SEQ ID n°1092	Prot n°PL-196.1	Contig41	323453	324028		74%	Identities = 121/190 (63%), Positives = 155/190 (80%) sp P45467 YRAP_ECOLI HYPOTHETICAL 20.0 KD PROTEIN IN AGAI-MTR INTERGENIC REGION PRECURSOR (O191) pir J065105 hypothetical 20.0 kD protein in agai-mtr intergenic region - Escherichia coli (strain K- 12) gb AAA57953.1 (U18997) ORF_o191 [Escherichia coli] gb AAC76184.1 (AE000396) putative periplasmic protein [Escherichia coli] Length = 191

TABLEAU I

SEQ ID n°1093	Prot n°PL-1960.1	Contig41	1087234	1087977	56%	<p>Identities = 101/245 (41%), Positives = 143/245 (58%), Gaps = 1/245 (0%) sp O54438 FABG_PSEAE 3-OXOACYL-ACYL-CARRIER PROTEIN[REDUCTASE (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE) pir T12020 3-oxoacyl-acyl carrier protein reductase - Pseudomonas aeruginosa gb AAB94395.1 (U91631) 3-oxoacyl-acyl carrier protein reductase [Pseudomonas aeruginosa] gb AAG06355.1 AE004722_11 Identities = 30/77 (38%), Positives = 42/77 (53%), Gaps = 7/77 (9%) pir J70613 hypothetical protein Rv0636 - Mycobacterium tuberculosis (strain H37RV) emb CAB07125.1 (Z92772) hypothetical protein Rv0636 [Mycobacterium tuberculosis] Length = 142</p>
SEQ ID n°1094	Prot n°PL-1961.1	Contig41	1086362	1087177	15%	<p>Identities = 165/418 (39%), Positives = 238/418 (55%), Gaps = 13/418 (3%) pir B70448 3-oxoacyl-acyl-carrier-protein] synthase (EC 2.3.1.41) II - Aquifex aeolicus gb AAC07574.1 (AE000752) 3-oxoacyl-acyl-carrier-protein] synthase II [Aquifex aeolicus] Length = 415</p>
SEQ ID n°1095	Prot n°PL-1962.1	Contig41	1085100	1086365	55%	<p>Identities = 141/397 (35%), Positives = 220/397 (54%), Gaps = 14/397 (3%) gb AAG01802.1 AF278772_1 (AF278772) cysteine desulfurase Nifs [Methanosarcina thermophila] Length = 404</p>
SEQ ID n°1096	Prot n°PL-1963.1	Contig41	1083485	1084675	54%	<p>Identities = 95/345 (27%), Positives = 162/345 (46%), Gaps = 15/345 (4%) pir S15161 long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) - Photobacterium phosphoreum emb CAA39107.1 (X55459) fatty acyl-protein synthetase [Photobacterium phosphoreum] Length = 373</p>
SEQ ID n°1097	Prot n°PL-1964.1	Contig41	1081892	1083115	39%	<p>Identities = 109/344 (31%), Positives = 183/344 (52%), Gaps = 6/344 (1%) pir E69725 potassium uptake trkA - Bacillus subtilis gb AAB0908.1 (U93876) hypothetical protein YrdP [Bacillus subtilis] emb CAB14605.1 (Z99117) alternate gene name: yrdP [Bacillus subtilis] Length = 345</p>
SEQ ID n°1098	Prot n°PL-1965.1	Contig41	1080458	1081543	48%	<p>Identities = 53/227 (23%), Positives = 100/227 (43%), Gaps = 17/227 (7%) sp Q51872 LUMQ_PHOE PROBABLE TRANSCRIPTIONAL REGULATOR LUMQ pir JC4504 poir thermoregulatory protein EnvY homolog - Photobacterium leiognathi gb AA87846.1 (U35231) lumQ gene product [Photobacterium leiognathi] Length = 248</p>
SEQ ID n°1099	Prot n°PL-1966.1	Contig41	1079190	1080077	33%	<p>Identities = 202/294 (68%), Positives = 244/294 (82%) gb AAF33477.1 (AF233324) 98% identity to E. coli transcriptional activator protein (ILVY) (SP:P05827); contains similarity to Pfam (Bacterial regulatory helix-turn-helix protein, IysR family), score=207.1, E=2.7e-58, N=1 [Salmonella typhimurium LT2] Length = 287</p>
SEQ ID n°1100	Prot n°PL-1967.1	Contig41	1077761	1078642	76%	<p>Identities = 431/492 (87%), Positives = 452/492 (91%), Gaps = 1/492 (0%) gb AA24028.1 (M11889) acetoaldehyde acid isomerase [Escherichia coli] Length = 491</p>
SEQ ID n°1101	Prot n°PL-1968.1	Contig41	1076093	1077571	90%	

TABLEAU I

SEQ ID n°1102	Prot n°PL-1989.1	Contig41	1073856	1075883	88%	<p>Identities = 545/667 (81%), Positives = 603/667 (89%) gb AAF33474.1 (AF233324) 98% identity with E. coli ATP-dependent DNA helicase (REP) (SP:P09980); contains similarity to Piam family PF00580 (UvrD/REP helicase), score=817.3, E=5.5e-242, N=1 [Salmonella typhimurium LT2] Length = 674 "</p>
SEQ ID n°1103	Prot n°PL-197.1	Contig41	324160	324897	73%	<p>Identities = 153/233 (65%), Positives = 181/233 (77%) sp P46022 MTGA_ECOLI MONOFUNCTIONAL BIOSYNTHETIC PEPTIDOGLYCAN TRANSGLYCOSYLASE (MONOFUNCTIONAL TGASE) pir J865112 hypothetical 27.3 kD protein in pto-arcB intergenic region - Escherichia coli (strain K-12) gb AAA58010.1 (U18987) ORF_1242 [Escherichia coli] gb AAC76240.1 (AE000400) putative identities = 345/491 (70%), Positives = 407/491 (82%)</p>
SEQ ID n°1104	Prot n°PL-1970.1	Contig41	1072303	1073805	80%	<p>sp P25552 GPPA_ECOLI GUANOSINE-5'-TRIPHOSPHATE, 3'-DIPHOSPHATE PYROPHOSPHATASE (GUANOSINE PENTAPHOSPHATE PHOSPHOHYDROLASE) (PPPGPP-5'-PHOSPHOHYDROLASE) pir J448285 expolyposphatase (EC 3.6.1.11) - Escherichia coli gb AA67580.1 (M87049) guanosine pentaphosphatase [Escherichia coli] gb AAB27726.1 expolyposphatase, guanosine pentaphosphatase phosphohydrolase, GPP, expolyp(P)ase (EC 3.6.1.11) [Escherichia coli, Peptide, 494 aa] gb AAC76784.1 (AE000454) guanosine pentaphosphatase: expolyposphatase [Escherichia coli] identities = 357/428 (83%), Positives = 385/428 (89%), Gaps = 7/428 (1%)</p>
SEQ ID n°1105	Prot n°PL-1971.1	Contig41	1070993	1072297	88%	<p>sp P24229 RHLB_ECOLI PUTATIVE ATP-DEPENDENT RNA HELICASE RHLB pir J65181 rhlB protein - Escherichia coli (strain K-12) gb AAC76785.1 (AE000454) putative ATP-dependent RNA helicase [Escherichia coli] Length = 421</p>
SEQ ID n°1106	Prot n°PL-1972.1	Contig41	1068830	1070089	98%	<p>Identities = 408/419 (97%), Positives = 417/419 (99%) sp P03002 RHO_ECOLI TRANSCRIPTION TERMINATION FACTOR RHO pir JTWECR transcription termination factor rho - Escherichia coli gb AA24532.1 (J01673) transcription termination factor [Escherichia coli] gb AA67583.1 (M87049) transcription termination factor rho [Escherichia coli] gb AAC76788.1 (AE000454) transcription termination factor Rho: polarity suppressor [Escherichia coli] Length = 419 "</p>
SEQ ID n°1107	Prot n°PL-1973.1	Contig41	1067324	1068409	83%	<p>Identities = 263/358 (73%), Positives = 312/358 (86%) sp P24235 RFE_ECOLI PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE pir J65182 probable undecaprenyl-phosphate alpha-n-acetylglucosaminyltransferase - Escherichia coli (strain K-12) gb AAC76789.1 (AE000454) UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase: synthesis of enterobacterial common antigen (ECA) [Escherichia coli] Length = 367 "</p>

TABLEAU I

SEQ ID n°1108	Prot n°PL-1974.1	Contig41	1066239	1067330	72%	<p>Identities = 209/336 (62%), Positives = 264/336 (78%), Gaps = 2/336 (0%) sp P25905 WZXE_ECOLI LIPOPOLYSACCHARIDE BIOSYNTHESIS PROTEIN WZXE pir D65182 hypothetical 39.5K protein (rfe 5' region) - Escherichia coli gb AAC76790.1 (AE000454) putative transport protein [Escherichia coli] Length = 349</p>
SEQ ID n°1108	Prot n°PL-1976.1	Contig41	1084991	1066112	84%	<p>Identities = 295/373 (79%), Positives = 331/373 (88%) sp P27828 WECB_ECOLI UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE (UDP-GLCNAC-2-EPIMERASE) (BACTERIOPHAGE N4 ADSORPTION PROTEIN C) pir A49350 bacteriophage N4 adsorption protein nrfC - Escherichia coli gb AAC36847.1 (L18799) cytoplasmic protein [Escherichia coli] Length = 376</p>
SEQ ID n°1110	Prot n°PL-1976.1	Contig41	1063709	1064986	86%	<p>Identities = 334/420 (79%), Positives = 373/420 (88%) pir B49350 hypothetical protein 379 (nrfC 3' region) - Escherichia coli Length = 420</p>
SEQ ID n°1111	Prot n°PL-1977.1	Contig41	1062642	1063712	85%	<p>Identities = 288/353 (81%), Positives = 315/353 (88%) sp P27830 RFFG_ECOLI DTDP-GLUCOSE 4,6-DEHYDRATASE pir G65182 dTDPglucose 4,6-dehydratase [EC 4.2.1.46] - Escherichia coli (strain K-12) pdb 1BXKJB Chain B, Dtdp-Glucose 4,6-Dehydratase From E. Coli pdb 1BXKJA Chain A, Dtdp-Glucose 4,6-Dehydratase From E. Coli gb AAC76793.1 (AE000455) dTDP-glucose 4,6-dehydratase [Escherichia coli] Identities = 241/293 (82%), Positives = 266/293 (90%)</p>
SEQ ID n°1112	Prot n°PL-1978.1	Contig41	1061739	1062635	88%	<p>sp P27831 RFFH_ECOLI GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (DTDP-GLUCOSE SYNTHASE) (DTDP-GLUCOSE PYROPHOSPHORYLASE) pir H65182 glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) - Escherichia coli gb AAC76794.1 (AE000455) glucose-1-phosphate thymidyltransferase [Escherichia coli] Identities = 99/195 (50%), Positives = 123/195 (62%), Gaps = 14/195 (7%) pir J30684 hypothetical protein o181 - Escherichia coli Length = 181</p>
SEQ ID n°1113	Prot n°PL-1979.1	Contig41	1061042	1061632	48%	<p>Identities = 127/217 (58%), Positives = 170/217 (77%) sp P26428 S27A_ECOLI SIGMA CROSS-REACTING PROTEIN 27A (SCRIP-Identities = 283/376 (75%), Positives = 329/376 (87%) gb AAF33462.1 (AF233324) 92% identity with E. coli lipopolysaccharide biosynthesis protein (WECE) (SP:P27833); contains similarity to Pfam family PF01041 (DegT/DmrJ/EryC1/SrS family), score=295.0, E=9.2e-85, N=1 [Salmonella typhimurium LT2] Length = 376 "</p>
SEQ ID n°1114	Prot n°PL-198.1	Contig41	324890	325543	77%	
SEQ ID n°1115	Prot n°PL-1980.1	Contig41	1059910	1061040	80%	
SEQ ID n°1116	Prot n°PL-1981.1	Contig41	1058658	1059908	84%	<p>Identities = 311/416 (74%), Positives = 366/416 (87%) gb AAF33461.1 (AF233324) 89% identity with E. coli lipopolysaccharide biosynthesis protein (WZXE) (SP:P2783) [Salmonella typhimurium LT2] Length = 416</p>
SEQ ID n°1117	Prot n°PL-1982.1	Contig41	1057576	1058661	75%	<p>Identities = 220/359 (61%), Positives = 273/359 (75%), Gaps = 2/359 (0%) sp P56258 YIFM_ECOLI HYPOTHETICAL 40.6 KDA PROTEIN IN WZXE-WECE INTERGENIC REGION Length = 359</p>

TABLEAU I

SEQ ID n°1118	Prot n°PL-1983.1	Contig41	1058200	1057579	83%	<p>Identities = 347/443 (78%), Positives = 394/443 (88%), Gaps = 3/443 (0%) gb AAA67593.1 (M87049) 4-alpha-L-fucosyltransferase [Escherichia coli] Length = 808</p> <p>Identities = 170/239 (71%), Positives = 209/239 (87%) sp P37457 WECG_SALTY_PROBABLE_UDP-N-ACETYL-D-MANNOSAMINURONIC_ACID_TRANSFERASE (UDP-MANNACA TRANSFERASE) pir S27727 hypothetical protein - Salmonella typhimurium gb AAA92025.1 (M95047) rfm gene product [Salmonella typhimurium] gb AAF33458.1 (AF233324) S. typhimurium putative UDP-N-acetyl-D-mannosamine transferase (WECG) (SP: P37457 [Salmonella typhimurium LT2]) Length = 246</p>
SEQ ID n°1120	Prot n°PL-1985.1	Contig41	1053837	1055228	81%	<p>Identities = 344/445 (77%), Positives = 399/445 (89%) sp P37456 YIFK_SALTY_PROBABLE_TRANSPORT_PROTEIN_YIFK pir S27728 probable transport protein - Salmonella typhimurium gb AA92026.1 (M95047) transport protein [Salmonella typhimurium] Identities = 87/394 (22%), Positives = 164/394 (41%), Gaps = 66/394 (16%) gb AAG00842.1 AF272977.2 (AF272977) transposase [Mycoplasma hyopneumoniae] Length = 552</p>
SEQ ID n°1121	Prot n°PL-1986.1	Contig41	1050500	1052146	29%	<p>Identities = 267/393 (67%), Positives = 324/393 (81%) sp P09128 HEMY_ECOLI_HEMY_PROTEIN pir S01694 hemY protein - Escherichia coli emb CAA31135.1 (X12614) ORF Y (AA 1 - 398) [Escherichia coli] gb AAA67598.1 (M87049) hemY [Escherichia coli] gb AAC76805.1 (AE000456) a late step of protoheme IX synthesis [Escherichia coli] Identities = 220/376 (58%), Positives = 290/376 (76%), Gaps = 1/376 (0%) sp P09127 HEMX_ECOLI_PUTATIVE_UROPORPHYRIN-III_C-METHYLTRANSFERASE (UROGEN III METHYLASE) (ORF X) pir S02185 uroporphyrin-III C-methyltransferase (EC 2.1.1.107) - Escherichia coli emb CAA31134.1 (X12614) ORF X (AA 1 - 393) [Escherichia coli] emb CAA31772.1 (X13406) put. urogen III methylase (AA 1 - 393); hemX gene [Escherichia coli] gb AAA67599.1 (M87049) uroporphyrinogen III methylase [Escherichia coli] gb AAC76806.1 (AE000456) uroporphyrinogen III methylase [Escherichia coli] Length = 393</p>
SEQ ID n°1122	Prot n°PL-1987.1	Contig41	1048955	1050193	78%	<p>Identities = 137/246 (55%), Positives = 180/246 (72%) sp P09128 HEM4_ECOLI_UROPORPHYRINOGEN-III_SYNTHASE (UROS) (UROPORPHYRINOGEN-III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE [CYCLIZING]) pir E65184 uroporphyrinogen-III synthase (EC 4.2.1.75) - Escherichia coli (strain K-12) emb CAA31133.1 (X12614) uroporphyrinogen III cosynthetase (AA 1 - 246) [Escherichia coli] gb AAA67600.1 (M87049) uroporphyrinogen III synthase [Escherichia coli] gb AAC76807.1 (AE000456) uroporphyrinogen III synthase [Escherichia coli] Length = 246</p>
SEQ ID n°1124	Prot n°PL-1989.1	Contig41	1047066	1047806	66%	

TABLEAU I

SEQ ID n°1125	Prot n°PL-199.1	Contig41	325781	328126	84%	Identities = 584/781 (74%), Positives = 673/781 (86%), Gaps = 3/781 (0%) emb CAA37397.1 X53315 arcB [Escherichia coli] Length = 778
SEQ ID n°1126	Prot n°PL-1990.1	Contig41	1046128	1047069	86%	Identities = 252/310 (81%), Positives = 275/310 (88%) sp Q59684 HEM3_PROMI PORPHOBILINOGEN DEAMINASE (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) gb AAC44328.1 (U22969) porphobilinogen deaminase [Proteus mirabilis] Length = 313
SEQ ID n°1127	Prot n°PL-1991.1	Contig41	1042959	1045529	85%	Identities = 683/836 (81%), Positives = 750/836 (89%), Gaps = 1/836 (0%) sp Q59685 CYAA_PROMI ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE) gb AAC44330.1 (U22969) adenylate cyclase [Proteus mirabilis] Length = 865
SEQ ID n°1128	Prot n°PL-1992.1	Contig41	1041473	1042297	86%	Identities = 228/274 (82%), Positives = 245/274 (88%) diaminopimelate epimerase (EC 5.1.1.7) - Escherichia coli (strain K-12) gb AAC76812.1 (AE000457) diaminopimelate epimerase [Escherichia coli] Length = 275
SEQ ID n°1129	Prot n°PL-1993.1	Contig41	1040736	1041440	89%	Identities = 132/235 (56%), Positives = 175/235 (74%), Gaps = 1/235 (0%) gb AAF33444.1 (AF233324) 86% identity with E. coli hypothetical protein (YGA) (SP:P233305) [Salmonella typhimurium LT2] Length = 235
SEQ ID n°1130	Prot n°PL-1994.1	Contig41	1039828	1040739	83%	Identities = 215/296 (72%), Positives = 255/296 (85%) (AF028736) site specific recombinase [Serratia marcescens] Length = 296
SEQ ID n°1131	Prot n°PL-1995.1	Contig41	1039112	1039828	88%	Identities = 139/238 (57%), Positives = 173/238 (71%) (AF028736) No definition line found [Serratia marcescens] Length = 238
SEQ ID n°1132	Prot n°PL-1996.1	Contig41	1036883	1039045	91%	Identities = 621/720 (86%), Positives = 674/720 (93%) (AF233324) 98% identity with E. coli DNA helicase (UVRD) (SP:P03018); contains similarity to Pfam family PF00580 (UvrD/REP helicase), score=812.9, E=1.2e-240, N=1 [Salmonella typhimurium LT2] Length = 720
SEQ ID n°1133	Prot n°PL-1997.1	Contig41	1035837	1036787	92%	Identities = 271/316 (85%), Positives = 284/316 (92%) sp P31138 CORA_SALTY MAGNESIUM AND COBALT TRANSPORT PROTEIN CORA pir A47157 magnesium transport protein CorA - Salmonella typhimurium gb AAO2986.1 (L11043) Mg2+ transport protein [Salmonella typhimurium] gb AAF33440.1 (AF233324) S. typhimurium magnesium transport protein (CORA) (SP:P31138) [Salmonella typhimurium LT2]
SEQ ID n°1134	Prot n°PL-1998.1	Contig41	1033793	1034683	78%	Identities = 193/293 (65%), Positives = 237/293 (80%) (AF233324) 90% identity with E. coli rad gene product (RAD) (SP:P27844); contains similarity to Pfam family PF00892 (Integral membrane protein), score=17.4, E=0.05, N=1 [Salmonella typhimurium LT2] Length = 294
SEQ ID n°1135	Prot n°PL-1999.1	Contig41	1030480	1032915	51%	Identities = 321/608 (52%), Positives = 421/608 (68%), Gaps = 10/608 (1%) gb AAB40620.1 (U61153) AicC [Bordetella bronchiseptica] Length = 608

TABLEAU I

SEQ ID n°1136	Prot n°PL-2.1	Contig41	1135	2328	37%	Identities = 88/288 (30%), Positives = 151/288 (51%), Gaps = 10/288 (3%) gb AAG07125.1 AE004793_2 (AE004793) integrase/recombinase XerD [Pseudomonas aeruginosa] Length = 298
SEQ ID n°1137	Prot n°PL-20.1	Contig41	34909	35592	44%	Identities = 59/208 (28%), Positives = 101/208 (48%), Gaps = 9/208 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°1138	Prot n°PL-200.1	Contig41	328874	333331	89%	Identities = 1243/1490 (83%), Positives = 1353/1490 (90%), Gaps = 1/1490 (0%) sp P09831 GLTB_ECOLI GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN PRECURSOR (GLUTAMATE SYNTHASE ALPHA SUBUNIT) (NADPH-GOGAT) (GLTS ALPHA CHAIN) pif F65112 glutamate synthase (NADPH) (EC 1.4.1.13) large chain precursor - Escherichia coli gb AAA58014.1 (U18997) glutamate synthase, large subunit [Escherichia coli] gb AAC76244.1 (AE000400) glutamate synthase, large subunit [Escherichia coli] Length = 1517
SEQ ID n°1139	Prot n°PL-2000.1	Contig41	1029197	1030498	68%	Identities = 218/420 (51%), Positives = 303/420 (71%), Gaps = 8/420 (1%) emb CAB87220.1 (AL163641) putative monooxygenase [Streptomyces coelicolor A3(2)] Length = 413
SEQ ID n°1140	Prot n°PL-2001.1	Contig41	1027610	1028166	63%	Identities = 255/483 (52%), Positives = 328/483 (67%), Gaps = 14/483 (2%) emb CAB87219.1 (AL163641) putative pyridoxal-dependent decarboxylase [Streptomyces coelicolor A3(2)] Length = 480
SEQ ID n°1141	Prot n°PL-2002.1	Contig41	1028463	1027263	46%	Identities = 82/212 (38%), Positives = 124/212 (57%), Gaps = 2/212 (0%) sp P39405 FHUF_ECOLI FERRIC IRON REDUCTASE PROTEIN FHUF pif S56594 hypothetical 30.1K protein (dnaT-hold intergenic region) - Escherichia coli gb AAA97266.1 (U14003) ORF_f262b [Escherichia coli] gb AAC77323.1 (AE000507) orf, hypothetical protein [Escherichia coli] Length = 262
SEQ ID n°1142	Prot n°PL-2003.1	Contig41	1025497	1026309	68%	Identities = 144/260 (55%), Positives = 190/260 (72%), Gaps = 1/260 (0%) pif T36888 probable iron-siderophore uptake system ATP-binding component - Streptomyces coelicolor emb CAB52849.1 (AL109848) putative iron-siderophore uptake system ATP-binding component [Streptomyces coelicolor A3(2)] Length = 301
SEQ ID n°1143	Prot n°PL-2004.1	Contig41	1024442	1025512	50%	Identities = 122/352 (34%), Positives = 193/352 (54%), Gaps = 10/352 (2%) gb AAD4882.1 (U52150) cytoplasmic membrane permease [Vibrio cholerae] gb AAF93943.1 (AE004163) ferric vibriobactin ABC transporter, permease protein [Vibrio cholerae] Length = 358
SEQ ID n°1144	Prot n°PL-2005.1	Contig41	1023454	1024467	62%	Identities = 145/327 (44%), Positives = 212/327 (64%), Gaps = 3/327 (0%) pif T36890 probable iron-siderophore uptake system transmembrane component - Streptomyces coelicolor emb CAB52851.1 (AL109848) putative iron-siderophore uptake system transmembrane component [Streptomyces coelicolor A3(2)] Length = 348

TABLEAU I

SEQ ID n°1145	Prot n°PL-2008.1	Contig41	1022390	1023457	46%	<p>Identities = 84/325 (28%), Positives = 165/325 (49%), Gaps = 13/325 (4%) gb AAB97475.1 (U02617) DlxR/iron regulated lipoprotein precursor [Conyebacterium diptheriae] Length = 355</p>
SEQ ID n°1146	Prot n°PL-2007.1	Contig41	1020117	1022372	55%	<p>Identities = 278/723 (38%), Positives = 416/723 (57%), Gaps = 30/723 (4%) gb AAD26430.1 AF135154_1 (AF135154) ferric alcaligin siderophore receptor [Bordetella pertussis] Length = 734</p>
SEQ ID n°1147	Prot n°PL-2008.1	Contig41	1018264	1020078	64%	<p>Identities = 285/588 (48%), Positives = 398/588 (66%), Gaps = 7/588 (1%) gb AAB40620.1 (U61153) AlC [Bordetella bronchiseptica] Length = Identities = 484/606 (76%), Positives = 529/606 (86%), Gaps = 1/606 (0%) gb AAF33434.1 (AF233324) S. typhimurium DNA-dependent ATPase DNA helicase (RECQ) (SP:P40724); contains similarity to Pfam families PF0057 (HRDC domain, score=130.4, E=3.3e-35, N=1), PF00270 (DEAD/DEAH box helicase, score=121.6, E=1.5e-37, N=1) and PF00271 (Helicases) Length = 615 "</p>
SEQ ID n°1148	Prot n°PL-2009.1	Contig41	1015980	1017818	84%	<p>Identities = 375/472 (79%), Positives = 424/472 (89%) sp P09832 GLTD_ECOLI GLUTAMATE SYNTHASE [NADPH] SMALL CHAIN (GLUTAMATE SYNTHASE BETA SUBUNIT) (NADPH-GOGAT) (GLTS BETA CHAIN) pr G65112 glutamate synthase (NADPH) (EC 1.4.1.13) small chain - Escherichia coli gb AAA58015.1 (U18987) glutamate synthase, small subunit [Escherichia coli] gb AAC76245.1 (AE000400) glutamate synthase, small subunit [Escherichia coli] Length = 472</p>
SEQ ID n°1149	Prot n°PL-201.1	Contig41	333341	334759	89%	<p>Identities = 171/326 (52%), Positives = 229/326 (69%), Gaps = 1/326 (0%) emb CAA26932.1 (X03155) lysophospholipase L2 (aa 1-340) [Escherichia coli] pr I111247A lysophospholipase L2 [Escherichia coli] Length =</p>
SEQ ID n°1150	Prot n°PL-2010.1	Contig41	1014967	1015985	66%	<p>Identities = 174/264 (65%), Positives = 207/264 (77%) gb AAF33430.1 (AF233324) 78-92% identity (with one gap) to E. coli hypothetical protein (YIGL) (SP:P27848) [Salmonella typhimurium LT2] Length = 266</p>
SEQ ID n°1151	Prot n°PL-2011.1	Contig41	1014144	1014944	67%	
SEQ ID n°1152	Prot n°PL-2012.1	Contig41	1011322	1012815	No Hits found	<p>Identities = 56/229 (24%), Positives = 103/229 (44%), Gaps = 8/229 (3%) pir T08276 probable transposase - Halobacterium sp. (strain NRC-1) insertion sequence [SH8 plasmid pNRC100 gb AAC82843.1 (AF016485) ORF H0846 [Halobacterium sp. NRC-1] gb AAC82834.1 (AF016485) ORF H1709 [Halobacterium sp. NRC-1] gb AAG18697.1 (AE004975) Vng0059h [Halobacterium sp. NRC-1] gb AAG18910.1 (AE004993) Vng0337h [Halobacterium sp. NRC-1] gb AAG20310.1 (AE005105) Vng2175h [Halobacterium sp. NRC-1] gb AAG20766.1 (AE005145) Vng6079h [Halobacterium sp. NRC-1] gb AAG20820.1 (AE005150) Vng8147h [Halobacterium sp. NRC-1] gb AAG21042.1 (AE005169) Vng6447h [Halobacterium sp. NRC-1] Length = 424</p>
SEQ ID n°1154	Prot n°PL-2014.1	Contig41	1008356	1009123	No Hits found	
SEQ ID n°1155	Prot n°PL-2016.1	Contig41	1006548	1007306	No Hits found	

TABLEAU I

SEQ ID n°1156	Prot n°PL-2017.1	Contig41	1005876	1006523	33%	Identities = 47/185 (25%), Positives = 73/185 (39%), Gaps = 28/185 (15%) gb AAG07294.1 AE004808_4 (AE004808) hypothetical protein [Pseudomonas aeruginosa] Length = 261
SEQ ID n°1157	Prot n°PL-2018.1	Contig41	1004739	1005461	36%	Identities = 45/198 (22%), Positives = 89/198 (44%), Gaps = 14/198 (7%) gb AAG07295.1 AE004808_5 (AE004808) hypothetical protein [Pseudomonas aeruginosa] Length = 239
SEQ ID n°1158	Prot n°PL-2019.1	Contig41	1004092	1004715	36%	Identities = 50/191 (26%), Positives = 76/191 (39%), Gaps = 23/191 (12%) gb AAG07294.1 AE004808_4 (AE004808) hypothetical protein [Pseudomonas aeruginosa] Length = 261
SEQ ID n°1159	Prot n°PL-202.1	Contig41	336075	336716	89%	Identities = 178/212 (83%), Positives = 196/212 (91%) gb AAG01334.1 AF288218_1 (AF288218) SspA [Providencia stuartii] Length = 213
SEQ ID n°1160	Prot n°PL-2020.1	Contig41	1001294	1003270	53%	Identities = 246/674 (36%), Positives = 362/674 (53%), Gaps = 34/674 (5%) gb AAF65932.1 AE004346) vgrG protein [Vibrio cholerae] Length =
SEQ ID n°1161	Prot n°PL-2021.1	Contig41	999516	1001279	43%	Identities = 143/582 (24%), Positives = 255/592 (42%), Gaps = 25/592 (4%) gb AAF96024.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 589
SEQ ID n°1162	Prot n°PL-2022.1	Contig41	995602	998937	78%	Identities = 692/1111 (62%), Positives = 882/1111 (79%), Gaps = 4/1111 (0%) sp P39285 YJEP_EC01 HYPOTHETICAL 123.8 KD PROTEIN IN GENX-PSD INTERGENIC REGION PRECURSOR pir E65228 hypothetical 123.8 kD protein in genX-psd intergenic region - Escherichia coli (strain K-12) gb AAC77119.1 (AE000488) putative periplasmic binding protein [Escherichia coli] Length = 1107
SEQ ID n°1163	Prot n°PL-2023.1	Contig41	994682	995575	73%	Identities = 185/284 (65%), Positives = 234/284 (82%) sp P10740 DPSD_EC01 PHOSPHATIDYL SERINE DECARBOXYLASE PROENZYME pir A29234 phosphatidylserine decarboxylase (EC 4.1.1.65) precursor - Escherichia coli gb AAA97059.1 (U14003) phosphatidylserine decarboxylase [Escherichia coli] gb AAA83896.1 (J03916) phosphatidylserine decarboxylase [Escherichia coli] gb AAC77120.1 (AE000488) phosphatidylserine decarboxylase; phospholipid synthesis
SEQ ID n°1164	Prot n°PL-2024.1	Contig41	993552	994607	82%	Identities = 261/350 (74%), Positives = 292/350 (82%), Gaps = 1/350 (0%) sp P39286 YJEP_EC01 HYPOTHETICAL 39.2 KD PROTEIN IN PSD-AMIB INTERGENIC REGION Length = 350
SEQ ID n°1165	Prot n°PL-2025.1	Contig41	998958	990869	47%	Identities = 85/309 (27%), Positives = 162/309 (51%), Gaps = 5/309 (1%) dbj BAB04109.1 (AP001508) unknown conserved protein [Bacillus halodurans] Length = 311
SEQ ID n°1166	Prot n°PL-2026.1	Contig41	998644	998655	31%	Identities = 71/282 (24%), Positives = 129/282 (43%), Gaps = 29/282 (9%) pir J127169 hypothetical protein Y54G11A.4 - Caenorhabditis elegans emb CAA22449.1 (AL034488) predicted using GeneFinder [Caenorhabditis elegans] Length = 497

TABLEAU I

SEQ ID n°1167	Prot n°PL-2027.1	Contig41	987599	988689	46%	<p>Identities = 97/292 (33%), Positives = 165/292 (56%), Gaps = 7/292 (2%) epiO32265YVBU_BACSU HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YVBU pir E70030 transcription regulator LysR family homolog yvbU - Bacillus subtilis emb CAB15404.1 (Z99121) similar to transcriptional regulator (LysR family) [Bacillus subtilis] Length = Identities = 239/614 (38%), Positives = 341/614 (54%), Gaps = 49/614 (7%) sp P40803 PKSK_BACSU PUTATIVE POLYKETIDE SYNTHASE PKSK (PKS) pir A69679 polyketide synthase pksK - Bacillus subtilis gb AA85144.1 (U11039) polyketide synthase [Bacillus subtilis] emb CAB13590.1 (Z99112) polyketide synthase of type I [Bacillus subtilis] emb CAB13601.1 (Z99113) polyketide synthase of type I [Bacillus subtilis] Length = 4447</p>	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°1168	Prot n°PL-2028.1	Contig32	158260	160122	54%	<p>Identities = 241/371 (64%), Positives = 295/371 (78%), Gaps = 1/371 (0%) sp P46442 YHGM_ECOLI HYPOTHETICAL 43.1 KD PROTEIN IN RPLM- H10A INTERGENIC REGION (F375) pir B65115 hypothetical 43.1 kD protein in rplM-h10A intergenic region - Escherichia coli (strain K-12) gb AAA58034.1 (U18997) ORF_375 [Escherichia coli] gb AAC76284.1 (AE000402) orf, hypothetical protein [Escherichia coli] Length = 375 Identities = 103/411 (25%), Positives = 172/411 (41%), Gaps = 37/411 (9%) db BAB06372.1 (AP001516) pyruvate dehydrogenase E2 (dihydrolipoamide acetyltransferase) [Bacillus halodurans] Length = 426 Identities = 176/530 (33%), Positives = 280/530 (52%), Gaps = 36/530 (6%) pir H72128 oxoisovalerate dehydrogenase (pyruvate) alpha and beta fusion - Chlamydia pneumoniae (strain CWL028) gb AAD18186.1 (AE001588) (pyruvate) Oxoisovalerate Dehydrogenase Alpha & Beta [Chlamydia pneumoniae] gb AAF38548.1 (AE002233) 2-oxoisovalerate dehydrogenase, E1 component, alpha and beta subunit [Chlamydia pneumoniae pneumoniae AR39] Length = 678 Identities = 242/448 (54%), Positives = 328/448 (73%), Gaps = 15/448 (3%) gb AAB71432.1 (U82290) putative glycoprotein [Escherichia coli] Length = 464</p>	
SEQ ID n°1170	Prot n°PL-2030.1	Contig32	158705	158279	32%	<p>Identities = 713/2196 (32%), Positives = 1133/2196 (51%), Gaps = 140/2196 (6%) gb AAF17281.1 (AF204805) NosD [Nostoc sp. GSV224] Length = 2450</p>	
SEQ ID n°1171	Prot n°PL-2031.1	Contig32	154684	156420	48%	<p>Identities = 139/388 (35%), Positives = 205/388 (52%), Gaps = 5/388 (1%) pir H75515 tetracycline-efflux transporter - Deinococcus radiodurans (strain R1) gb AAF10051.1 (AE001906) tetracycline-efflux transporter [Deinococcus radiodurans] Length = 407</p>	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°1172	Prot n°PL-2032.1	Contig32	151629	153058	68%		
SEQ ID n°1173	Prot n°PL-2033.1	Contig32	149778	150608	No Hits found		
SEQ ID n°1174	Prot n°PL-2034.1	Contig32	137160	149753	26%		
SEQ ID n°1175	Prot n°PL-2035.1	Contig32	135898	137244	45%		

TABLEAU I

SEQ ID n°1176	Prot n°PL-2036.1	Contig32	132672	136869	60%	Identities = 472/1057 (44%), Positives = 644/1057 (60%), Gaps = 28/1057 (2%) pir T14591 actinomycin synthetase II - Streptomyces chrysomallus gb AAC38442.1 (AF047717) actinomycin synthetase II [Streptomyces chrysomallus] Length = 2611	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°1177	Prot n°PL-2037.1	Contig32	130805	131873	No Hits found	Identities = 75/306 (24%), Positives = 123/306 (39%), Gaps = 61/306 (19%) gb AAF86178.1 (AE004366) multidrug resistance protein D [Vibrio cholerae] Length = 379	
SEQ ID n°1178	Prot n°PL-2038.1	Contig32	129638	130888	29%		
SEQ ID n°1179	Prot n°PL-2039.1	Contig32	128493	129653	No Hits found		
SEQ ID n°1180	Prot n°PL-204.1	Contig41	340270	341646	83%	Identities = 308/459 (67%), Positives = 385/459 (83%), Gaps = 64/459 (1%) spiP39009 DEGQ_ECOLI_PROTEASE DEQ PRECURSOR pir JC8051 trypsin-like proteinase (EC 3.4.21.-) hhoA precursor - Escherichia coli gb AAC43992.1 (U15661) hhoA [Escherichia coli] gb AAA58036.1 (U18997) ORF_0465 [Escherichia coli] gb AAC44005.1 (U32485) DegQ [Escherichia coli] gb AAC76266.1 (AE000402) serine endoprotease [Escherichia coli] pir 2206396A hhoA gene [Escherichia coli] Length = 455	
SEQ ID n°1181	Prot n°PL-2040.1	Contig32	127354	128517	28%	Identities = 64/270 (23%), Positives = 112/270 (40%), Gaps = 37/270 (13%) emb CAC1141.1 (AJ250591) NKS protein [Streptomyces tendae] Length = 424	
SEQ ID n°1182	Prot n°PL-2041.1	Contig32	126063	126896	29%	Identities = 49/167 (29%), Positives = 82/167 (48%), Gaps = 9/167 (5%) emb CAC12469.1 (AL445067) conserved hypothetical protein [Thermoplasma acidophilum] Length = 251	
SEQ ID n°1183	Prot n°PL-2042.1	Contig32	124323	125564	53%	Identities = 157/408 (38%), Positives = 226/408 (54%), Gaps = 17/408 (4%) pir C72394 hypothetical protein TM0291 - Thermotoga maritima (strain MSB8) gb AAD35378.1AE001711_2 (AE001711) 3-isopropylmalate dehydratase, large subunit, putative [Thermotoga maritima] Length = 418	
SEQ ID n°1184	Prot n°PL-2043.1	Contig32	123178	123876	54%	Identities = 92/222 (41%), Positives = 126/222 (57%) emb CAB91068.1 (AJ239032) homocitrate synthase 2 [Anabaena variabilis] Length = 379	
SEQ ID n°1185	Prot n°PL-2044.1	Contig32	121822	123153	66%	Identities = 219/443 (49%), Positives = 309/443 (69%), Gaps = 6/443 (1%) spiP54950 YXEK_BACSU_HYPOTHETICAL 49.3 KD PROTEIN IN IDH-DEOR INTERGENIC REGION pir E70075 nitroacetate monooxygenase (EC 1.14.13.-) component A homolog yxeK - Bacillus subtilis dbj BAA08327.1 (D45912) homologous to deaA gene product of Rhodococcus sp. [Bacillus subtilis] emb CAB15988.1 (Z99124) similar to monooxygenase [Bacillus subtilis] Length = 441	
SEQ ID n°1186	Prot n°PL-2045.1	Contig32	120885	121640	67%	Identities = 118/250 (47%), Positives = 169/250 (67%), Gaps = 2/250 (0%) pir S0206 phosphoenolpyruvate phosphomutase FOM1 - Streptomyces wedmorensis dbj BAA32495.1 (AB016934) phosphoenolpyruvate phosphomutase [Streptomyces wedmorensis] Length = 435	
SEQ ID n°1187	Prot n°PL-2046.1	Contig32	119130	119807	50%	Identities = 76/203 (37%), Positives = 115/203 (56%), Gaps = 1/203 (0%) pir 1919484A impB gene [Klebsiella pneumoniae] Length = 296	

TABLEAU I

SEQ ID n°1188	Prot n°PL-2047.1	Contig32	117743	118393	81%	Identities = 151/211 (71%), Positives = 180/211 (84%), Gaps = 2/211 (0%) sp P07800 CHEZ_SALTY CHEMOTAXIS PROTEIN CHEZ pir A27088 chemotaxis protein cheZ - Salmonella typhimurium gb AAD15120.1 (M18891) cheZ gene product [Salmonella typhimurium] Length = 214
SEQ ID n°1189	Prot n°PL-2048.1	Contig32	115972	117024	89%	Identities = 277/352 (78%), Positives = 318/352 (89%), Gaps = 5/352 (1%) sp P07330 CHEB_ECOLI PROTEIN-GLUTAMATE METHYLESTERASE pir XYECEB protein-glutamate methyltransferase (EC 3.1.1.61) - Escherichia coli db BAA15689.1 (D90830) Protein-glutamate methyltransferase (EC 3.1.1.61). [Escherichia coli] gb AAC74953.1 (AE000282) response regulator for chemotaxis (cheA sensor); protein methyltransferase [Escherichia coli] Length = 349 "
SEQ ID n°1190	Prot n°PL-2049.1	Contig32	115092	115979	73%	Identities = 189/283 (66%), Positives = 220/283 (76%), Gaps = 3/283 (1%) sp P07801 CHER_SALTY CHEMOTAXIS PROTEIN METHYLTRANSFERASE pir XYEBGM protein-glutamate O-methyltransferase (EC 2.1.1.80) - Salmonella typhimurium gb AA27035.1 (J02757) methyltransferase (cheR; EC 2.1.1.24) [Salmonella typhimurium] Length = 288 "
SEQ ID n°1191	Prot n°PL-205.1	Contig41	341798	342681	42%	Identities = 88/241 (36%), Positives = 122/241 (50%), Gaps = 5/241 (2%) db BAB16031.1 (AB030747) transposase [Streptococcus pyogenes] Length = 428
SEQ ID n°1192	Prot n°PL-2050.1	Contig32	113451	115085	63%	Identities = 267/519 (51%), Positives = 357/519 (68%), Gaps = 6/519 (1%) sp P02942 MCP1_ECOLI METHYL-ACCEPTING CHEMOTAXIS PROTEIN I (MCP-I) (SERINE CHEMORECEPTOR PROTEIN) pir QRECS serine chemoreceptor protein - Escherichia coli gb AA24700.1 (J01718) methyl- accepting chemotaxis protein I [Escherichia coli] gb AAC77311.1 (AE000506) methyl-accepting chemotaxis protein I, serine sensor receptor [Escherichia coli] Length = 551
SEQ ID n°1193	Prot n°PL-2051.1	Contig32	111703	113397	75%	Identities = 334/567 (58%), Positives = 429/567 (74%), Gaps = 13/567 (2%) sp P21822 MCP5_ENTAE METHYL-ACCEPTING CHEMOTAXIS SERINE TRANSDUCER pir JC32302 serine transducer tse - Enterobacter aerogenes gb AA24787.1 (M26411) tse [Enterobacter aerogenes] Length = 557
SEQ ID n°1194	Prot n°PL-2052.1	Contig32	108924	110975	77%	Identities = 461/676 (68%), Positives = 536/676 (79%), Gaps = 17/676 (2%) sp P09384 CHEA_SALTY CHEMOTAXIS PROTEIN CHEA pir A28959 chemotaxis protein cheA - Salmonella typhimurium gb AA27034.1 (J03811) sensory protein (cheA; gta start codon) [Salmonella typhimurium] Length = 671 "

TABLEAU I

SEQ ID n°1195	Prot n°PL-2053.1	Contig32	107920	108921	69%	<p>Identities = 187/310 (60%), Positives = 233/310 (74%), Gaps = 9/310 (2%) sp P08349 MOTB_ECOLI_CHEMOTAXIS MOTB PROTEIN (MOTILITY PROTEIN B) pir JQRECMB chemotaxis protein motB - Escherichia coli gb AAA24178.1 (J01652) motB protein for chemotaxis [Escherichia coli] dbj BAA15710.1 (D90831) Chemotaxis MotB protein (Motility protein B) [Escherichia coli] gb AAC74959.1 (AE000282) enables flagellar motor rotation, linking torque machinery to cell wall [Escherichia coli]</p>
SEQ ID n°1196	Prot n°PL-2054.1	Contig32	106823	107923	69%	<p>Identities = 217/294 (73%), Positives = 255/294 (85%) sp P56891 MOTA_SALTY_CHEMOTAXIS MOTA PROTEIN (MOTILITY PROTEIN A) gb AAC45265.1 (U81861) MotA [Salmonella typhimurium] dbj BAA85316.1 (D43640) MotA protein [Salmonella typhimurium]</p>
SEQ ID n°1197	Prot n°PL-2055.1	Contig32	101453	102163	69%	<p>Identities = 140/233 (60%), Positives = 172/233 (73%), Gaps = 2/233 (0%) sp P22037 ATMC_SALTY MG(2+) TRANSPORT ATPASE PROTEIN C pir A39083 Mg2+-transporting ATPase (EC 3.6.1.-) mgcC - Salmonella typhimurium gb AAA72083.1 (M57715) Mg2+ transport ATPase [Salmonella typhimurium] gb AAD16960.1 (AF106566) MgtC [Salmonella typhimurium]</p>
SEQ ID n°1198	Prot n°PL-2056.1	Contig32	98336	98421	No Hits found	Length = 231
SEQ ID n°1199	Prot n°PL-2057.1	Contig32	95332	96435	66%	<p>Identities = 200/333 (60%), Positives = 243/333 (72%), Gaps = 4/333 (1%) sp P38347 INTB_ECOLI_PROPHAGE P4 INTEGRASE (INT(P4)) pir S56496 prophage P4 integrase - Escherichia coli gb AAA97167.1 (U14003) ORF_o396 [Escherichia coli] gb AAC77227.1 (AE000498) prophage P4 integrase [Escherichia coli] Length = 396</p>
SEQ ID n°1200	Prot n°PL-2058.1	Contig32	93503	95248	20%	<p>Identities = 66/289 (22%), Positives = 119/289 (40%), Gaps = 48/289 (16%) pir T18372 repeat organellar protein - Plasmodium chabaudi gb AAC63403.1 (U43145) repeat organellar protein [Plasmodium chabaudi] Length =</p>
SEQ ID n°1201	Prot n°PL-2059.1	Contig32	92352	93455	No Hits found	
SEQ ID n°1202	Prot n°PL-206.1	Contig41	344446	345504	79%	<p>Identities = 236/351 (67%), Positives = 284/351 (80%), Gaps = 1/351 (0%) sp P31137 DEGS_ECOLI_PROTEASE DEGS PRECURSOR pir JC6062 trypsin-like proteinase (EC 3.4.21.-) hhoB - Escherichia coli gb AAC43983.1 (U15661) hhoB [Escherichia coli] gb AAA58037.1 (U18997) ORF_o355 [Escherichia coli] gb AAC44006.1 (U32495) DegS [Escherichia coli] gb AAC76267.1 (AE000402) protease [Escherichia coli] pir J2206396B hhoB gene [Escherichia coli] Length = 355</p>
SEQ ID n°1203	Prot n°PL-2060.1	Contig32	90058	91680	5%	<p>Identities = 20/50 (40%), Positives = 32/50 (64%), Gaps = 1/50 (2%) gb AAF70012.1 AF250878_173 (AF250878)orf; hypothetical protein [Salmonella typhi] Length = 357 "</p>
SEQ ID n°1204	Prot n°PL-2061.1	Contig32	89022	90062	No Hits found	
SEQ ID n°1205	Prot n°PL-2062.1	Contig32	85673	87202	25%	<p>Identities = 87/242 (35%), Positives = 131/242 (53%), Gaps = 32/242 (13%) gb AAC55983.1 (AE001272) nicking enzyme (traA) [Lactococcus lactis]</p>
						Length = 680

TABLEAU I

SEQ ID n°1206	Prot n°PL-2063.1	Contig32	83738	85615	47%	Identities = 178/618 (28%), Positives = 295/618 (46%), Gaps = 90/618 (14%) pir S77439 hypothetical protein sir1135 - <i>Synechocystis</i> sp. (strain PCC 6803) dbj BAA17286.1 (D90905) hypothetical protein [<i>Synechocystis</i> sp.] Length = 715
SEQ ID n°1207	Prot n°PL-2064.1	Contig32	81390	82358	60%	Identities = 168/314 (53%), Positives = 213/314 (67%), Gaps = 4/314 (1%) emb CAB84714.1 (AL162756) putative transposase for IS1655 [<i>Neisseria meningitidis</i>] emb CAB84719.1 (AL162756) putative transposase for IS1655 [<i>Neisseria meningitidis</i>] Length = 321
SEQ ID n°1208	Prot n°PL-2065.1	Contig32	79181	80059	No Hits found	Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U83995) putative protease [<i>Porphyromonas gingivalis</i>] Length = 300
SEQ ID n°1210	Prot n°PL-2067.1	Contig32	76537	77589	78%	Identities = 247/347 (71%), Positives = 287/347 (82%) sp P05020 PYRC_ECOLI DIHYDROOROTASE (DHOASE) pir JDEECOO dihydroorotase (EC 3.5.2.3) - <i>Escherichia coli</i> emb CAA28157.1 (X04468) dihydroorotase [<i>Escherichia coli</i>] gb AAA24482.1 (M16752) dihydroorotase (EC 3.5.2.3) [<i>Escherichia coli</i>] dbj BAA35870.1 (D90743) Dihydroorotase (EC 3.5.2.3) [<i>Escherichia coli</i>] gb AAC74146.1 (AE000207) dihydro-orotase [<i>Escherichia coli</i>] Length = 348
SEQ ID n°1211	Prot n°PL-2068.1	Contig32	75284	75946	40%	Identities = 49/191 (25%), Positives = 89/191 (45%), Gaps = 7/191 (3%) pir AA5828 colanic acid capsular biosynthesis activation protein A - <i>Erwinia amylovora</i> Length = 211
SEQ ID n°1212	Prot n°PL-2069.1	Contig32	74180	75238	83%	Identities = 263/343 (76%), Positives = 288/343 (86%) protein 39.9 - <i>Escherichia coli</i> emb CAA43318.1 (X61000) Orf39.9 [<i>Escherichia coli</i>] Length = 350
SEQ ID n°1213	Prot n°PL-207.1	Contig41	348288	347733	9%	Identities = 30/83 (36%), Positives = 48/83 (57%), Gaps = 3/83 (3%) gb AAC72032.1 (AF047554) unknown [<i>Myxococcus xanthus</i>] Length = Identities = 189/308 (65%), Positives = 246/308 (80%)
SEQ ID n°1214	Prot n°PL-2070.1	Contig32	72472	73413	77%	sp P24187 HTRB_ECOLI LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (HEAT SHOCK PROTEIN B) pir J16888 lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-) - <i>Escherichia coli</i> emb CAA43317.1 (X61000) HtrB protein [<i>Escherichia coli</i>] dbj BAA35863.1 (D90743) HtrB protein. [<i>Escherichia coli</i>] gb AAC74138.1 (AE000206) heat shock protein [<i>Escherichia coli</i>] dbj BAA35852.1 (D90742) HtrB protein. Identities = 192/505 (38%), Positives = 288/505 (57%), Gaps = 28/505 (5%)
SEQ ID n°1215	Prot n°PL-2071.1	Contig32	70210	71748	55%	sp P94408 YCLF_BACSU HYPOTHETICAL 53.3 KD PROTEIN IN SFP- GERKA INTERGENIC REGION pir J69762 di-tripeptide ABC transporter (membrane pt) homolog ycf - <i>Bacillus subtilis</i> dbj BAA09000.1 (D50453) homologue of di-tripeptide transporter Dtp of <i>L. lactis</i> [<i>Bacillus subtilis</i>] emb CAB12175.1 (Z99106) similar to di-tripeptide ABC transporter (membrane protein) [<i>Bacillus subtilis</i>] Length = 492

TABLEAU I

SEQ ID n°1216	Prot n°PL-2072.1	Contig32	68599	69306	47%	Identities = 79/244 (32%), Positives = 114/244 (48%), Gaps = 19/244 (7%) gb AAG06608.1 AE004745_5 (AE004745) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 254
SEQ ID n°1217	Prot n°PL-2073.1	Contig32	66479	67369	38%	Identities = 60/220 (27%), Positives = 114/220 (51%), Gaps = 10/220 (4%) dbj BAB08659.1 (AP001517) unknown conserved protein [Bacillus halodurans] Length = 284
SEQ ID n°1218	Prot n°PL-2074.1	Contig32	64721	66232	67%	Identities = 282/502 (56%), Positives = 371/502 (73%), Gaps = 5/502 (0%) gb AAG03520.1 AE004451_1 (AE004451) probable aldehyde dehydrogenase [Pseudomonas aeruginosa] Length = 497
SEQ ID n°1219	Prot n°PL-2075.1	Contig32	62770	64704	70%	Identities = 358/647 (55%), Positives = 484/647 (71%), Gaps = 13/647 (2%) dbj BAB06037.1 (AP001515) myo-inositol catabolism [Bacillus halodurans] Length = 637
SEQ ID n°1220	Prot n°PL-2076.1	Contig32	61418	62404	57%	Identities = 151/323 (46%), Positives = 202/323 (61%) sp O68965 M2D_RHIME MYO-INOSITOL 2-DEHYDROGENASE gb AAC70005.1 (AF059313) myo-inositol dehydrogenase [Sinorhizobium] Identities = 245/545 (44%), Positives = 364/545 (65%), Gaps = 7/545 (1%)
SEQ ID n°1221	Prot n°PL-2077.1	Contig32	59599	61314	60%	sp P31448 YIDK_ECOLI HYPOTHETICAL 62.1 KD PROTEIN IN EMRD-GLVG INTERGENIC REGION pir H65169 probable transport protein yidK - Escherichia coli (strain K-12) gb AA62031.1 (L10328) similar to glucose transport proteins [Escherichia coli] gb AAC76702.1 (AE000445) putative cotransporter [Escherichia coli] Length = 571
SEQ ID n°1222	Prot n°PL-2078.1	Contig32	57931	59064	56%	Identities = 140/388 (36%), Positives = 221/388 (56%), Gaps = 12/388 (3%) dbj BAB04428.1 (AP001509) unknown conserved protein [Bacillus halodurans] Length = 388
SEQ ID n°1223	Prot n°PL-2079.1	Contig32	55951	57891	27%	Identities = 104/341 (30%), Positives = 175/341 (50%), Gaps = 21/341 (6%) dbj BAB06038.1 (AP001515) myo-inositol catabolism [Bacillus halodurans] Length = 331
SEQ ID n°1224	Prot n°PL-208.1	Contig41	347739	350237	26%	Identities = 128/552 (23%), Positives = 220/552 (39%), Gaps = 77/552 (13%) pir S72284 DNA-directed RNA polymerase (EC 2.7.7.6) beta-2 chain - Plasmodium falciparum plasid emb CAA64574.1 (X95275) frameshift [Plasmodium falciparum] Length = 960
SEQ ID n°1225	Prot n°PL-2080.1	Contig32	55031	55921	64%	Identities = 164/295 (55%), Positives = 203/295 (68%), Gaps = 31/295 (10%) (AF076240) MocC [Rhizobium leguminosarum bv. viciae] Length = 295
SEQ ID n°1226	Prot n°PL-2081.1	Contig32	54156	54983	57%	Identities = 136/268 (50%), Positives = 175/268 (64%), Gaps = 4/268 (1%) sp P42413 IOLB_BACSU IOLB PROTEIN pir B69645 myo-inositol catabolism iolB - Bacillus subtilis dbj BAA03291.1 (D14399) hypothetical protein [Bacillus subtilis] emb CAB16011.1 (Z99124) alternate gene name: yxdB~myo-inositol catabolism [Bacillus subtilis] Length = 271
SEQ ID n°1227	Prot n°PL-2082.1	Contig32	50949	52007	No Hits found	
SEQ ID n°1228	Prot n°PL-2083.1	Contig32	49984	50970	No Hits found	
SEQ ID n°1229	Prot n°PL-2084.1	Contig32	48641	50005	No Hits found	

TABLEAU I

SEQ ID n°1231	Prot n°PL-2085.1	Contig32	44290	47613	No Hits found	
SEQ ID n°1231	Prot n°PL-2086.1	Contig32	41620	42687	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°1232	Prot n°PL-2087.1	Contig32	34025	36079	76%	Identities = 424/684 (61%), Positives = 527/684 (76%) sp P15038 HELD_ECOLI_HELICASE_IV (75 KD HELICASE) db JHJEC44 helicase (EC 3.6.1.-) IV - Escherichia coli db BAA35727.1 (D90734) Helicase (EC 3.6.1.-) IV. [Escherichia coli] gb AAC74048.1 (AE000198) DNA helicase IV [Escherichia coli] Length = 684
SEQ ID n°1233	Prot n°PL-2088.1	Contig32	31673	33814	76%	Identities = 446/706 (63%), Positives = 555/706 (78%), Gaps = 2/706 (0%) sp P75870 YCCS_ECOLI_HYPOTHETICAL_82.0 KDA PROTEIN IN SULA-HELD INTERGENIC REGION pir IG64836 probable membrane protein yccS - Escherichia coli gb AAC74046.1 (AE000198) orf, hypothetical protein [Escherichia coli] db BAA35718.1 (D90733) Hypothetical protein HI1680 [Escherichia coli] db BAA35725.1 (D90734) Hypothetical protein HI1680 [Escherichia coli] Length = 720
SEQ ID n°1234	Prot n°PL-2089.1	Contig32	31002	31613	47%	Identities = 74/196 (37%), Positives = 101/196 (50%), Gaps = 1/196 (0%) sp P75869 YCCR_ECOLI_HYPOTHETICAL_24.1 KDA PROTEIN IN SULA-HELD INTERGENIC REGION pir IF64836 probable membrane protein b0959 - Escherichia coli gb AAC74045.1 (AE000198) orf, hypothetical protein [Escherichia coli] db BAA35717.1 (D90733) ORF_ID:0223#4 [Escherichia coli] db BAA35724.1 (D90734) ORF_ID:0223#4 [Escherichia coli] Length = 209
SEQ ID n°1235	Prot n°PL-209.1	Contig41	350896	352555	88%	Identities = 421/520 (80%), Positives = 474/520 (90%), Gaps = 1/520 (0%) gb AAC08739.1 (AF021839) 4-hydroxyphenylacetic acid hydroxylase [Photobacterium luminescens] Length = 520
SEQ ID n°1236	Prot n°PL-2090.1	Contig40	314808	315824	55%	Identities = 132/320 (41%), Positives = 190/320 (59%), Gaps = 13/320 (4%) gb AAC31479.1 (AF067849) phospholipase A [Yersinia enterocolitica (type 0:8)] Length = 324
SEQ ID n°1237	Prot n°PL-2091.1	Contig40	313369	314049	81%	Identities = 170/224 (75%), Positives = 189/224 (83%) (AE004306) uracil-DNA glycosylase [Vibrio cholerae] Length = 226
SEQ ID n°1238	Prot n°PL-2092.1	Contig40	312719	313300	68%	Identities = 118/196 (60%), Positives = 147/196 (74%), Gaps = 5/196 (2%) sp P09372 GRPE_ECOLI_GRPE_PROTEIN (HSP-70 COFACTOR) (HEAT SHOCK PROTEIN B25.3) (HSP24) pir S01240 heat shock protein grpE (heat shock protein b25.3) (hsp24) - Escherichia coli emb CAA30711.1 (X07863) grpE protein (AA 1-197) [Escherichia coli] gb AAB32515.1 GrpE=heat shock protein [Escherichia coli, mutant grpE25, Peptide Mutant, 197 aa] gb AAC75663.1 (AE000347) phage lambda replication; host DNA synthesis; heat shock protein; protein repair [Escherichia coli] db BAA16498.1 (D90888) heat shock protein B25.3 [Escherichia coli]

TABLEAU I

SEQ ID n°1238	Prot n°PL-2093.1	Contig40	311716	312594	85%	<p>Identities = 226/292 (77%), Positives = 255/292 (86%)</p> <p>sp P37081 YJB_ECOLI HYPOTHETICAL 32.8 KDA PROTEIN IN GRPE-RECN INTERGENIC REGION pir B65040 yfB protein - Escherichia coli (strain K-12) gb AAC76664.1 (AE000347) orf, hypothetical protein [Escherichia coli] dbj BAA16500.1 (D90888) similar to [SwissProt Accession Number P37768] [Escherichia coli] Length = 292</p>
SEQ ID n°1240	Prot n°PL-2094.1	Contig40	309966	311627	80%	<p>Identities = 401/553 (72%), Positives = 458/553 (82%) pir RQECN recN protein - Escherichia coli gb AAC75665.1 (AE000347) protein used in recombination and DNA repair [Escherichia coli] Length = 553</p>
SEQ ID n°1241	Prot n°PL-2095.1	Contig40	304459	305877	19%	<p>Identities = 62/170 (36%), Positives = 90/170 (52%), Gaps = 24/170 (14%)</p> <p>ref NP_050653.1 S sp Q9T1V0 VPS_BPMU TAIL FIBER PROTEIN (GPS) gb AAF01127.1 (AF083977) S [Bacteriophage Mu] Length = 504</p>
SEQ ID n°1242	Prot n°PL-2096.1	Contig40	303942	304547	No Hits found	
SEQ ID n°1243	Prot n°PL-2097.1	Contig40	302616	303941	28%	<p>Identities = 74/300 (24%), Positives = 124/300 (40%), Gaps = 13/300 (4%)</p> <p>gb AAF84513.1 (AE0003994) hypothetical protein [Xylella fastidiosa] Length = 387</p>
SEQ ID n°1244	Prot n°PL-2098.1	Contig40	299397	300359	No Hits found	
SEQ ID n°1245	Prot n°PL-2099.1	Contig40	298277	299164	No Hits found	
SEQ ID n°1246	Prot n°PL-21.1	Contig41	36698	37372	38%	<p>Identities = 52/212 (24%), Positives = 87/212 (40%), Gaps = 15/212 (7%)</p> <p>gb AAG04736.1 (AE004564_5) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230</p>
SEQ ID n°1247	Prot n°PL-210.1	Contig41	352980	354245	92%	<p>Identities = 371/417 (88%), Positives = 395/417 (93%)</p> <p>sp P33038 MURA_ENTCL UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (ENOYL-PYRUVATE TRANSFERASE) (EPT) pir S22372 UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) - Enterobacter cloacae pdb 1NAW A Chain A, Enolpyruvyl Transferase pdb 1NAW B Chain B, Enolpyruvyl Transferase emb CAA77856.1 (Z11835) UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Enterobacter cloacae]</p>
SEQ ID n°1248	Prot n°PL-2100.1	Contig40	296220	298343	19%	<p>Identities = 93/316 (29%), Positives = 139/316 (43%), Gaps = 57/316 (18%)</p> <p>pir T09486 structural lytic transglycosylase homolog - phage P1 gb AAB88193.1 (AF035607) structural lytic transglycosylase [enterobacteria phage P1] Length = 1140</p>
SEQ ID n°1249	Prot n°PL-2101.1	Contig40	293662	295173	37%	<p>Identities = 110/500 (22%), Positives = 190/500 (38%), Gaps = 53/500 (10%)</p> <p>gb AAF84392.1 (AE003986_22) (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84497.1 (AE003993_16) (AE003993) hypothetical protein [Xylella fastidiosa] Length = 498</p>
SEQ ID n°1250	Prot n°PL-2102.1	Contig40	293082	293705	No Hits found	
SEQ ID n°1251	Prot n°PL-2103.1	Contig40	290495	291556	No Hits found	

TABLEAU I

SEQ ID n°1252	Prot n°PL-2104.1	Contig40	288888	290043	25%	Identities = 69/281 (24%), Positives = 113/281 (39%), Gaps = 46/281 (16%) gb AAF84394.1 AE003986_14 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84489.1 AE003993_8 (AE003993) hypothetical protein [Xylella fastidiosa] Length = 397
SEQ ID n°1253	Prot n°PL-2105.1	Contig40	287822	288700	39%	Identities = 65/256 (25%), Positives = 115/256 (44%), Gaps = 11/256 (4%) sp P71385 YE07_HAEIN HYPOTHETICAL PROTEIN HI1407 pir B64122 hypothetical protein HI1407 - Haemophilus influenzae (strain Rd KW20) gb AAC23048.1 (U32820) traN-related protein [Haemophilus influenzae Rd] Length = 447
SEQ ID n°1254	Prot n°PL-2108.1	Contig40	286285	287922	28%	Identities = 85/366 (23%), Positives = 156/366 (42%), Gaps = 25/366 (6%) gb AAF84380.1 AE003986_10 (AE003986) conserved hypothetical protein [Xylella fastidiosa] gb AAF84485.1 AE003993_4 (AE003993) conserved hypothetical protein [Xylella fastidiosa] Length = 467
SEQ ID n°1255	Prot n°PL-2107.1	Contig40	285114	288439	25%	Identities = 81/180 (45%), Positives = 117/180 (61%), Gaps = 7/180 (3%) sp P44184 YE10_HAEIN HYPOTHETICAL PROTEIN HI1410 pir E64028 hypothetical protein HI1410 - Haemophilus influenzae (strain Rd KW20) gb AAC23056.1 (U32820) H. influenzae predicted coding region HI1410 [Haemophilus influenzae Rd] Length = 394
SEQ ID n°1256	Prot n°PL-2108.1	Contig40	281721	282665	No Hits found	Identities = 158/211 (74%), Positives = 180/211 (84%), Gaps = 2/211 (0%) sp P45390 YRBC_ECOLI HYPOTHETICAL 24.0 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (F211) pir B65110 hypothetical 24.0 kD protein in murZ-poN intergenic region - Escherichia coli (strain K-12) gb AAA57893.1 (U18997) ORF_7211 [Escherichia coli] gb AAC76224.1 (AE000389) orf, hypothetical protein [Escherichia coli] gb AAF21249.1 AF053073_2 (AF053073) Yrbc [Shigella flexneri] Length = 211
SEQ ID n°1257	Prot n°PL-211.1	Contig41	355245	355874	84%	Identities = 117/178 (65%), Positives = 139/178 (77%) ref NP_046950.1 gp54 sp O64362 LYCV_BPN15 LYSOZYME (LYSIS PROTEIN) (MURAMIDASE) (ENDOLYSIN) (PROTEIN GP54) pir T13141 lysozyme homolog - phage N15 gb AAC19089.1 (AF064539) gp54 [Bacteriophage N15] Length = 178
SEQ ID n°1258	Prot n°PL-2111.1	Contig40	275128	276367	25%	Identities = 78/152 (51%), Positives = 104/152 (68%), Gaps = 1/152 (0%) db BAA76527.2 (AB017338) tail fiber [Pectobacterium carotovorum] Length = 667
SEQ ID n°1260	Prot n°PL-2112.1	Contig40	274876	275388	54%	Identities = 97/140 (69%), Positives = 115/140 (81%) db BAA76526.1 (AB017338) tail fiber [Pectobacterium carotovorum] Length = 182
SEQ ID n°1261	Prot n°PL-2113.1	Contig40	273717	274820	78%	Identities = 251/367 (68%), Positives = 297/367 (80%) db BAA96863.1 (AB045036) baseplate [Pectobacterium carotovorum subsp. carotovorum] Length = 367

TABLEAU I

SEQ ID n°1262	Prot n°PL-2114.1	Contig40	272721	273328	75%	Identities = 130/196 (66%), Positives = 162/196 (82%), Gaps = 4/196 (2%) dbj BAA96861.1 (AB045036) tail spike [Pectobacterium carotovorum subsp. carotovorum] Length = 193
SEQ ID n°1263	Prot n°PL-2115.1	Contig40	271516	272724	73%	Identities = 251/378 (66%), Positives = 297/378 (78%), Gaps = 9/378 (2%) dbj BAA96860.1 (AB045036) orf7 [Pectobacterium carotovorum subsp. carotovorum] Length = 386
SEQ ID n°1264	Prot n°PL-2118.1	Contig40	270459	271343	68%	Identities = 154/303 (50%), Positives = 210/303 (68%), Gaps = 11/303 (3%) dbj BAA96859.1 (AB045036) orf8 [Pectobacterium carotovorum subsp. carotovorum] Length = 309
SEQ ID n°1265	Prot n°PL-2117.1	Contig40	267904	270459	54%	Identities = 270/873 (30%), Positives = 461/873 (51%), Gaps = 78/873 (8%) dbj BAA96858.1 (AB045036) tail protein [Pectobacterium carotovorum subsp. carotovorum] Length = 835
SEQ ID n°1266	Prot n°PL-2118.1	Contig40	265289	266716	88%	Identities = 383/475 (80%), Positives = 429/475 (89%), Gaps = 11/475 (2%) (AB017338) tail sheath protein [Pectobacterium carotovorum] Length = 475
SEQ ID n°1267	Prot n°PL-2119.1	Contig40	262885	263820	No Hits found	Identities = 206/260 (79%), Positives = 238/260 (91%) sp P45392 YRBE_ECOLI_HYPOTHETICAL_27.9_KD_PROTEIN_IN_MURA-RPON_INTERGENIC_REGION_F260 p I D65110 hypothetical 27.9 kD protein in murz-rpon intergenic region - Escherichia coli (strain K-12) gb AA57995.1 (U18997) ORF_260 [Escherichia coli] gb AAC76226.1 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 260
SEQ ID n°1268	Prot n°PL-2120.1	Contig40	261741	262853	No Hits found	Identities = 111/251 (44%), Positives = 148/251 (58%), Gaps = 5/251 (1%) ref NP_050634.1 gp30 gb AAAF01108.1 AF083977_27 (AF083977) gp30 [Bacteriophage Mu] Length = 439
SEQ ID n°1270	Prot n°PL-2121.1	Contig40	280243	261112	51%	Identities = 105/403 (26%), Positives = 180/403 (44%), Gaps = 21/403 (5%) emb CAB85074.1 (AL162757) conserved hypothetical protein [Neisseria meningitidis] Length = 519
SEQ ID n°1271	Prot n°PL-2122.1	Contig40	258742	260301	34%	Identities = 225/470 (47%), Positives = 301/470 (63%), Gaps = 8/470 (1%) ref NP_050632.1 gp28 sp Q8T1W6 VG28_BP MU PROTEIN GP28 gb AAAF01108.1 AF083977_25 (AF083977) gp28 [Bacteriophage Mu] Length = 551
SEQ ID n°1272	Prot n°PL-2123.1	Contig40	257204	258808	56%	Identities = 225/470 (47%), Positives = 301/470 (63%), Gaps = 8/470 (1%) ref NP_050632.1 gp28 sp Q8T1W6 VG28_BP MU PROTEIN GP28 gb AAAF01108.1 AF083977_25 (AF083977) gp28 [Bacteriophage Mu] Length = 551
SEQ ID n°1273	Prot n°PL-2124.1	Contig40	255304	256110	No Hits found	Identities = 41/132 (31%), Positives = 65/132 (49%), Gaps = 14/132 (10%) sp P44587 YFHD_HAEIN_HYPOTHETICAL_PROTEIN_H10232 p I H64145 hypothetical protein H10232 - Haemophilus influenzae (strain Rd KW20) gb AAC21901.1 (U32709) conserved hypothetical protein [Haemophilus influenzae Rd] Length = 462
SEQ ID n°1274	Prot n°PL-2125.1	Contig40	254754	255497	26%	Identities = 64/230 (27%), Positives = 105/230 (44%), Gaps = 14/230 (6%) gb AAAF83745.1 AE003932_9 (AE003932) methyltransferase [Xylella fastidiosa] Length = 311
SEQ ID n°1275	Prot n°PL-2126.1	Contig40	253506	254324	38%	Identities = 64/230 (27%), Positives = 105/230 (44%), Gaps = 14/230 (6%) gb AAAF83745.1 AE003932_9 (AE003932) methyltransferase [Xylella fastidiosa] Length = 311

TABLEAU I

SEQ ID n°1276	Prot n°PL-2127.1	Contig40	250148	251071	47%	Identities = 102/286 (35%), Positives = 154/286 (53%), Gaps = 7/286 (2%) gb AAF41403.1 (AE002451) hypothetical protein [Neisseria meningitidis MC58] Length = 291
SEQ ID n°1277	Prot n°PL-2128.1	Contig40	248310	250094	52%	Identities = 193/591 (32%), Positives = 317/591 (52%), Gaps = 31/591 (5%) gb AAF94948.1 (AE004256) hypothetical protein [Vibrio cholerae] Length = 585
SEQ ID n°1278	Prot n°PL-2129.1	Contig40	246899	248083	47%	Identities = 154/229 (67%), Positives = 188/229 (81%) gb AAC64124.1 (AF091717) Eha [Salmonella typhi] Length = 322 Identities = 205/266 (77%), Positives = 239/266 (89%)
SEQ ID n°1279	Prot n°PL-2131.1	Contig41	357212	358015	87%	sp P45393 NRBF_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN MURA-RPON INTERGENIC REGION pir E55110 hypothetical protein b3195 - Escherichia coli (strain K-12) gb AAA57986.1 (U18997) ORF_269 [Escherichia coli] gb AAC76227.1 (AE000399) putative ATP-binding component of a transport system
SEQ ID n°1280	Prot n°PL-2130.1	Contig40	241514	242719	36%	Identities = 89/307 (28%), Positives = 147/307 (46%), Gaps = 18/307 (5%) pir T36177 probable DNA-binding protein - Streptomyces coelicolor emb CAB41077.1 (ALD49645) putative DNA-binding protein [Streptomyces coelicolor A3(2)] Length = 390
SEQ ID n°1281	Prot n°PL-2131.1	Contig40	239040	240407	60%	Identities = 209/460 (45%), Positives = 286/460 (61%), Gaps = 17/460 (3%) ref NP_037740.1 Gp55 gb AAF31133.1 (AF069529) Gp55 [Bacteriophage HK97] Length = 458
SEQ ID n°1282	Prot n°PL-2132.1	Contig40	237675	238445	28%	Identities = 50/142 (35%), Positives = 74/142 (51%), Gaps = 22/142 (15%) pir T03010 probable replication protein - Salmonella typhimurium gb AAC28071.1 (AF001386) unknown [Salmonella typhimurium] Length = 325
SEQ ID n°1283	Prot n°PL-2133.1	Contig40	233634	234701	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°1284	Prot n°PL-2134.1	Contig40	231695	233494	8%	Identities = 31/99 (31%), Positives = 53/99 (53%), Gaps = 2/99 (2%) pir T03004 exodeoxyribonuclease VIII homolog - Salmonella typhimurium gb AAC26062.1 (AF001386) exodeoxyribonuclease VIII [Salmonella typhimurium] Length = 975

TABLEAU I

SEQ ID n°1285	Prot n°PL-2135.1	Contig40	228866	229954	46%	Identities = 108/374 (28%), Positives = 168/374 (44%), Gaps = 51/374 (13%) ref NP_047363.1 integrase pil S33667 probable integrase - Pseudomonas aeruginosa phage CTX dbj BAA02675.1 (D13409) integrase [Pseudomonas aeruginosa phage phi CTX] emb CAA74224.1 (Y13918) integrase [Pseudomonas aeruginosa phage phi CTX] dbj BAA36272.1 (AB008650) Integrase [Pseudomonas aeruginosa phage phi CTX] gb AAD14164.1 S75107_1 (S75107) pore-forming cytotoxin integrase [bacteriophage phi CTX] gb AAF06112.1 AF140576_1 (AF140576) integrase [Integration vector mini-CTX1] gb AAF06114.1 AF140577_1 (AF140577) integrase [Integration vector mini-CTX2] gb AAF08118.1 AF140578_2 (AF140578) integrase [Integration vector mini-CTX-GFP] gb AAF06121.1 AF140579_2 (AF140579) integrase [Integration vector mini-CTX-lacZ] gb AAG09888.1 AF251497_6 (AF251497) integrase [cloning vector HKBS1] Length = 389
SEQ ID n°1286	Prot n°PL-2136.1	Contig40	224892	226391	61%	Identities = 198/502 (39%), Positives = 306/502 (60%), Gaps = 20/502 (3%) ref NP_043506.1 orf35 sp P51739 YO35_BPHP1 HYPOTHETICAL 58.7 KD PROTEIN IN LYS 3'REGION (ORF35) pil S69543 hypothetical protein 35 - phage HP1 gb AAB09222.1 (U24159) orf35 [Bacteriophage HP1] Length = 533
SEQ ID n°1287	Prot n°PL-2137.1	Contig40	223644	224384	42%	Identities = 63/244 (25%), Positives = 104/244 (41%), Gaps = 13/244 (5%) ref NP_043504.1 orf33 sp P51737 YO33_BPHP1 HYPOTHETICAL 28.3 KD PROTEIN IN LYS 3'REGION (ORF33) pil S69541 hypothetical protein 33 - phage HP1 gb AAB09220.1 (U24159) orf33 [Bacteriophage HP1] Length = 258
SEQ ID n°1288	Prot n°PL-2138.1	Contig40	222989	223813	36%	Identities = 73/187 (39%), Positives = 101/187 (53%), Gaps = 6/187 (3%) ref NP_037719.1 Gp29 gb AAF31112.1 (AF089529) Gp29 [Bacteriophage HK97] Length = 202
SEQ ID n°1289	Prot n°PL-2139.1	Contig40	221238	223037	43%	Identities = 172/564 (30%), Positives = 261/564 (46%), Gaps = 88/564 (15%) ref NP_043502.1 orf31 sp P51735 VPH_BPHP1 PROBABLE TAIL FIBER PROTEIN (ORF31) pil S69539 hypothetical protein 31 - phage HP1 gb AAB09218.1 (U24159) orf31 [Bacteriophage HP1] Length = 925
SEQ ID n°1290	Prot n°PL-214.1	Contig41	358244	359218	62%	Identities = 171/317 (53%), Positives = 228/317 (70%) sp P45394 YRBG_ECOLI HYPOTHETICAL 34.7 KD PROTEIN IN MURA-RPON INTERGENIC REGION (O325) pil F65110 hypothetical 34.7 kD protein in murZ-rpoN intergenic region - Escherichia coli (strain K-12) gb AAA57997.1 (U18997) ORF_0325 [Escherichia coli] gb AAC76228.1 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 325

TABLEAU I

SEQ ID n°1291	Prot n°PL-2140.1	Contig40	217620	218204	58%	Identities = 88/195 (45%), Positives = 120/195 (61%) CELL FILAMENTATION PROTEIN FIC fic - Escherichia coli gb AA58158.1 (U18997) CG Site No. 18361; filamentation in presence of cyclic AMP in mutant [Escherichia coli] gb AAC76386.1 (AE000412) induced in stationary phase, recognized by rpoS, affects cell division [Escherichia coli] Length = 200 "
SEQ ID n°1292	Prot n°PL-2141.1	Contig40	218651	216310	65%	Identities = 107/221 (48%), Positives = 146/221 (65%), Gaps = 4/221 (1%) emb CAA03911.1 (AJ000084) Ccm1 protein [Proteus mirabilis] Length = 228
SEQ ID n°1293	Prot n°PL-2142.1	Contig40	210826	212775	82%	Identities = 487/655 (74%), Positives = 546/655 (83%), Gaps = 16/655 (2%) sp P40601 LIP1_PHOLU_LIPASE 1 PRECURSOR (TRIACYLGLYCEROL LIPASE) pir A47081 triacylglycerol lipase (EC 3.1.1.3) - Xenorhabdus luminescens emb CAA47020.1 (X66379) triacylglycerol lipase [Xenorhabdus luminescens] Length = 845
SEQ ID n°1294	Prot n°PL-2143.1	Contig40	209097	209864	57%	Identities = 95/257 (36%), Positives = 151/257 (57%), Gaps = 11/257 (4%) gb AAC83227.1 (AF070473) TonB [Pasteurella multocida] Length = 256
SEQ ID n°1295	Prot n°PL-2144.1	Contig40	205967	209014	25%	Identities = 173/533 (32%), Positives = 258/533 (47%), Gaps = 62/533 (11%) gb AAG08282.1 AE004902_10 (AE004902) hypothetical protein [Pseudomonas aeruginosa] Length = 989
SEQ ID n°1296	Prot n°PL-2145.1	Contig40	204211	205713	36%	Identities = 103/443 (23%), Positives = 183/443 (41%), Gaps = 49/443 (11%) gb AAF42300.1 (AE002545) conserved hypothetical protein [Neisseria meningitidis MC58] Length = 505
SEQ ID n°1297	Prot n°PL-2146.1	Contig40	203370	204131	20%	Identities = 37/108 (34%), Positives = 51/108 (46%), Gaps = 12/108 (11%) gb AAC44892.1 (U73112) hemoglobin-haptoglobin utilization protein A [Neisseria meningitidis] Length = 341
SEQ ID n°1298	Prot n°PL-2147.1	Contig40	201135	202496	54%	Identities = 147/431 (34%), Positives = 248/431 (57%), Gaps = 3/431 (0%) gb AAF94694.1 (AE004232) multidrug resistance protein NorM, putative [Vibrio cholerae] Length = 461
SEQ ID n°1299	Prot n°PL-2148.1	Contig40	199179	200453	88%	Identities = 341/423 (80%), Positives = 381/423 (89%) gb AAG08410.1 AE004915_5 (AE004915) homocysteine synthase [Pseudomonas aeruginosa] Length = 425
SEQ ID n°1300	Prot n°PL-2149.1	Contig40	197772	198566	37%	Identities = 59/269 (21%), Positives = 99/269 (35%), Gaps = 58/269 (21%) sp P23903 E138_BACCI GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE A1) pir JQ0420 beta-1,3-glucanase A1 precursor - Bacillus circulans gb AA22474.1 (M34503) beta-1,3-glucanase A1 (gicA) [Bacillus circulans] Length = 682

TABLEAU I

SEQ ID n°1301	Prot n°PL-215.1	Contig41	359243	360211	86%	<p>Identities = 238/321 (74%), Positives = 281/321 (87%)</p> <p>sp P45395 YRBH_ECOLI_HYPOTHETICAL_35.2_KDA_PROTEIN_IN_MJRA-RPON INTERGENIC REGION (Q328) pir G65110 hypothetical 35.2 kD protein in murZ-rpoN intergenic region - Escherichia coli (strain K-12) gb AA57898.1 (U18997) ORF_0328 [Escherichia coli] gb AAC76229.1 (AE000399) putative isomerase [Escherichia coli] Length = 328</p> <p>Identities = 407/663 (60%), Positives = 476/663 (71%), Gaps = 46/663 (6%)</p> <p>dbj BAA05664.1 (D28119) outer membrane protein C [Pseudomonas aeruginosa] gb AAG07177.1 (AE004797_12 (AE004797) outer membrane protein OprC [Pseudomonas aeruginosa] Length = 723</p>
SEQ ID n°1302	Prot n°PL-2150.1	Contig40	195622	197724	67%	<p>Identities = 56/213 (26%), Positives = 97/213 (45%), Gaps = 16/213 (7%)</p> <p>gb AAG04736.1 (AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230</p> <p>Identities = 45/205 (21%), Positives = 102/205 (48%), Gaps = 13/205 (6%)</p> <p>gb AAG04736.1 (AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230</p> <p>Identities = 237/359 (66%), Positives = 283/359 (78%)</p> <p>sp P45545 YHFS_ECOLI_HYPOTHETICAL_38.6_KD_PROTEIN_IN_CYSG-TRPS INTERGENIC REGION (F361) pir C65132 hypothetical 38.6 kD protein in cysG-trpS intergenic region - Escherichia coli (strain K-12) gb AAA58173.1 (U18997) ORF_1361 [Escherichia coli] gb AAC76401.1 (AE000413) orf. hypothetical protein [Escherichia coli] Length = 361</p> <p>Identities = 212/433 (48%), Positives = 301/433 (68%), Gaps = 19/433 (4%)</p> <p>dbj BAB04308.1 (AP001509) unknown conserved protein in others [Bacillus halodurans] Length = 429</p> <p>Identities = 207/288 (71%), Positives = 243/288 (83%) pdj 1BF6 B Chain B, Phosphotriesterase Homology Protein From Escherichia Coli pdj 1BF6 A Chain A, Phosphotriesterase Homology Protein From Escherichia Coli Length = 291</p> <p>Identities = 234/385 (60%), Positives = 294/385 (75%), Gaps = 1/385 (0%)</p> <p>sp P45550 YHFX_ECOLI_HYPOTHETICAL_44.3_KD_PROTEIN_IN_CYSG-TRPS INTERGENIC REGION (F387) pir H65132 hypothetical 44.3 kD protein in cysG-trpS intergenic region - Escherichia coli (strain K-12) gb AAA58178.1 (U18997) ORF_1387 [Escherichia coli] gb AAC76406.1 (AE000413) orf. hypothetical protein [Escherichia coli] Length = 387</p> <p>Identities = 184/273 (67%), Positives = 222/273 (80%)</p> <p>sp P45552 YHFX_ECOLI_HYPOTHETICAL_30.3_KD_PROTEIN_IN_CYSG-TRPS INTERGENIC REGION Length = 273</p>
SEQ ID n°1303	Prot n°PL-2151.2	Contig40	192900	194483		
SEQ ID n°1304	Prot n°PL-2152.1	Contig31	181	867	42%	
SEQ ID n°1305	Prot n°PL-2153.1	Contig31	1005	1710	43%	
SEQ ID n°1306	Prot n°PL-2154.1	Contig31	1997	3133	73%	
SEQ ID n°1307	Prot n°PL-2155.1	Contig31	3181	4515	64%	
SEQ ID n°1308	Prot n°PL-2156.1	Contig31	4924	5949	71%	
SEQ ID n°1309	Prot n°PL-2157.1	Contig31	5858	7036	73%	
SEQ ID n°1310	Prot n°PL-2158.1	Contig31	7533	8438	72%	

TABLEAU I

SEQ ID n°1311	Prot n°PL-2159.1	Contig31	8591	10261	81%	<p>Identities = 417/555 (75%), Positives = 474/555 (85%), Gaps = 6/555 (1%) sp P20966 PTFB_ECOLI PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EIIF-FRU) pir J34962 phosphotransferase system enzyme II (EC 2.7.1.69), fructose-specific - Escherichia coli gb AAA60524.1 (U00007) fructose-specific IIBC component [Escherichia coli] gb AAA62624.1 (M23196) enzyme II-fru [Escherichia coli] gb AAC75228.1 (AE000306) PTS system, fructose-specific transport protein [Escherichia coli] prf J2014253BN fruA gene [Escherichia coli] Length = 563 Identities = 39/134 (29%), Positives = 63/134 (46%), Gaps = 10/134 (7%) gil 6320628 Type 1 membrane protein with EF hand motif, Hkr1p pir J569703 HKR1 protein precursor - yeast (Saccharomyces cerevisiae) gb AAB64857.1 (U33007) Hkr1p; YDR420W; CAI: 0.10 [Saccharomyces cerevisiae] Length = 1802 "</p>
SEQ ID n°1312	Prot n°PL-216.1	Contig41	359467	360225	24%	<p>Identities = 235/375 (62%), Positives = 287/375 (75%), Gaps = 3/375 (0%) sp P24217 PTFA_ECOLI PTS SYSTEM, FRUCTOSE-SPECIFIC IIA/FPR COMPONENT (EIIA-FRU) (FRUCTOSE-PERMEASE IIA/FPR COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A/FPR COMPONENT) (PHOSPHOTRANSFERASE FPR PROTEIN) (PSEUDO-HPR) (EIIIF-FRU) (FRUCTOSE PTS DIPHOSPHORYL TRANSFER PROTEIN) pir J53564 phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli gb AAA60534.1 (U00007) fructose-specific IIA/FPR component [Escherichia coli] gb AAB31084.1 (S72443) DTP, FruB=phosphoenolpyruvate: sugar phosphotransferase system diphosphoryl transfer protein [Escherichia coli, Peptide, 376 aa] gb AAC75230.1 (AE000306) PTS system, fructose-specific IIA/fpr component [Escherichia coli] prf J2014253BV phosphotransferase FPr protein [Escherichia coli] Length = 376 Identities = 111/188 (59%), Positives = 135/188 (73%) pir J53063 FimB protein - Escherichia coli emb CAA85725.1 (Z37500) FimB protein [Escherichia coli] Length = 200</p>
SEQ ID n°1313	Prot n°PL-2160.1	Contig31	10331	11458	74%	<p>Identities = 190/513 (37%), Positives = 295/513 (57%), Gaps = 15/513 (2%) pir J070180 phosphotransferase system enzyme II (EC 2.7.1.69), glucose-specific, factor II - Lyme disease spirochete gb AAC66988.1 (AE001166) PTS system, glucose-specific IIBC component (ptsG) [Borrelia burgdorferi] Length = 514</p>
SEQ ID n°1314	Prot n°PL-2161.1	Contig31	12033	12853	66%	<p>Identities = 210/440 (47%), Positives = 301/440 (67%), Gaps = 6/440 (1%) sp O06901 MALH_FUSMR MALTOL-6-PHOSPHATE GLUCOSIDASE (6-PHOSPHO-ALPHA-D-GLUCOSIDASE) gb AAB63015.1 (U81185) MalH [Fusobacterium mortiferum] Length = 441</p>

TABLEAU I

SEQ ID n°1317	Prot n°PL-2164.1	Contig31	16797	17579	42%	Identities = 58/244 (23%), Positives = 110/244 (44%), Gaps = 20/244 (8%) gb AAD11507.1 (U60828) unknown [Lactococcus lactis] Length = 244
SEQ ID n°1318	Prot n°PL-2165.1	Contig31	19296	20000	43%	Identities = 54/208 (25%), Positives = 102/208 (48%), Gaps = 9/208 (4%) gb AAG04736.1 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°1319	Prot n°PL-2166.1	Contig31	20320	21576	68%	Identities = 211/439 (48%), Positives = 293/439 (66%), Gaps = 26/439 (5%) pir T37066 probable integral membrane protein - Streptomyces coelicolor emb CAB52363.1 (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)] Length = 516
SEQ ID n°1320	Prot n°PL-2167.1	Contig31	22580	23632	43%	Identities = 101/288 (35%), Positives = 154/288 (53%), Gaps = 2/288 (0%) sp P46860 GNTR_ECOLI GLUCONATE UTILIZATION SYSTEM GNT-1 TRANSCRIPTIONAL REPRESSOR dbj BAA12324.1 (D84362) repressor [Escherichia coli] Length = 331
SEQ ID n°1321	Prot n°PL-2168.1	Contig31	24945	26000	76%	Identities = 249/350 (71%), Positives = 286/350 (81%), Gaps = 1/350 (0%) gb AAG07744.1 (AE004851) xenobiotic reductase [Pseudomonas aeruginosa] Length = 350
SEQ ID n°1322	Prot n°PL-2169.1	Contig31	27434	29155	72%	Identities = 335/579 (57%), Positives = 426/579 (72%), Gaps = 15/579 (2%) pir T14986 toxin protein - Yersinia pestis plasmid pMT1 gb AAC82729.1 (AF074611) murine toxin [Yersinia pestis] Length = 587
SEQ ID n°1323	Prot n°PL-217.1	Contig41	361912	362637	91%	Identities = 207/241 (85%), Positives = 223/241 (91%) ABC transporter (ntrA/roN 5'region) - Escherichia coli (strain K-12) gb AAA56003.1 (U18997) ORF_0241 [Escherichia coli] gb AAC76233.1 (AE000399) putative ATP-binding component of a transport system [Escherichia coli] Length = 241
SEQ ID n°1324	Prot n°PL-2170.1	Contig31	29373	30704	76%	Identities = 324/442 (73%), Positives = 370/442 (83%) sp P00926 SDHD_ECOLI D-SERINE DEHYDRATASE (D-SERINE DEAMINASE) pir JDWEC5 D-serine dehydratase (EC 4.2.1.14) - Escherichia coli gb AAC75425.1 (AE000324) D-serine dehydratase (deaminase) [Escherichia coli] dbj BAA16229.1 (D90866) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] dbj BAA16237.1 (D90867) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] Length = 442
SEQ ID n°1325	Prot n°PL-2171.1	Contig31	31389	32726	89%	Identities = 358/443 (80%), Positives = 399/443 (89%) sp P08555 DSDX_ECOLI DSDX PERMEASE pir S64140 D-serine permease - Escherichia coli emb CAA60138.1 (X86379) D-serine permease [Escherichia coli] emb CAA62932.1 (X91821) dsdX [Escherichia coli] gb AAC75424.1 (AE000324) transport system permease (serine?) [Escherichia coli] dbj BAA16225.1 (D90866) DSDX PERMEASE [Escherichia coli] dbj BAA16233.1 (D90867) DSDX PERMEASE [Escherichia coli] Length = 445

TABLEAU I

SEQ ID n°1326	Prot n°PL-2172.1	Contig31	32968	33906	73%	<p>Identities = 180/300 (60%), Positives = 234/300 (78%), Gaps = 1/300 (0%) sp P48068 DSDC_ECOLI D-SERINE DEAMINASE ACTIVATOR pir A65010 D-serine deaminase activator - Escherichia coli (strain K-12) gb AAC75423.1 (AE000324) D-serine dehydratase (deaminase) transcriptional activator [Escherichia coli] dbj BAA16224.1 (D90866) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] dbj BAA16232.1 (D90867) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] Length = 311</p>
SEQ ID n°1327	Prot n°PL-2173.1	Contig31	35380	36234	13%	<p>Identities = 28/55 (50%), Positives = 39/55 (70%), Gaps = 1/55 (1%) dbj BAA96865.1 (AB045036) tail fiber [Pectobacterium carotovorum subsp. carotovorum] Length = 832</p>
SEQ ID n°1328	Prot n°PL-2174.1	Contig31	35947	38353	81%	<p>Identities = 338/449 (75%), Positives = 398/449 (88%) sp P39312 CYCA_ECOLI D-SERINE/D-ALANINE/GLYCINE TRANSPORTER pir S58433 D-serine/D-alanine/glycine transporter - Escherichia coli gb AAA97104.1 (U14003) ORF_o470 [Escherichia coli] gb AAC77165.1 (AE000492) transport of D-alanine, D-serine, and glycine [Escherichia coli] Length = 146/197 (74%), Positives = 168/197 (84%), Gaps = 1/197 (0%) sp P30849 WRBA_ECOLI TRP REPRESSOR BINDING PROTEIN pir B64842 trp repressor-binding protein - Escherichia coli gb AAC74089.1 (AE000202) trp repressor binding protein; affects association of trp repressor and operator [Escherichia coli] dbj BAA35771.1 (D90737) Trp repressor binding protein [Escherichia coli] dbj BAA35781.1 (D90738) Trp repressor binding protein [Escherichia coli] Length = 198</p>
SEQ ID n°1330	Prot n°PL-2176.2	Contig31	39962	41200		<p>Identities = 44/201 (21%), Positives = 97/201 (47%), Gaps = 18/201 (8%) pir B75150 chromosome segregation protein (smc1) PAB2109 - Pyrococcus abyssi (strain Orsay) emb CAB49281.1 (AJ248284) chromosome segregation protein (smc1) [Pyrococcus abyssi] Length = 1177 Identities = 277/333 (83%), Positives = 308/333 (92%), Gaps = 4/333 (1%) gb AAA25324.1 (L34345) xyitol dehydrogenase [Morganella morganii] Length = 338</p>
SEQ ID n°1331	Prot n°PL-2177.1	Contig31	41240	41878	45%	<p>Identities = 255/494 (51%), Positives = 335/494 (67%), Gaps = 7/494 (1%) gb AAC04473.1 (AF007800) xyloase kinase [Pseudomonas fluorescens] Length = 493</p>
SEQ ID n°1332	Prot n°PL-2178.1	Contig31	42911	43939	82%	<p>Identities = 368/480 (76%), Positives = 423/480 (87%), Gaps = 3/480 (0%) sp P24255 RP54_ECOLI RNA POLYMERASE SIGMA-54 FACTOR. pir I57054 sigma factor - Escherichia coli pir A35695 transcription initiation factor sigma-54 - Escherichia coli emb CAA81617.1 (Z27094) sigma factor [Escherichia coli] gb AAB80163.1 (U12684) sigma-N (sigma-54) [Escherichia coli] gb AAA58004.1 (U18997) sigma-N (sigma-54) [Escherichia coli] gb AAC76234.1 (AE000399) RNA polymerase, sigma(54 or 60) factor; nitrogen and fermentation regulation [Escherichia coli] Length =</p>
SEQ ID n°1334	Prot n°PL-218.1	Contig41	362665	364107	87%	

TABLEAU I

SEQ ID n°1337	Prot n°PL-2180.1	Contig31	45533	47017	80%	<p>Identities = 377/491 (76%), Positives = 429/491 (86%)</p> <p>sp P07117 PUTP_ECOLI_SODIUM/PROLINE SYMPORTER (PROLINE PERMEASE) pir JGECPP sodium/proline symporter - Escherichia coli emb CAA29143.1 (X05653) putP proline carrier (AA 1-502) [Escherichia coli] dbj BAA35793.1 (D90738) Proline carrier protein [Escherichia coli] gb AAC74100.1 (AE000203) major sodium/proline symporter [Escherichia coli] pf 1404369A Pro carrier protein [Escherichia coli] Length = 502</p> <p>Identities = 1029/1330 (77%), Positives = 1158/1330 (86%), Gaps = 14/1330</p> <p>(1%) sp P09546 PUTA_ECOLI_BIFUNCTIONAL PUTA PROTEIN [INCLUDES: PROLINE DEHYDROGENASE (PROLINE OXIDASE); DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (P5C DEHYDROGENASE)] pir D64843 proline dehydrogenase (EC 1.5.99.8) / 1-proline-5-carboxylate dehydrogenase (EC 1.5.1.12) - Escherichia coli dbj BAA35791.1 (D90738) Proline dehydrogenase (EC 1.5.99.8) (proline oxidase) / delta-1- pyroline-5-carboxylate dehydrogenase (EC 1.5.1.12) (p5c dehydrogenase), [Escherichia coli] gb AAC74099.1 (AE000203) proline dehydrogenase, P5C dehydrogenase [Escherichia coli] Length = 1320 "</p>
SEQ ID n°1338	Prot n°PL-2181.1	Contig31	47504	51484	87%	<p>Identities = 214/230 (93%), Positives = 222/230 (96%) emb CAB46360.1 (AJ131736) FliA, sigma 28 [Xenorhabdus nematophilus] Length = 230</p> <p>Identities = 228/360 (63%), Positives = 288/360 (74%), Gaps = 14/360 (3%)</p> <p>sp P13713 FLIC_SERMA_FLAGELLIN pir JU0056 flagellin - Serratia marcescens gb AAA26556.1 (M27219) flagellin [Serratia marcescens] Length = 351</p>
SEQ ID n°1339	Prot n°PL-2184.1	Contig31	54437	55858	83%	<p>Identities = 337/490 (68%), Positives = 398/490 (80%), Gaps = 24/490 (4%)</p> <p>pir JC5755 hook-associated protein 2 - Xenorhabdus nematophilus emb CAA62510.1 (X91047) hook-associated protein 2 [Xenorhabdus nematophilus] Length = 489</p>
SEQ ID n°1340	Prot n°PL-2185.1	Contig31	57060	57881	No Hits found	
SEQ ID n°1341	Prot n°PL-2186.1	Contig31	59067	60770	76%	<p>Identities = 342/555 (61%), Positives = 437/555 (78%), Gaps = 21/555 (3%)</p> <p>sp P25798 FLIF_ECOLI_FLAGELLAR M-RING PROTEIN pir G64957 flagellar basal-body M-ring protein - Escherichia coli dbj BAA15763.1 (D80834) Flagellar M-ring protein (fragments), [Escherichia coli] gb AAC75005.1 (AE000286) flagellar biosynthesis; basal-body MS(membrane and supramembrane)-ring and collar protein [Escherichia coli] Length = 552 "</p>
SEQ ID n°1342	Prot n°PL-2187.1	Contig31	60767	61759	91%	<p>Identities = 260/329 (79%), Positives = 305/329 (92%)</p> <p>sp P15933 FLIG_SALTY_FLAGELLAR MOTOR SWITCH PROTEIN FLIG pir A30929 flagellar motor switch protein flig - Salmonella typhimurium gb AAA27097.1 (M24462) flig flagellar switch protein [Salmonella</p>

TABLEAU I

SEQ ID n°1343	Prot n°PL-2188.1	Contig31	61734	62456	68%	<p>Identities = 128/237 (54%), Positives = 166/237 (70%), Gaps = 8/237 (3%) pir A04958 flagellar assembly protein flh - Escherichia coli gb AAC75007.1 (AE000286) flagellar biosynthesis; export of flagellar proteins? [Escherichia coli] Length = 235 "</p>	
SEQ ID n°1344	Prot n°PL-2189.1	Contig31	62456	63820	86%	<p>Identities = 362/455 (79%), Positives = 405/455 (88%), Gaps = 1/455 (0%) sp P52612 FLII_ECOLI FLAGELLUM-SPECIFIC ATP SYNTHASE pir B04958 H⁺-transporting ATP synthase (EC 3.6.1.34), flagellum-specific - Escherichia coli dbj BAA15766.1 (D90834) Flagellum-specific ATP synthase (EC 3.6.1.34). [Escherichia coli] gb AAC75008.1 (AE000286) flagellum- specific ATP synthase [Escherichia coli] Length = 457</p>	
SEQ ID n°1345	Prot n°PL-219.1	Contig41	385093	385944	95%	<p>Identities = 269/283 (95%), Positives = 279/283 (98%) sp P17183 YHBJ_KLEPN HYPOTHETICAL 32.5 KD PROTEIN IN PTSN- PTSO INTERGENIC REGION (ORF4) pir S60666 probable ATP-binding protein - Klebsiella pneumoniae emb CAA90684.1 (Z50803) orfIV [Klebsiella pneumoniae]</p>	
SEQ ID n°1346	Prot n°PL-2190.1	Contig31	64303	65634	40%	<p>Identities = 118/388 (30%), Positives = 179/388 (45%), Gaps = 44/388 (11%) sp P52614 FLIK_ECOLI FLAGELLAR HOOK-LENGTH CONTROL PROTEIN pir D64988 flagellar hook-length control protein flhK - Escherichia coli gb AAB06632.1 (L43491) flhK gene product [Escherichia coli] dbj BAA15768.1 (D90834) Flagellar hook-length control protein. [Escherichia coli] gb AAC75010.1 (AE000286) flagellar hook-length control protein [Escherichia coli] Length = 375</p>	
SEQ ID n°1347	Prot n°PL-2191.1	Contig31	66290	67294	85%	<p>Identities = 272/333 (81%), Positives = 304/333 (90%), Gaps = 1/333 (0%) sp P06974 FLIM_ECOLI FLAGELLAR MOTOR SWITCH PROTEIN FLIM pir XMECF2 flagellar motor switch protein flm - Escherichia coli gb AAA23786.1 (M12784) FlhA protein [Escherichia coli] dbj BAA15770.1 (D90834) Flagellar motor switch protein FLIM. [Escherichia coli] gb AAC75012.1 (AE000286) flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction [Escherichia coli] Length = 334</p>	
SEQ ID n°1348	Prot n°PL-2192.1	Contig31	68171	68926	80%	<p>Identities = 192/236 (81%), Positives = 214/236 (90%), Gaps = 1/236 (0%) sp P33133 FLIP_ECOLI FLAGELLAR BIOSYNTHETIC PROTEIN FLIP pir B36869 probable export protein flp precursor - Escherichia coli gb AAC36859.1 (L22182) flagellar protein [Escherichia coli] dbj BAA15773.1 (D90834) Flagellar biosynthetic protein Flp. [Escherichia coli] dbj BAA15779.1 (D90835) Flagellar biosynthetic protein Flp. [Escherichia coli] gb AAC75015.1 (AE000287) flagellar biosynthesis [Escherichia coli] Identities = 155/256 (60%), Positives = 208/256 (81%)</p>	
SEQ ID n°1349	Prot n°PL-2193.1	Contig31	69219	70001	76%	<p>sp P34202 FLIR_ERWCA FLAGELLAR BIOSYNTHETIC PROTEIN FLIR (FLAGELLAR BIOSYNTHETIC PROTEIN MOPE) pir S42698 probable export protein mopE - Erwinia carotovora subsp. atroseptica emb CAA51478.1 (X72969) mopE [Erwinia carotovora] Length = 261</p>	

TABLEAU I

SEQ ID n°1350	Prot n°PL-2194.1	Contig31	70425	72521	15%	Identities = 58/223 (26%), Positives = 106/223 (47%), Gaps = 28/223 (11%) pir C09543 hypothetical protein AF2347 - Archaeoglobus fulgidus gb AAB91316.1 (AE001114) A. fulgidus predicted coding region AF2347 [Archaeoglobus fulgidus] Length = 453
SEQ ID n°1351	Prot n°PL-2195.1	Contig31	72613	73365	No Hits found	
SEQ ID n°1352	Prot n°PL-2196.1	Contig31	75938	77065	No Hits found	
SEQ ID n°1353	Prot n°PL-2197.1	Contig31	76965	78578	No Hits found	
SEQ ID n°1354	Prot n°PL-2198.1	Contig31	78587	79519	No Hits found	
SEQ ID n°1355	Prot n°PL-2199.1	Contig31	79513	81480	50%	Identities = 243/571 (42%), Positives = 340/571 (58%), Gaps = 6/571 (1%) gb AAC62387.1 (AF044506) VgrG protein [Escherichia coli] Length = Identities = 266/354 (75%), Positives = 300/354 (84%) gb AAA85578.1 (U23806) extended ORF of mgtE gene; transcription from this start point is unlikely [Providencia stuartii] Length = 356 "
SEQ ID n°1356	Prot n°PL-22.1	Contig41	37886	38956	77%	Identities = 211/550 (38%), Positives = 330/550 (59%), Gaps = 20/550 (3%) ref NP_043508.1 orf35 sp P51739 YO35_BPHP1 HYPOTHETICAL 58.7 KD PROTEIN IN LYS 3'REGION (ORF35) pir S69543 hypothetical protein 35 - phage HP1 gb AAB09222.1 (U24159) orf35 [Bacteriophage HP1] Length = 533
SEQ ID n°1357	Prot n°PL-220.1	Contig41	368828	370477	59%	
SEQ ID n°1358	Prot n°PL-2200.1	Contig31	82093	83058	72%	Identities = 171/321 (53%), Positives = 239/321 (74%), Gaps = 4/321 (1%) sp P16326 FLGL_SALTY FLAGELLAR HOOK-ASSOCIATED PROTEIN 3 (HAP3) (HOOK-FILAMENT JUNCTION PROTEIN) pir S10362 hook- associated protein 3 - Salmonella typhimurium emb CAA36028.1 (X51739) HAP3 [Salmonella typhimurium] Length = 317
SEQ ID n°1359	Prot n°PL-2201.1	Contig31	83133	84785	63%	Identities = 263/548 (47%), Positives = 353/548 (63%), Gaps = 4/548 (0%) sp P33235 FLGK_ECOLI FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1) pir G84851 flagellar hook-associated protein 1 - Escherichia coli dbj BAA35891.1 (D90744) Flagellar hook-associated protein 1 (hap1) . [Escherichia coli] gb AAC74166.1 (AE000209) flagellar biosynthesis, hook-filament junction protein 1 [Escherichia coli] Length = 547
SEQ ID n°1360	Prot n°PL-2202.1	Contig31	84909	85853	69%	Identities = 178/316 (56%), Positives = 235/316 (74%), Gaps = 2/316 (0%) sp P15931 FLGJ_SALTY FLAGELLAR PROTEIN FLGJ pir C30930 flagellar protein flgJ - Salmonella typhimurium gb AAA27070.1 (M24466) flgJ flagellar protein [Salmonella typhimurium] Length = 316
SEQ ID n°1361	Prot n°PL-2203.1	Contig31	85850	86965	83%	Identities = 276/361 (76%), Positives = 314/361 (86%) sp P75941 FLGI_ECOLI FLAGELLAR P-RING PROTEIN PRECURSOR pir E84851 flagellar basal body P-ring protein precursor - Escherichia coli gb AAC74164.1 (AE000208) homolog of Salmonella P-ring of flagella basal body [Escherichia coli] dbj BAA35889.1 (D90744) Flagellar basal body P-ring protein precursor [Escherichia coli] Length = 365

TABLEAU I

SEQ ID n°1362	Prot n°PL-2204.1	Contig31	86972	87783	70%	Identities = 167/232 (71%), Positives = 192/232 (81%), Gaps = 1/232 (0%) dbj BAA36888.1 (D90744) Flagellar basal body L-ring protein precursor [Escherichia coli] Length = 235
SEQ ID n°1363	Prot n°PL-2205.1	Contig31	87799	88581	86%	sp P16439 FLGG_SALTY FLAGELLAR BASAL-BODY ROD PROTEIN FLGG (DISTAL ROD PROTEIN) pir XMEBFG flagellar basal body rod protein figG - Salmonella typhimurium emb CAA36314.1 (X52094) figG protein product (AA 1-260) [Salmonella typhimurium] Length = 260
SEQ ID n°1364	Prot n°PL-2206.1	Contig31	88605	89360	76%	sp P16323 FLGF_SALTY FLAGELLAR BASAL-BODY ROD PROTEIN FLGF (PUTATIVE PROXIMAL ROD PROTEIN) pir XMEBFF flagellar basal body rod protein figF - Salmonella typhimurium emb CAA36313.1 (X52094) figF protein product (AA 1-251) [Salmonella typhimurium] Length = 251
SEQ ID n°1365	Prot n°PL-2208.1	Contig31	89379	90593	72%	sp P16322 FLGE_SALTY FLAGELLAR HOOK PROTEIN FLGE pir S10365 flagellar hook protein figE - Salmonella typhimurium emb CAA36022.1 (X51737) figE protein (AA 1-403) [Salmonella typhimurium] Length = 403
SEQ ID n°1366	Prot n°PL-2209.1	Contig31	90621	91316	74%	Identities = 133/234 (56%), Positives = 173/234 (73%), Gaps = 5/234 (2%) sp P16321 FLGD_SALTY BASAL-BODY ROD MODIFICATION PROTEIN FLGD pir S47641 flagellar hook formation protein figD - Salmonella typhimurium dbj BAA04982.1 (D25293) flagella [Salmonella typhimurium]
SEQ ID n°1367	Prot n°PL-221.1	Contig41	370985	371725	42%	Identities = 62/244 (25%), Positives = 105/244 (42%), Gaps = 13/244 (5%) ref NP_043504.1 orf33 sp P51737 YO33_BPHP1 HYPOTHETICAL 28.3 KD PROTEIN IN LYS 3 REGION (ORF33) pir S69541 hypothetical protein 33 - phage HP1 gb AA809220.1 (U24159) orf33 [Bacteriophage HP1] Length = 258
SEQ ID n°1368	Prot n°PL-2210.1	Contig31	92400	93059	62%	Identities = 99/219 (45%), Positives = 149/219 (67%), Gaps = 1/219 (0%) gb AAC45658.1 (U82214) FlpA [Proteus mirabilis] Length = 218
SEQ ID n°1369	Prot n°PL-2211.1	Contig31	94221	95414	28%	Identities = 56/272 (20%), Positives = 114/272 (41%), Gaps = 32/272 (11%) pir A45592 liver stage antigen LSA-1 - Plasmodium falciparum emb CAA39863.1 (X56203) liver stage antigen [Plasmodium falciparum] Length = 1909
SEQ ID n°1370	Prot n°PL-2212.1	Contig31	95551	97032	No Hits found	
SEQ ID n°1371	Prot n°PL-2213.1	Contig31	98106	99584	No Hits found	
SEQ ID n°1372	Prot n°PL-2214.1	Contig31	99637	101127	No Hits found	
SEQ ID n°1373	Prot n°PL-2215.2	Contig32	179040	180542		
SEQ ID n°1374	Prot n°PL-2216.2	Contig32	180591	182054		
SEQ ID n°1375	Prot n°PL-2217.2	Contig31	101149	102192		
SEQ ID n°1376	Prot n°PL-2218.2	Contig40	95501	98287		

TABLEAU I

SEQ ID n°1377	Prot n°PL-2219.1	Contig40	98789	99473	28%	Identities = 53/95 (55%), Positives = 67/95 (69%), Gaps = 2/95 (2%) gb AAFF82314.1 (AE002420) MatB-related protein [Neisseria meningitidis MC58] Length = 422
SEQ ID n°1378	Prot n°PL-222.1	Contig41	372329	374146	28%	Identities = 119/277 (42%), Positives = 170/277 (60%), Gaps = 6/277 (2%) ref NP_043502.1 orf31 sp P51735 VPH_BPHP1 PROBABLE TAIL FIBER PROTEIN (ORF31) pir S69539 hypothetical protein 31 - phage HP-1 gb AAB09218.1 (U24159) orf31 [Bacteriophage HP-1] Length = 925
SEQ ID n°1379	Prot n°PL-2220.1	Contig40	99764	101095	21%	Identities = 58/224 (25%), Positives = 94/224 (41%), Gaps = 17/224 (7%) emb CAB72079.1 (AJ391284) hypothetical protein [Neisseria meningitidis] Length = 500
SEQ ID n°1380	Prot n°PL-2221.1	Contig40	103854	105533	60%	Identities = 243/547 (44%), Positives = 342/547 (62%), Gaps = 5/547 (0%) gb AAC31980.1 (L39897) HecB [Pectobacterium chrysanthemi] Length = 558
SEQ ID n°1381	Prot n°PL-2222.1	Contig40	106397	107068	17%	Identities = 39/101 (38%), Positives = 40/101 (38%) emb CAB38044.1 (AL034559) HesB-like domain protein [Plasmodium falciparum] Length = 404
SEQ ID n°1382	Prot n°PL-2223.1	Contig40	107035	108102	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°1383	Prot n°PL-2224.1	Contig40	109927	111360	61%	Identities = 223/474 (47%), Positives = 294/474 (61%), Gaps = 7/474 (1%) pir S30159 N-formimidoyl formicin A synthase - Micromonospora olivasterospora dbj BAA00940.1 (D10050) formimidoyl formicin A synthetase [Micromonospora olivasterospora] Length = 482
SEQ ID n°1384	Prot n°PL-2225.1	Contig40	111348	112208	41%	Identities = 77/207 (37%), Positives = 118/207 (56%), Gaps = 17/207 (8%) emb CAB84532.1 (AL359152) putative methylase [Streptomyces coelicolor A3(2)] Length = 281
SEQ ID n°1385	Prot n°PL-2226.1	Contig40	112230	113507	41%	Identities = 101/374 (27%), Positives = 177/374 (47%), Gaps = 31/374 (8%) pir F75017 5-aminolevulinic acid synthase (8 amino-7-oxononanoate synthase) PAB1244 - Pyrococcus abyssi (strain Orsay) emb CAB50580.1 (AJ248288) 5-AMINOLEVULINIC ACID SYNTHASE (8 AMINO-7-OXONONANOATE SYNTHASE) [Pyrococcus abyssi] Length = 300/698 (42%), Positives = 406/698 (57%), Gaps = 28/698 (4%)
SEQ ID n°1386	Prot n°PL-2227.1	Contig40	113891	115868	58%	gb AAC44868.1 (U60417) PapA [Streptomyces pristinaespiralis] Length = 719
SEQ ID n°1387	Prot n°PL-2228.1	Contig40	115809	116846	40%	Identities = 95/290 (32%), Positives = 139/290 (47%), Gaps = 3/290 (1%) gb AAC44867.1 (U60417) PapC [Streptomyces pristinaespiralis] Length = 296
SEQ ID n°1388	Prot n°PL-2229.1	Contig40	116868	118400	63%	Identities = 228/491 (46%), Positives = 328/491 (66%), Gaps = 5/491 (1%) gb AAC43550.1 (U40487) proton antiporter efflux pump [Mycobacterium smegmatis] pir J2207392A efflux pump [Mycobacterium smegmatis] Length = 504

TABLEAU I

SEQ ID n°1388	Prot n°PL-223.1	Contig41	375876	377216	88%	<p>Identities = 367/446 (82%), Positives = 397/446 (88%)</p> <p>sp P24231 PMBA_ECOLI PMBA PROTEIN (TLDE PROTEIN) pir S13730 pmbA protein - Escherichia coli emb CAA38091.1 (X54152) pmbA is involved in the production of antibiotic MccB17 [Escherichia coli] gb AAA97132.1 (U14003) pmbA gene product [Escherichia coli] dbj BAA07915.1 (D44452) TldE protein [Escherichia coli] gb AAC77192.1 (AE000494) maturation of antibiotic MccB17, see tld genes [Escherichia coli]</p>
SEQ ID n°1390	Prot n°PL-2230.1	Contig40	118966	120291	22%	<p>Identities = 91/222 (40%), Positives = 101/222 (44%), Gaps = 40/222 (18%)</p> <p>pir E70806 hypothetical glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain H37RV) emb CAA17744.1 (AL022022) PE_PGRS [Mycobacterium tuberculosis] Length = 1381</p>
SEQ ID n°1391	Prot n°PL-2231.1	Contig40	120878	122275	24%	<p>Identities = 94/242 (38%), Positives = 115/242 (46%), Gaps = 17/242 (7%)</p> <p>pir H70846 hypothetical glycine-rich protein Rv3345c - Mycobacterium tuberculosis (strain H37RV) emb CAA17117.1 (AL021841) PE_PGRS [Mycobacterium tuberculosis] Length = 1538</p>
SEQ ID n°1392	Prot n°PL-2232.1	Contig40	123207	123878	48%	<p>Identities = 75/196 (38%), Positives = 109/196 (55%), Gaps = 4/196 (2%)</p> <p>pir E75485 hypothetical protein - Deinococcus radiodurans (strain R1) gb AAF10288.1 AE001927_7 (AE001927) hypothetical protein [Deinococcus radiodurans] Length = 198</p>
SEQ ID n°1393	Prot n°PL-2233.1	Contig40	123824	124813	79%	<p>Identities = 219/325 (67%), Positives = 265/325 (81%), Gaps = 4/325 (1%)</p> <p>sp P39179 UP14_ECOLI UNKNOWN PROTEIN FROM 2D-PAGE (SPOT PR51) pir JB65074 hypothetical protein b2898 - Escherichia coli (strain K-12) gb AAA83079.1 (U28375) ORF_0326 [Escherichia coli] gb AAC75936.1 (AE000373) orf, hypothetical protein [Escherichia coli] Length = 328</p>
SEQ ID n°1394	Prot n°PL-2234.1	Contig40	126323	127213	86%	<p>Identities = 228/292 (78%), Positives = 265/292 (90%) gb AAB87499.1 (AF033487) site-specific recombinase [Proteus mirabilis] Length = 313</p>
SEQ ID n°1395	Prot n°PL-2235.1	Contig40	127237	127944	66%	<p>Identities = 139/228 (60%), Positives = 181/228 (78%), Gaps = 1/228 (0%)</p> <p>sp P39691 DSBC_ERWICH THIOI:DISULFIDE INTERCHANGE PROTEIN DSBC PRECURSOR pir S44444 protein disulfide-isomerase (EC 5.3.4.1) dsbC precursor - Erwinia chrysanthemi emb CAA54108.1 (X76687) dsbC [Erwinia chrysanthemi] Length = 238</p>
SEQ ID n°1396	Prot n°PL-2236.1	Contig40	127944	129677	83%	<p>Identities = 399/573 (69%), Positives = 484/573 (83%)</p> <p>sp P21893 RECJ_ECOLI SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ pir JD65073 single-stranded DNA-specific exonuclease (EC 3.1.-.-) - Escherichia coli gb AAA83073.1 (U28375) single-stranded DNA-specific exonuclease [Escherichia coli] gb AAC75930.1 (AE000373) ssDNA exonuclease, 5' -> 3' specific</p>

TABLEAU I

SEQ ID n°1397	Prot n°PL-2237.1	Contig40	129899	130833	94%	Identities = 311/343 (90%), Positives = 327/343 (94%) sp P07012 RF2_ECOLI PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) pir FCECR2 translation releasing factor RF-2 - Escherichia coli (strain K-12) gb AAC75929.1 (AE000372) peptide chain release factor RF-2 [Escherichia coli] prf 1806186A peptide chain-releasing factor:ISOTYPE=2 [Escherichia coli] Length = 505 "
SEQ ID n°1398	Prot n°PL-2238.1	Contig40	130943	132457	88%	Identities = 415/502 (82%), Positives = 452/502 (89%) sp P13030 SYK1_ECOLI LYSYL-TRNA SYNTHETASE (LYSINE-TRNA LIGASE) (LYSRS) pir SYECKT lysine--RNA ligase (EC 6.1.1.6) - Escherichia coli gb AAA23959.1 (J03795) herC protein [Escherichia coli] gb AAA83071.1 (U28375) lysyl tRNA synthetase (LysRS), constitutive [Escherichia coli] gb AAC75928.1 (AE000372) lysine tRNA synthetase, constitutive; suppressor of ColE1 mutation in primer RNA [Escherichia coli] Length = 505 "
SEQ ID n°1399	Prot n°PL-2239.1	Contig40	132933	133556	81%	Identities = 153/210 (72%), Positives = 176/210 (82%) gb AAF96164.1 (AE004365) antibiotic acetyltransferase [Vibrio cholerae] Length = 232 Identities = 131/181 (72%), Positives = 152/181 (83%), Gaps = 3/181 (1%) sp P26850 YJGA_ECOLI HYPOTHETICAL 21.4 KD PROTEIN IN FBP-PMBA INTERGENIC REGION (X96 PROTEIN) (F183) pir S56460
SEQ ID n°1400	Prot n°PL-224.1	Contig41	377418	377957	74%	hypothetical 21.4K protein (fbp-pmba intergenic region) - Escherichia coli gb AAA24760.1 (M95096) X96 [Escherichia coli] gb AAA97131.1 (U14003) alternate gene name yjgA [Escherichia coli] dbj BAA07914.1 (D44452) 21K protein [Escherichia coli] gb AAC77191.1 (AE000494) putative alpha helix protein [Escherichia coli] Length = 183
SEQ ID n°1401	Prot n°PL-2240.1	Contig40	133760	134767	72%	Identities = 184/336 (54%), Positives = 261/336 (73%), Gaps = 24/336 (7%) sp P37415 YTL2_SALTY HYPOTHETICAL 35.3 KD PROTEIN NEAR TLPA OPERON pir S41385 hypothetical yadD homolog - Salmonella typhimurium emb CAA82634.1 (Z29513) 30 kDa protein similar to E. coli yadD and yjgA [Salmonella typhimurium] Length = 313
SEQ ID n°1402	Prot n°PL-2241.1	Contig40	136516	136340	40%	Identities = 74/191 (38%), Positives = 110/191 (56%) pir T35272 hypothetical protein SC5F2A.30 - Streptomyces coelicolor emb CAB40897.1 (AL049587) hypothetical protein [Streptomyces coelicolor A3(2)] Length = 211
SEQ ID n°1403	Prot n°PL-2242.1	Contig40	136591	137562	57%	Identities = 151/322 (46%), Positives = 198/322 (60%), Gaps = 12/322 (3%) gb AAG05239.1 AE004611_4 (AE004611) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 334
SEQ ID n°1404	Prot n°PL-2243.1	Contig40	137576	138243	71%	Identities = 339/547 (61%), Positives = 408/547 (73%), Gaps = 15/547 (2%) sp P74839 PRPR_SALTY PROPIONATE CATABOLISM OPERON REGULATORY PROTEIN gb AAC44813.1 (U51879) PtpR [Salmonella typhimurium] Length = 541

TABLEAU I

SEQ ID n°1406	Prot n°PL-2244.1	Contig40	139576	140466	86%	<p>Identities = 237/295 (80%), Positives = 266/295 (89%) sp Q56062 CPPM_SALTY PUTATIVE CARBOXYVINYL-CARBOXYPHOSPHONATE PHOSPHORYLMUTASE (CARBOXYPHOSPHONOLPYRUVATE PHOSPHONOMUTASE) (CPEP PHOSPHONOMUTASE) gb AAC44814.1 (U51879) PrpB [Salmonella typhimurium] Length = 295</p>	
SEQ ID n°1408	Prot n°PL-2245.1	Contig40	140527	141693	82%	<p>Identities = 308/388 (78%), Positives = 337/388 (85%), Gaps = 1/388 (0%) sp P31680 CISZ_ECOLI METHYL CITRATE SYNTHASE (CITRATE SYNTHASE 2) pir E64760 citrate (sl)-synthase (EC 4.1.3.7) - Escherichia coli gb AAB18057.1 (U73857) similar to E. coli gltA citrate synthase [Escherichia coli] gb AAC73436.1 (AE000140) putative citrate synthase; propionate metabolism? [Escherichia coli] Length = 389 "</p>	
SEQ ID n°1407	Prot n°PL-2246.1	Contig40	141748	143199	88%	<p>Identities = 391/483 (80%), Positives = 432/483 (88%) sp P74840 PRPD_SALTY PRPD PROTEIN gb AAC44816.1 (U51879) PrpD [Salmonella typhimurium] Length = 483</p>	
SEQ ID n°1408	Prot n°PL-2247.1	Contig40	144334	145038	No Hits found		
SEQ ID n°1408	Prot n°PL-2248.1	Contig40	143272	145158	81%	<p>Identities = 452/626 (72%), Positives = 531/626 (84%) gb AAC44817.2 (U51879) PrpE [Salmonella typhimurium] Length = 628</p>	
SEQ ID n°1410	Prot n°PL-2249.1	Contig40	146311	147621	60%	<p>Identities = 208/412 (50%), Positives = 274/412 (66%), Gaps = 3/412 (0%) dbj BAB04638.1 (AP001510) diaminobutyric acid aminotransferase [Bacillus halodurans] Length = 427</p>	
SEQ ID n°1411	Prot n°PL-225.1	Contig41	378770	380215	90%	<p>Identities = 400/481 (83%), Positives = 440/481 (91%) sp P46473 TLDD_ECOLI TLDD PROTEIN pir F65116 tld protein - Escherichia coli (strain K-12) gb AAA58046.1 (U18997) ORF_481 [Escherichia coli] dbj BAA07913.1 (D44451) TldD protein [Escherichia coli] gb AAC76276.1 (AE000403) suppresses inhibitory activity of CsrA</p>	
SEQ ID n°1412	Prot n°PL-2250.1	Contig40	147626	148495	30%	<p>Identities = 53/242 (21%), Positives = 89/242 (35%), Gaps = 54/242 (22%) dbj BAB10550.1 (AB008265) gene_id:MDC12.4-unknown protein [Arabidopsis thaliana] Length = 440</p>	
SEQ ID n°1413	Prot n°PL-2251.1	Contig40	148987	158886	53%	<p>Identities = 1153/3328 (34%), Positives = 1766/3328 (52%), Gaps = 206/3328 (6%) pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] Length = 9376</p>	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°1414	Prot n°PL-2252.1	Contig40	158886	168698	53%	<p>Identities = 1167/3233 (36%), Positives = 1772/3233 (54%), Gaps = 95/3233 (2%) pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] Length = 9376</p>	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°1415	Prot n°PL-2253.1	Contig40	168683	172102	52%	<p>Identities = 392/1139 (34%), Positives = 699/1139 (62%), Gaps = 43/1139 (3%) gb AAF17280.1 (AF204805) NosC [Nostoc sp. GSV224] Length = 3317</p>	Unknown, similar to proteins involved in antibiotic biosynthesis

TABLEAU I

SEQ ID n°1416	Prot n°PL-2254.1	Contig40	172089	181914	52%	Identities = 1118/3375 (33%), Positives = 1724/3375 (50%), Gaps = 189/3375 (5%) gb AAAF17280.1 (AF204805) NosC [Nostoc sp. GSV224] Length = 3317	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°1417	Prot n°PL-2255.1	Contig40	181941	183788	12%	Identities = 451/158 (28%), Positives = 74/158 (46%), Gaps = 19/158 (12%) gb AAA448787.1 (J03860) fatty acid synthase (EC 3.2.1.23) [Gallus gallus] Length = 2447	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°1418	Prot n°PL-2256.1	Contig40	183805	185505	50%	Identities = 165/513 (32%), Positives = 284/513 (55%), Gaps = 8/513 (1%) sp P33941 YOJL_EC01_HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YOJL pir J064991 hypothetical ABC transporter in eco-alkB intergenic region - Escherichia coli (strain K-12) gb AAA16403.1 (U00008) yojl [Escherichia coli] dbj BAA15994.1 (D90850) ATP-binding protein SyoD [Escherichia coli] gb AAC7627.1 (AE000310) putative ATP-binding component of a transport system [Escherichia coli]	
SEQ ID n°1419	Prot n°PL-2257.1	Contig40	185606	186397	34%	Identities = 58/185 (29%), Positives = 91/185 (45%), Gaps = 1/185 (0%) gb AAB50779.1 (S83325) aspartyl(asparaginyl)beta-hydroxylase, HAAH [human, hepatoblastoma cell line HepG2, Peptide, 758 aa] [Homo sapiens] Length = 758	
SEQ ID n°1420	Prot n°PL-2258.1	Contig40	186534	187565	35%	Identities = 79/266 (29%), Positives = 123/266 (45%), Gaps = 9/266 (3%) emb CAB92259.1 (AL356595) putative oxynase [Streptomyces coelicolor A3(2)] Length = 333	
SEQ ID n°1421	Prot n°PL-2259.1	Contig40	187481	189991	44%	Identities = 242/780 (31%), Positives = 373/780 (47%), Gaps = 84/780 (10%) gb AAG05773.1 AE004664_10 (AE004664) probable acylase [Pseudomonas aeruginosa] Length = 762	
SEQ ID n°1422	Prot n°PL-226.1	Contig41	380221	381078	61%	Identities = 127/270 (47%), Positives = 177/270 (65%), Gaps = 5/270 (1%) gb AAF93594.1 (AE004129) conserved hypothetical protein [Vibrio cholerae] Length = 275	
SEQ ID n°1423	Prot n°PL-2260.1	Contig40	190143	191006	37%	Identities = 73/231 (31%), Positives = 108/231 (46%), Gaps = 21/231 (9%) gb AAF71807.1 AC013430_16 (AC013430) F3F9.18 [Arabidopsis thaliana] Length = 919	
SEQ ID n°1424	Prot n°PL-2261.1	Contig40	191580	192548	No Hits found		
SEQ ID n°1425	Prot n°PL-2262.2	Contig41	871505	872278			
SEQ ID n°1426	Prot n°PL-2263.1	Contig41	868132	871068	88%	Identities = 787/951 (82%), Positives = 864/951 (90%) emb CAA29322.1 (X05891) valyl-tRNA synthetase [Escherichia coli] Length = 951	

TABLEAU I

SEQ ID n°1427	Prot n°PL-2264.1	Contig41	866124	867644	92%	<p>Identities = 429/501 (85%), Positives = 473/501 (93%) sp P11648 AMPA_ECOLI_CYTOSOL_AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (AMINOPEPTIDASE A1) pir JAPECA leucyl aminopeptidase (EC 3.4.11.1) A - Escherichia coli emb CAA33225.1 (X15130) aminopeptidase A1 (AA 1 - 503) [Escherichia coli] gb AAA97157.1 (U14003) aminopeptidase A1 [Escherichia coli] emb CAA60184.1 (X86443) aminopeptidase A [Escherichia coli] gb AAC77217.1 (AE000496) aminopeptidase A1 [Escherichia coli]</p> <p>Identities = 246/364 (67%), Positives = 309/364 (84%) sp P39340 YJGP_ECOLI_HYPOTHETICAL_40.4_KD_PROTEIN_IN_PEPAGNTV INTERGENIC REGION (O366) pir S56487 hypothetical 40.4K protein (pepa-gntv intergenic region) - Escherichia coli gb AAA97158.1 (U14003) ORF_o366 [Escherichia coli] gb AAC77218.1 (AE000497) orf, hypothetical protein [Escherichia coli] Length = 388</p>
SEQ ID n°1428	Prot n°PL-2265.1	Contig41	864738	865838	77%	<p>Identities = 254/356 (71%), Positives = 311/356 (87%) sp P39341 YJGQ_ECOLI_HYPOTHETICAL_39.8_KD_PROTEIN_IN_PEPAGNTV INTERGENIC REGION (O361) pir S66488 hypothetical 39.8K protein (pepa-gntv intergenic region) - Escherichia coli gb AAA97159.1 (U14003) ORF_o361 [Escherichia coli] gb AAC77219.1 (AE000497) orf, hypothetical protein [Escherichia coli] Length = 381</p> <p>Identities = 203/350 (58%), Positives = 258/350 (73%), Gaps = 2/350 (0%) pir H84785 yaiH protein - Escherichia coli gb AAC73479.1 (AE000144) putative enzyme [Escherichia coli] Length = 385</p> <p>Identities = 241/390 (61%), Positives = 309/390 (78%), Gaps = 3/390 (0%) sp P39347 INTB_ECOLI_PROPHAGE_P4_INTEGRASE (INT(P4)) pir S56496 prophage P4 integrase - Escherichia coli gb AAA97167.1 (U14003) ORF_o396 [Escherichia coli] gb AAC77227.1 (AE000498) prophage P4 integrase [Escherichia coli] Length = 396</p>
SEQ ID n°1432	Prot n°PL-2269.1	Contig41	859281	860234	No Hits found	Identities = 426/990 (43%), Positives = 609/990 (61%), Gaps = 14/990 (1%) sp P48474 YHDP_ECOLI_HYPOTHETICAL_107.7_KD_PROTEIN_IN_ARGR-CAFA INTERGENIC REGION pir G65116 hypothetical protein b3245 - Escherichia coli (strain K-12) gb AAC76277.1 (AE000403) orf, hypothetical protein [Escherichia coli] Length = 986
SEQ ID n°1433	Prot n°PL-227.1	Contig41	381075	384908	47%	Identities = 59/188 (31%), Positives = 86/188 (45%), Gaps = 17/188 (9%) pir A36134 RepA protein - Escherichia coli plasmid TF-FC2 gb AAA27381.1 (M73777) replication protein A [Plasmid pTF-FC2] Length = 290
SEQ ID n°1434	Prot n°PL-2270.1	Contig41	856307	857449	22%	Identities = 75/284 (26%), Positives = 120/284 (41%), Gaps = 41/284 (14%) gb AAC12937.1 (AF056345) Orf3 [Francisella tularensis] Length = 275
SEQ ID n°1436	Prot n°PL-2271.1	Contig41	855275	856153	40%	
SEQ ID n°1438	Prot n°PL-2272.1	Contig41	852064	853452	No Hits found	
SEQ ID n°1437	Prot n°PL-2273.1	Contig41	850968	851848	No Hits found	

TABLEAU I

SEQ ID n°1438	Prot n°PL-2274.1	Contig41	849989	850973	No Hits found		Identities = 294/422 (69%), Positives = 348/422 (81%) gb AAF06982.1 AF157599.1 (AF157599) P4 integrase-like protein [Escherichia coli] Length = 428
SEQ ID n°1439	Prot n°PL-2275.1	Contig41	848207	849472	81%		
SEQ ID n°1440	Prot n°PL-2276.1	Contig41	845043	847268	56%		Identities = 262/745 (35%), Positives = 419/745 (56%), Gaps = 20/745 (2%) gb AAA64865.1 U23723 orf732 [Escherichia coli] Length = 732
SEQ ID n°1441	Prot n°PL-2277.1	Contig41	843881	845020	45%		Identities = 116/277 (41%), Positives = 174/277 (61%), Gaps = 12/277 (4%) gb AAA64864.1 U23723 orf300 [Escherichia coli] Length = 300
SEQ ID n°1442	Prot n°PL-2278.1	Contig41	842264	843097	No Hits found		
SEQ ID n°1443	Prot n°PL-2279.1	Contig41	842261	843175	26%		Identities = 51/167 (30%), Positives = 81/167 (47%), Gaps = 6/167 (3%) dbj BAB06239.1 AP001515 transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°1444	Prot n°PL-228.1	Contig41	384917	386386	92%		Identities = 423/433 (95%), Positives = 460/493 (92%) pir JAG5117 cytosolic axial filament protein cafa - Escherichia coli gb AAA58050.1 (U18997) ORF_1495; orf of ECMRED, uses 2nd start [Escherichia coli] gb AAC76279.1 (AE000404) bundles of cytoplasmic filaments [Escherichia coli] Length = 495 "
SEQ ID n°1445	Prot n°PL-2280.1	Contig41	839434	840903	26%		Identities = 79/309 (25%), Positives = 129/309 (41%), Gaps = 30/309 (9%) gb AAF93226.1 (AE004096) smf protein [Vibrio cholerae] Length = 371
SEQ ID n°1446	Prot n°PL-2281.1	Contig41	837362	839485	56%		Identities = 293/706 (41%), Positives = 401/706 (56%), Gaps = 43/706 (6%) pir T35189 probable ATP-dependent DNA helicase - Streptomyces coelicolor emb CAA18513.1 (AL022374) SC588.05, probable ATP-dependent DNA helicase, len: 719 aa; similar in N-terminal half to many e.g. RECQ_EC01P1 5043 atp-dependent dna helicase reqc (607 aa), fasta score s; opt: 546 z-score: 615.9 E0: 4.1e-27, 35.9% identity in 362 aa ov> Length = 719 "
SEQ ID n°1447	Prot n°PL-2282.1	Contig41	833886	837215	11%		Identities = 76/321 (23%), Positives = 129/321 (39%), Gaps = 65/321 (20%) gil4506479 regulator of nonsense transcripts 1 gb AAC50771.1 (U65533) regulator of nonsense transcript stability [Homo sapiens] Length = 1118
SEQ ID n°1448	Prot n°PL-2283.1	Contig41	832608	833375	82%		Identities = 174/254 (68%), Positives = 212/254 (82%) spiP15031 FECE_EC01 IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE pir QRECM3 membrane-bound iron(III) dicitrate transport protein - Escherichia coli gb AAA23765.1 (M26397) fecE [Escherichia coli] gb AAA97183.1 (U14003) fecE gene product [Escherichia coli] gb AAC77243.1 (AE000499) ATP-binding component of citrate-dependent iron(III) transport protein [Escherichia coli] Length = 255

TABLEAU I

SEQ ID n°1448	Prot n°PL-2284.1	Contig41	831312	832807	60%	<p>Identities = 212/318 (66%), Positives = 260/318 (81%)</p> <p>sp P15029 FECD_ECOLI_IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD pir S56513 citrate-dependent iron transport protein feCD - Escherichia coli pir QRECD2 iron(III) dicitrate transport protein 2, cytosolic - Escherichia coli gb AAA97184.1 (U14003) CG Site No. 18394 [Escherichia coli] gb AAC77244.1 (AE000499) citrate-dependent iron transport, membrane-bound protein [Escherichia coli] Length =</p>
SEQ ID n°1450	Prot n°PL-2285.1	Contig41	830656	831654	83%	<p>Identities = 248/326 (75%), Positives = 281/326 (85%)</p> <p>sp P15030 FECC_ECOLI_IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECC pir S56514 fecC protein - Escherichia coli pir QRECD1 iron(III) dicitrate transport protein 1, cytosolic - Escherichia coli gb AAA97185.1 (U14003) fecC gene product [Escherichia coli] gb AAC77245.1 (AE000499) citrate-dependent iron(III) transport protein, cytosolic [Escherichia coli] Length = 332</p>
SEQ ID n°1451	Prot n°PL-2286.1	Contig41	829751	830659	82%	<p>Identities = 214/298 (71%), Positives = 250/298 (83%), Gaps = 2/298 (0%)</p> <p>sp P15028 FECB_ECOLI_IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR Length = 300</p>
SEQ ID n°1452	Prot n°PL-2287.1	Contig41	827355	829691	89%	<p>Identities = 653/779 (83%), Positives = 711/779 (90%), Gaps = 7/779 (0%)</p> <p>sp P13036 FECA_ECOLI_IRON(III) DICITRATE TRANSPORT PROTEIN FECA PRECURSOR pir QRECFE iron(III) dicitrate transport system outer membrane receptor precursor - Escherichia coli (strain K-12) gb AAC77247.1 (AE000499) outer membrane receptor, citrate-dependent iron transport, outer membrane receptor [Escherichia coli] Length = 774</p>
SEQ ID n°1453	Prot n°PL-2288.1	Contig41	826281	827246	71%	<p>Identities = 212/316 (67%), Positives = 246/316 (77%), Gaps = 1/316 (0%)</p> <p>sp P23485 FECE_ECOLI_FECR PROTEIN pir JB37804 fecR protein - Escherichia coli gb AAA23767.1 (M63115) fecR [Escherichia coli] gb AAA97188.1 (U14003) fecR gene product [Escherichia coli] gb AAC77248.1 (AE000500) regulator for fec operon, periplasmic [Escherichia coli] Length = 317</p>
SEQ ID n°1454	Prot n°PL-2289.1	Contig41	821896	822709	72%	<p>Identities = 198/329 (60%), Positives = 245/329 (74%) db BAA01531.1 (D10869) M5 protein [Salmonella choleraesuis] Length = 345</p> <p>Identities = 247/325 (76%), Positives = 279/325 (85%)</p>
SEQ ID n°1455	Prot n°PL-229.1	Contig41	387624	388658	75%	<p>sp P16926 MREC_ECOLI_ROD SHAPE-DETERMINING PROTEIN MREC pir J00059 rod shape-determining protein mreC - Escherichia coli gb AAA24155.1 (M31792) MreC protein [Escherichia coli] gb AAA58053.1 (U18997) called mreB in ECOMREB; Geneplot suggests frameshift near end [Escherichia coli] gb AAC76282.1 (AE000404) rod shape-determining protein [Escherichia coli] Length = 367</p>
SEQ ID n°1456	Prot n°PL-2290.1	Contig41	817797	818864	21%	<p>Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%)</p> <p>db BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188</p>

TABLEAU I

SEQ ID n°1457	Prot n°PL-2291.1	Contig41	815729	816985	53%	<p>Identities = 126/399 (31%), Positives = 223/399 (55%), Gaps = 21/399 (5%) gb AAC63217.1 (AF039135) juvenile hormone esterase-related protein [Leptinotarsa decemlineata] Length = 523</p>	Unknown, similar to insecticidal toxins
SEQ ID n°1458	Prot n°PL-2292.1	Contig41	812739	814328	15%	<p>Identities = 58/193 (30%), Positives = 83/193 (42%), Gaps = 40/193 (20%) gb AAG06678.1 (AE004751_4) (AE004751) hypothetical protein [Pseudomonas aeruginosa] Length = 882</p>	
SEQ ID n°1459	Prot n°PL-2293.1	Contig41	810013	810765	66%	<p>Identities = 106/242 (43%), Positives = 166/242 (67%), Gaps = 2/242 (0%) gb AAG07162.1 (AE004786_7) (AE004786) hypothetical protein [Pseudomonas aeruginosa] Length = 260</p>	
SEQ ID n°1460	Prot n°PL-2294.1	Contig41	808708	809967	53%	<p>Identities = 146/368 (39%), Positives = 226/368 (60%), Gaps = 13/368 (3%) gb AAG08696.1 (AE004943_12) (AE004943) probable MFS transporter [Pseudomonas aeruginosa] Length = 387</p>	
SEQ ID n°1461	Prot n°PL-2295.1	Contig41	806980	808326	85%	<p>Identities = 347/438 (79%), Positives = 397/438 (90%), Gaps = 1/438 (0%) sp P32702 YJCD_ECOLI_HYPOTHETICAL_45.7_KD_PROTEIN_IN_SOXR-ACS_INTERGENIC_REGION (O449) pir J365214 hypothetical 45.7 kD protein in soxR-acs intergenic region - Escherichia coli (strain K-12) gb AAC43158.1 (U00006) matches PS00017: ATP/GTP-binding site motif A [Escherichia coli] gb AAC77034.1 (AE000479) orf, hypothetical protein [Escherichia coli] Length = 449</p>	
SEQ ID n°1462	Prot n°PL-2296.1	Contig41	805058	806707	84%	<p>Identities = 381/547 (69%), Positives = 469/547 (85%) sp P32703 YJCE_ECOLI_PUTATIVE_NA(+)/H(+) EXCHANGER YJCE pir JH65214 hypothetical 80.5 kD protein in soxR-acs intergenic region - Escherichia coli (strain K-12) gb AAC43159.1 (U00006) similar to eukaryotic Na⁺/H⁺ exchangers [Escherichia coli] gb AAC77035.1 (AE000480) orf, hypothetical protein [Escherichia coli] Length = 546</p>	
SEQ ID n°1463	Prot n°PL-2297.1	Contig41	803896	804831	83%	<p>Identities = 236/305 (77%), Positives = 284/305 (96%) (M87049) trans-activator of metE and metH [Escherichia coli] Length = 317 Identities = 611/754 (81%), Positives = 671/754 (89%), Gaps = 3/754 (0%) sp P25665 METE_ECOLI_5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE-HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE) pir J42863 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase (EC 2.1.1.14) - Escherichia coli (strain K-12) gb AAC76832.1 (AE000458) tetrahydropteroyltriglutamate methyltransferase [Escherichia coli] Length = 753</p>	
SEQ ID n°1464	Prot n°PL-2298.1	Contig41	801511	803787	87%		
SEQ ID n°1465	Prot n°PL-2299.1	Contig41	800435	801280	19%	<p>Identities = 38/146 (26%), Positives = 56/146 (38%), Gaps = 31/146 (21%) pir J36711 probable dioxigenase - Streptomyces coelicolor emb CAB45209.1 (AL079308) putative dioxigenase [Streptomyces coelicolor A3(2)] Length = 284</p>	

TABLEAU I

SEQ ID n°1466	Prot n°PL-230.1	Contig41	40138	41364	37%	Identities = 88/366 (24%), Positives = 153/366 (41%), Gaps = 69/366 (18%) sp Q57550 Y085_METJA_HYPOTHETICAL PROTEIN MJ0085 pir E64310 iron transport system binding protein - Methanococcus jannaschii gb AAB98067.1 (U67466) iron transport periplasmic binding protein, putative (cauE) [Methanococcus jannaschii] Length = 373
SEQ ID n°1467	Prot n°PL-230.1	Contig41	388770	389873	92%	Identities = 340/367 (92%), Positives = 350/367 (94%) pir BVECEB rod shape- determining protein envB - Escherichia coli gb AAA58054.1 (U18997) frameshifts changes start relative to ECOMREB [Escherichia coli] gb AAC76283.1 (AE000404) regulator of ftsI, penicillin binding protein 3, separation function [Escherichia coli] Length = 367
SEQ ID n°1468	Prot n°PL-2300.1	Contig41	799534	800190	61%	Identities = 112/215 (52%), Positives = 150/215 (69%), Gaps = 1/215 (0%) sp P28618 PCP_BACSU_PYRROLIDONE-CARBOXYLATE PEPTIDASE (5- OXOPROLYL-PEPTIDASE) (PYROGLUTAMYL-PEPTIDASE I) (PGP-I) (PYRASE) pir S23432 pyroglutamyl-peptidase I (EC 3.4.19.3) pcp - Bacillus subtilis emb CAA46833.1 (X66034) TRANSFERRED ENTRY: 3.4.19.3 [Bacillus subtilis] dbj BAA06485.1 (D30808) pyrrolidone carboxy-peptidase [Bacillus subtilis] emb CAB12059.1 (Z99105) pyrrolidone-carboxylate peptidase [Bacillus subtilis] Length = 215
SEQ ID n°1469	Prot n°PL-2301.1	Contig41	797928	798683	89%	Identities = 219/250 (87%), Positives = 233/250 (92%) emb CAB94934.1 (AJ278525) uridine phosphorylase [Versinia pseudotuberculosis] Length = 253
SEQ ID n°1470	Prot n°PL-2302.1	Contig41	797051	797845	52%	Identities = 82/259 (31%), Positives = 138/259 (52%), Gaps = 5/259 (1%) dbj BAA81645.1 (AB028630) protein-tyrosine phosphatase [Clostridium perfringens] Length = 332
SEQ ID n°1471	Prot n°PL-2303.1	Contig41	796322	796936	41%	Identities = 57/152 (37%), Positives = 85/152 (55%) pir A64728 probable membrane protein yabl - Escherichia coli gb AAC73176.1 (AE000117) orf, hypothetical protein [Escherichia coli] Length = 254
SEQ ID n°1472	Prot n°PL-2304.1	Contig41	794861	796216	77%	Identities = 291/439 (66%), Positives = 359/439 (81%), Gaps = 4/439 (0%) gb AAF33423.1 (AF233324) 88% identity to E. coli hypothetical protein (Y1GN) (SP:P27850) [Salmonella typhimurium LT2] Length = 476
SEQ ID n°1473	Prot n°PL-2305.1	Contig41	794033	794812	83%	Identities = 199/251 (79%), Positives = 229/251 (90%) gb AAF33422.1 (AF233324) 98% identity with E. coli ubiquinone biosynthesis methyltransferase (UBIE) (SP:P27851); contains similarity to Pfam family PF01209 (ubie/COQ6 methyltransferase family), score=588.5, E=4.1e-173, N=1 [Salmonella typhimurium LT2] Length = 251 "
SEQ ID n°1474	Prot n°PL-2306.1	Contig41	793381	794016	62%	Identities = 99/197 (50%), Positives = 144/197 (72%) sp P27852 YIGP_ECOLI HYPOTHETICAL 22.2 KD PROTEIN IN UBIE-RFAH INTERGENIC REGION pir C65186 hypothetical 22.3 kD protein in udp-faH intergenic region - Escherichia coli (strain K-12) gb AAC76837.1 (AE000459) orf, hypothetical protein [Escherichia coli] Length = 201

TABLEAU I

SEQ ID n°1475	Prot n°PL-2307.1	Contig41	791757	793394	90%	Identities = 441/539 (81%), Positives = 496/539 (91%), Gaps = 1/539 (0%) sp O07443 AARF_PROST_UBIQUINONE BIOSYNTHESIS PROTEIN AARF (AMINOGLYCOSIDE ACETYLTRANSFERASE REGULATOR) gb AA096577.1 (AF002165) aminoglycoside acetyltransferase regulator [Providencia stuartii] Length = 544
SEQ ID n°1476	Prot n°PL-2308.1	Contig41	790019	790801	87%	Identities = 195/255 (76%), Positives = 230/255 (89%) gb AAF33418.1 (AF233324) 90% identity to E. coli SEC-independent protein translocase protein (TATC); contains similarity to Pfam family PF00902 (MttB family), score=147.4, E=2.6e-40, N=1 [Salmonella typhimurium LT2] Length = 259
SEQ ID n°1477	Prot n°PL-2309.1	Contig41	788896	789909	85%	Identities = 243/335 (72%), Positives = 290/335 (86%), Gaps = 1/335 (0%) gb AAF93283.1 (AE004101) delta-aminolevulinic acid dehydratase [Vibrio cholerae] Length = 347
SEQ ID n°1478	Prot n°PL-231.1	Contig41	390375	391352	71%	Identities = 222/324 (68%), Positives = 262/324 (80%), Gaps = 1/324 (0%) sp P26848 YHDH_ECOLI_PROTEIN_YHDH_pir J00688 hypothetical 35K protein (fabE 5' region) - Escherichia coli gb AAA23407.1 (M80458) 35 kDa protein [Escherichia coli] gb AAA68056.1 (U18997) ORF_o324;orf of ECOACOAC [Escherichia coli] gb AAC76285.1 (AE000404) putative dehydrogenase [Escherichia coli] Length = 324
SEQ ID n°1479	Prot n°PL-2310.1	Contig41	786259	787740	92%	Identities = 428/490 (87%), Positives = 459/490 (93%) gb AAF33412.1 (AF233324) 92% identity to E. coli hypothetical protein (YIGC) (SW:P26615) [Salmonella typhimurium LT2] Length = 492
SEQ ID n°1480	Prot n°PL-2311.1	Contig41	785547	786248	93%	Identities = 217/233 (93%), Positives = 224/233 (96%) sp P43129 UBIB_PHOLU_NAD(P)H-FLAVIN REDUCTASE (NAD(P)H-FLAVIN OXIDOREDUCTASE) db JBAA04597.1 (D17745) NAD(P)H-flavin reductase, Fre [Photobacterium luminescens] Length = 233
SEQ ID n°1481	Prot n°PL-2312.1	Contig41	784297	785463	82%	Identities = 299/387 (77%), Positives = 338/387 (87%) gb AAA23751.1 (M59368) fatty acid oxidizing complex [Escherichia coli] gb AAA62778.1 (M74164) 3-ketoacyl-coenzyme A thiolase [Escherichia coli] Length =
SEQ ID n°1482	Prot n°PL-2314.1	Contig41	888908	891046	87%	Identities = 578/709 (81%), Positives = 632/709 (88%), Gaps = 2/709 (0%) gb AAF60351.1 (AF242390) anaerobic ribonucleoside-triphosphate reductase [Salmonella typhimurium] Length = 712
SEQ ID n°1483	Prot n°PL-2315.1	Contig41	894304	895257	No Hits found	
SEQ ID n°1484	Prot n°PL-2316.1	Contig41	895230	897779	26%	Identities = 148/379 (39%), Positives = 228/379 (60%), Gaps = 7/379 (1%) sp Q58116 HMDH_METJA_3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (HMG-COA REDUCTASE) pir JA64388 3-hydroxy-3-methylglutaryl coenzyme A reductase (EC 1.1.1.-) - Methanococcus jannaschii gb AAB98699.1 (U67517) 3-hydroxy-3-methylglutaryl coenzyme A reductase [Methanococcus jannaschii] Length = 405

TABLEAU I

SEQ ID n°1485	Prot n°PL-2317.1	Contig41	897906	900689	18%	<p>Identities = 108/317 (34%), Positives = 170/317 (53%), Gaps = 13/317 (4%) sp O29548 PPSA_ARCFU PROBABLE PHOSPHOENOLPYRUVATE SYNTHASE (PYRUVATE, WATER DIKINASE) (PEP SYNTHASE) pir JF69338 pyruvate, water dikinase (EC 2.7.9.2) - Archaeoglobus fulgidus gb AAB90532.1 (AE001056) phosphoenolpyruvate synthase (ppsA) [Archaeoglobus fulgidus] Length = 753</p>
SEQ ID n°1486	Prot n°PL-2318.1	Contig41	900667	901737	17%	<p>Identities = 39/150 (26%), Positives = 63/150 (42%), Gaps = 8/150 (5%) pir JF65084 hypothetical protein b2981 - Escherichia coli (strain K-12) gb AAA69148.1 (U28377) ORF_f390 [Escherichia coli] gb AAC78017.1 (AE000381) orf, hypothetical protein [Escherichia coli] Length = 390</p>
SEQ ID n°1487	Prot n°PL-2319.1	Contig41	901650	903320	42%	<p>Identities = 149/568 (26%), Positives = 236/568 (41%), Gaps = 52/568 (9%) gb AAF85075.1 AE004039_10 (AE004039) peptide synthase [Xylella fastidiosa] Length = 563</p>
SEQ ID n°1488	Prot n°PL-232.1	Contig41	392527	393876	94%	<p>Identities = 408/448 (91%), Positives = 429/448 (95%) sp P24182 ACCC_ECOLI BIOTIN CARBOXYLASE (A SUBUNIT OF ACETYL-CoA CARBOXYLASE (ACC) pir J50632 acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxylase - Escherichia coli pdb 1DV1 A Chain A, Structure Of Biotin Carboxylase (Apo) pdb 1BNC A Chain A, Mol_Id: 1; Molecule: Biotin Carboxylase; Chain: A, B; Ec: 6.3.4.14 pdb 1BNC B Chain B, Mol_Id: 1; Molecule: Biotin Carboxylase; Chain: A, B; Ec: 6.3.4.14 gb AAA23409.1 (M80458) biotin carboxylase [Escherichia coli] gb AAA23746.1 (M83198) biotin carboxylase [Escherichia coli] gb AAA58059.1 (U18997) biotin carboxylase [Escherichia coli] gb AAC76288.1 (AE000404) acetyl CoA carboxylase, biotin carboxylase Identities = 39/121 (32%), Positives = 63/121 (51%), Gaps = 7/121 (5%)</p>
SEQ ID n°1489	Prot n°PL-2320.1	Contig41	903278	903940	28%	<p>sp P39823 PSS_BACSU CDP-DIACYLGLYCEROL-SERINE O-PHOSPHATIDYLTRANSFERASE (PHOSPHATIDYL-SERINE SYNTHASE) pir JAE5537 CDP-diacylglycerol-serine O-phosphatidyltransferase (EC 2.7.8.8) pssA - Bacillus subtilis db JBA07225.1 (D38022) phosphatidylserine synthase [Bacillus subtilis] emb JCA812021.1 (Z99105) phosphatidylserine synthase [Bacillus subtilis] db JBA033124.1 (AB006424) PHOSPHATIDYL-SERINE SYNTHASE [Bacillus</p>
SEQ ID n°1490	Prot n°PL-2321.1	Contig41	903801	904472	No Hits found	
SEQ ID n°1491	Prot n°PL-2322.2	Contig41	905262	906302		
SEQ ID n°1492	Prot n°PL-2323.1	Contig41	906302	907450	66%	<p>Identities = 184/375 (49%), Positives = 253/375 (67%), Gaps = 8/375 (2%) gb AAG06789.1 AE004761_5 (AE004761) hypothetical protein [Pseudomonas aeruginosa] Length = 390</p>
SEQ ID n°1493	Prot n°PL-2324.1	Contig41	907455	908426	76%	<p>Identities = 194/321 (60%), Positives = 249/321 (77%) gb AAG08790.1 AE004761_6 (AE004761) hypothetical protein [Pseudomonas aeruginosa] Length = 323</p>

TABLEAU I

SEQ ID n°1494	Prot n°PL-2325.1	Contig41	908598	909311	78%	<p>Identities = 154/205 (75%), Positives = 186/205 (90%)</p> <p>sp P33357 YEHU_ECOLI_HYPOTHETICAL_62.1_KD_PROTEIN_IN_MOLR-BGLX_INTERGENIC_REGION PRECURSOR pir E64980 hypothetical 62.1 kd protein in molR-bglX intergenic region - Escherichia coli (strain K-12) gb AAC75187.1 (AE000301) putative 2-component sensor protein</p> <p>Identities = 262/358 (73%), Positives = 307/358 (85%)</p> <p>sp P33357 YEHU_ECOLI_HYPOTHETICAL_62.1_KD_PROTEIN_IN_MOLR-BGLX_INTERGENIC_REGION PRECURSOR pir E64980 hypothetical 62.1 kd protein in molR-bglX intergenic region - Escherichia coli (strain K-12) gb AAC75187.1 (AE000301) putative 2-component sensor protein</p> <p>Identities = 172/238 (72%), Positives = 209/238 (87%), Gaps = 1/238 (0%)</p> <p>sp P33356 YEHT_ECOLI_HYPOTHETICAL_27.9_KD_PROTEIN_IN_MOLR-BGLX_INTERGENIC_REGION pir D64980 yehT protein - Escherichia coli (strain K-12) gb AAA60488.1 (U00007) yehT [Escherichia coli] gb AAC75186.1 (AE000301) orf, hypothetical protein [Escherichia coli] prf 2014253V yehT gene [Escherichia coli] Length = 244</p>
SEQ ID n°1495	Prot n°PL-2326.1	Contig41	910136	911284	80%	
SEQ ID n°1496	Prot n°PL-2327.1	Contig41	911281	912003	86%	
SEQ ID n°1497	Prot n°PL-2328.1	Contig41	912174	913976	83%	<p>Identities = 417/585 (71%), Positives = 512/585 (87%)</p> <p>sp P94532 CSTA_BACSU CARBON STARVATION PROTEIN A HOMOLOG pir A69609 carbon starvation-induced protein csiA - Bacillus subtilis emb CAA99598.1 (Z75208) carbon starvation induced protein [Bacillus subtilis] emb CAB14831.1 (Z99118) carbon starvation-induced protein [Bacillus subtilis] Length = 598</p>
SEQ ID n°1498	Prot n°PL-2329.1	Contig41	914115	916049	86%	<p>Identities = 530/637 (83%), Positives = 559/637 (87%), Gaps = 11/637 (1%)</p> <p>pir F65106 probable ATP-dependent RNA helicase dead - Escherichia coli gb AAA57965.1 (U18997) two frameshifts relative to ECODAD [Escherichia coli] gb AAC76196.1 (AE000397) inducible ATP-independent RNA helicase [Escherichia coli] Length = 646</p>
SEQ ID n°1499	Prot n°PL-233.1	Contig41	394468	395282	No Hits found	
SEQ ID n°1500	Prot n°PL-2330.1	Contig41	916206	917090	87%	<p>Identities = 236/294 (80%), Positives = 260/294 (88%)</p> <p>sp P39833 NLPI_ECOLI_LIPOPROTEIN_NLPI_PRECURSOR pir G65106 hypothetical 33.6 kd protein in dead-pnp intergenic region - Escherichia coli (strain K-12) gb AAA57966.1 (U18997) ORF_1294 [Escherichia coli] gb AAC76197.1 (AE000397) putative control proteins [Escherichia coli]</p>
SEQ ID n°1501	Prot n°PL-2331.1	Contig41	917338	919467	96%	<p>Identities = 675/709 (95%), Positives = 689/709 (96%)</p> <p>sp P41121 PNP_PHOLU_POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE) (CAP87K) pir S38883 polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) - Xenorhabdus luminescens emb CAA53671.1 (X76069) polynucleotide phosphorylase [Photorhabdus</p>

TABLEAU I

SEQ ID n°1502	Prot n°PL-2332.1	Contig41	920105	921052	78%	Identities = 229/308 (74%), Positives = 259/308 (83%), Gaps = 2/308 (0%) sp P09171 TRUB_ECOLI TRNA PSEUDOURIDINE SYNTHASE B (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) (P35 PROTEIN) pir Q9EC35 trna-pseudouridine synthase (EC 5.4.99.-) truB - Escherichia coli emb CAA32021.1 (X13775) P35 gene product (AA 1 - 314) [Escherichia coli] emb CAA31635.1 (X13270) P35 gene product (AA 1 - 314) [Escherichia coli] gb AAC76200.1 (AE000397) tRNA pseudouridine 5S synthase [Escherichia coli] Length = 314
SEQ ID n°1503	Prot n°PL-2333.1	Contig41	922845	923546	No Hits found	Identities = 750/913 (82%), Positives = 818/913 (89%), Gaps = 25/913 (2%) sp Q9ZF31 IF2_SALTY TRANSLATION INITIATION FACTOR IF-2 emb CAA05549.1 (AJ002552) Initiation factor IF2-alpha [Salmonella typhimurium] Length = 892
SEQ ID n°1504	Prot n°PL-2334.1	Contig41	921528	924257	88%	Identities = 64/221 (28%), Positives = 99/221 (43%), Gaps = 11/221 (4%) dbj BAA97453.1 (AB029393) streptococcal hemagglutinin [Streptococcus gordonii] Length = 2178
SEQ ID n°1505	Prot n°PL-2335.1	Contig41	923749	924510	38%	Identities = 430/502 (85%), Positives = 467/502 (92%), Gaps = 7/502 (1%) sp P03003 NUSA_ECOLI N UTILIZATION SUBSTANCE PROTEIN A (NUSA PROTEIN) (L FACTOR) pir FJEC transcription termination-antitermination factor nusa - Escherichia coli gb AAA57872.1 (U18987) L factor [Escherichia coli] gb AAC76203.1 (AE000397) transcription pausing; L factor [Escherichia coli] Length = 486
SEQ ID n°1506	Prot n°PL-2336.1	Contig41	924282	925790	81%	Identities = 377/443 (85%), Positives = 410/443 (92%), Gaps = 1/443 (0%) sp P31120 MRSA_ECOLI MRSA PROTEIN pir j41215 mrsa protein - Escherichia coli gb AAA16122.1 (L12988) putative [Escherichia coli] gb AAA57977.1 (U18997) yhbF [Escherichia coli] gb AAC76208.1 (AE000398) similar to phosphoglucomutases and phosphomannomutases [Escherichia coli] Length = 445
SEQ ID n°1507	Prot n°PL-2337.1	Contig41	927271	928608	87%	Identities = 199/282 (70%), Positives = 234/282 (82%), Gaps = 4/282 (1%) (U18997) dihydropteroate synthase [Escherichia coli] gb AAC76209.1 (AE000398) 7,8-dihydropteroate synthase [Escherichia coli] Length = 282 Identities = 574/651 (88%), Positives = 609/651 (93%), Gaps = 4/651 (0%) gb AAA97508.1 (U01378) ATP-binding protein [Escherichia coli] Length = 647
SEQ ID n°1508	Prot n°PL-2338.1	Contig41	928605	929450	82%	Identities = 73/309 (23%), Positives = 132/309 (42%), Gaps = 18/309 (5%) dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] Length = 345
SEQ ID n°1509	Prot n°PL-2339.1	Contig41	929533	931494	92%	
SEQ ID n°1510	Prot n°PL-234.1	Contig41	394351	395424	38%	

TABLEAU I

SEQ ID n°1511	Prot n°PL-2340.1	Contig41	931543	932184	92%	<p>Identities = 188/208 (90%), Positives = 188/208 (94%)</p> <p>sp P28692 RRMJ_ECOLI_RIBOSOMAL_RNA_LARGE_SUBUNIT_METHYLTRANSFERASE_J (RRNA (URIDINE-2'-O-)-METHYLTRANSFERASE) (23S RRNA M2U2552 METHYLTRANSFERASE) (CELL DIVISION PROTEIN FTSJ) pir S35108 cell division protein ftsJ - Escherichia coli gb AA23812.1 (M83138) ftsJ [Escherichia coli] gb AA57980.1 (U18997) ftsJ [Escherichia coli] gb AA97507.1 (U01376) regulatory protein [Escherichia coli]</p>
SEQ ID n°1512	Prot n°PL-2341.1	Contig41	933341	934924	75%	<p>Identities = 339/461 (73%), Positives = 398/461 (85%)</p> <p>sp P24228 PBP4_ECOLI_PENICILLIN-BINDING_PROTEIN_4_PRECURSOR (PBP-4) [INCLUDES: D-ALANYL-D-ALANINE CARBOXYPEPTIDASE (DD-PEPTIDASE) (DD-CARBOXYPEPTIDASE); D-ALANYL-D-ALANINE-ENDOPEPTIDASE (DD-ENDOPEPTIDASE)] pir A54535 serine-type D-Ala-D-Ala carboxypeptidase (EC 3.4.16.4) precursor - Escherichia coli emb CAA42070.1 (X59460) penicillin-binding protein 4 (PBP4) [Escherichia coli] emb CAA42643.1 (X60038) D-alanyl-D-alanine carboxypeptidase [Escherichia coli] gb AA57983.1 (U18997) D-alanyl-D-alanine carboxypeptidase, fraction B [Escherichia coli] gb AA97505.1 (U01376) ampicillin-binding protein [Escherichia coli] gb AAC76214.1 (AE000399) D-alanyl-D-alanine carboxypeptidase, fraction B; penicillin-binding protein 4 [Escherichia coli] Length = 477</p>
SEQ ID n°1513	Prot n°PL-2342.1	Contig41	934992	936167	81%	<p>Identities = 308/392 (78%), Positives = 350/392 (88%), Gaps = 3/392 (0%)</p> <p>sp P42841 YHBZ_ECOLI_HYPOTHETICAL_43_3_KD_GTP-BINDING_PROTEIN_IN_DACB-RPMA_INTERGENIC_REGION pir A65109 GTP-binding protein obg - Escherichia coli (strain K-12) gb AA57984.1 (U18997) ORF_930 [Escherichia coli] gb AAC76215.1 (AE000399) putative GTP-binding factor [Escherichia coli] Length = 390</p>
SEQ ID n°1514	Prot n°PL-2343.1	Contig41	937257	938228	85%	<p>Identities = 251/321 (78%), Positives = 287/321 (89%)</p> <p>sp P19841 ISPB_ECOLI_OCTAPRENYL-DIPHOSPHATE_SYNTHASE (OCTAPRENYL PYROPHOSPHATE SYNTHETASE) (OPP SYNTHETASE) pir E65109 octaprenyl-diphosphate synthase (EC 2.5.1.-) - Escherichia coli gb AA57988.1 (U18997) ORF_0323 [Escherichia coli] gb AAC76219.1 (AE000399) octaprenyl diphosphate synthase [Escherichia coli] Identities = 274/311 (88%), Positives = 295/311 (94%)</p>
SEQ ID n°1515	Prot n°PL-2344.1	Contig41	939735	940673	91%	<p>sp P06994 MDH_ECOLI_MALATE_DEHYDROGENASE pir DDEECM malate dehydrogenase [EC 1.1.1.37] - Escherichia coli gb AA58038.1 (U18997) malate dehydrogenase [Escherichia coli] gb AAC76268.1 (AE000403) malate dehydrogenase [Escherichia coli] Length = 312</p>

TABLEAU I

SEQ ID n°1516	Prot n°PL-2345.1	Contig41	941643	943013	81%	<p>Identities = 352/457 (77%), Positives = 394/457 (86%) sp P37773 MPL_ECOLI_UDP-N-ACETYLMURAMATE:L-ALANYL-GAMMA-D-GLUTAMYL-MESO-DIAMINOPIMELATE LIGASE (MUREIN PEPTIDE LIGASE) pir IS56459 hypothetical 48.5K protein (fbp-pmba intergenic region) - Escherichia coli gb AAA97130.1 (U14003) ORF_o457 [Escherichia coli] gb AAC77190.1 (AE000494) putative ligase [Escherichia coli] Length = 457</p>
SEQ ID n°1517	Prot n°PL-2346.1	Contig41	943179	944183	86%	<p>Identities = 279/333 (83%), Positives = 300/333 (89%), Gaps = 2/333 (0%) sp P09200 F16P_ECOLI FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE 1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) pir PAEC fructose-bisphosphatase (EC 3.1.3.11) - Escherichia coli emb CAA31062.1 (X12545) fructose-1,6-bisphosphatase (AA 1-332) [Escherichia coli] gb AAA97129.1 (U14003) fructose-1,6-bisphosphatase [Escherichia coli] gb AAC77189.1 (AE000494) fructose-bisphosphatase [Escherichia coli] Length = 332</p>
SEQ ID n°1518	Prot n°PL-2347.1	Contig41	944801	945331	76%	<p>Identities = 159/176 (90%), Positives = 169/176 (95%) sp P17288 PYR_ECOLI INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) pir PWEC inorganic pyrophosphatase (EC 3.6.1.1) - Escherichia coli gb AAB88583.1 (M23550) inorganic pyrophosphatase [Escherichia coli] gb AAA97123.1 (U14003) ppa gene product [Escherichia coli] gb AAC77183.1 (AE000494) inorganic pyrophosphatase [Escherichia coli] Length = 176</p>
SEQ ID n°1519	Prot n°PL-2348.1	Contig41	945781	949554	73%	<p>Identities = 679/1261 (53%), Positives = 926/1261 (72%), Gaps = 6/1261 (0%) sp P39321 YTFN_ECOLI HYPOTHETICAL 136.8 KD PROTEIN IN MSRA-CHPB INTERGENIC REGION pir H65233 yfN protein - Escherichia coli (strain K-12) gb AAC77178.1 (AE000493) orf, hypothetical protein [Escherichia coli] Length = 1259</p>
SEQ ID n°1520	Prot n°PL-2349.1	Contig41	949551	951293	74%	<p>Identities = 359/574 (62%), Positives = 437/574 (75%), Gaps = 3/574 (0%) sp P39320 YTFM_ECOLI HYPOTHETICAL 64.8 KD PROTEIN IN MSRA-CHPB INTERGENIC REGION PRECURSOR (O577) pir IS56445 hypothetical 64.8K protein (msra-chpb intergenic region) - Escherichia coli gb AAA97116.1 (U14003) ORF_o577 [Escherichia coli] gb AAC77177.1 (AE000493) orf, hypothetical protein [Escherichia coli] Length = 577</p>
SEQ ID n°1521	Prot n°PL-235.1	Contig41	396449	397375	35%	<p>Identities = 66/284 (23%), Positives = 110/284 (38%), Gaps = 48/284 (16%) pir C69122 hypothetical protein MTH1911 - Methanobacterium thermoautotrophicum (strain Delta H) gb AAB86371.1 (AE000942) unknown [Methanobacterium thermoautotrophicum] Length = 259</p>

TABLEAU I

SEQ ID n°1522	Prot n°PL-2350.1	Contig41	951408	952055	71%	<p>Identities = 133/205 (64%), Positives = 156/205 (75%)</p> <p>spiP2710 PMRSR_ECOLI PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O) REDUCTASE) pir S58444 protein-methionine-S-oxide reductase (EC 1.8.4.6) - Escherichia coli gb AAA24399.1 (M89992) peptide methionine sulfoxide reductase [Escherichia coli] gb AA97115.1 (U14003) peptide methionine sulfoxide reductase [Escherichia coli] gb AAC77176.1 (AE000493) peptide methionine sulfoxide reductase</p> <p>Identities = 325/444 (73%), Positives = 388/444 (86%), Gaps = 1/444 (0%)</p> <p>spiP39319 YTFLE_ECOLI HYPOTHETICAL 49.8 KD PROTEIN IN CYSQ-MSRA INTERGENIC REGION pir S58443 hypothetical 49.8K protein (cysq-msra intergenic region) - Escherichia coli gb AA97114.1 (U14003) ORF_1447 [Escherichia coli] gb AAC77175.1 (AE000493) putative transport protein [Escherichia coli] Length = 447</p> <p>Identities = 104/183 (56%), Positives = 133/183 (71%), Gaps = 1/183 (0%)</p> <p>gb AAF95691.1 (AE004324) conserved hypothetical protein [Vibrio cholerae] Length = 183</p>
SEQ ID n°1523	Prot n°PL-2351.1	Contig41	952210	953541	84%	<p>Identities = 165/247 (66%), Positives = 202/247 (80%), Gaps = 1/247 (0%)</p> <p>pir S56439 ammonium transport system structural protein - Escherichia coli gb AAA97110.1 (U14003) alternate gene name amtA [Escherichia coli] gb AAC77171.1 (AE000492) affects pool of 3'-phosphoadenosine-5'-phosphosulfate in pathway of sulfite synthesis [Escherichia coli] Length = 246</p> <p>Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%)</p> <p>dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188</p> <p>Identities = 160/209 (76%), Positives = 183/209 (87%) pir S56432 peptidylprolyl isomerase (EC 5.2.1.8) - Escherichia coli gb AAA97103.1 (U14003) ORF_o259a [Escherichia coli] gb AAC77164.1 (AE000492) FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli] Length = 259</p> <p>Identities = 75/235 (31%), Positives = 110/235 (45%), Gaps = 12/235 (5%)</p> <p>gb AAF01471.1 (AF190630_1 (AF190630) PhzR [Pseudomonas aeruginosa] gb AAG05287.1 (AE004616_1 (AE004616) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 237</p>
SEQ ID n°1524	Prot n°PL-2352.1	Contig41	954150	954704	63%	<p>Identities = 82/367 (22%), Positives = 162/367 (43%), Gaps = 20/367 (5%)</p> <p>emb CAB92558.1 (AL358812) putative integral membrane protein. [Streptomyces coelicolor A3(2)] Length = 411</p>
SEQ ID n°1525	Prot n°PL-2353.1	Contig41	954785	955528	79%	
SEQ ID n°1526	Prot n°PL-2354.1	Contig41	956340	957407	21%	
SEQ ID n°1527	Prot n°PL-2355.1	Contig41	957850	958488	85%	
SEQ ID n°1528	Prot n°PL-2356.1	Contig41	958684	959457	42%	
SEQ ID n°1529	Prot n°PL-2357.1	Contig41	959494	960873	No Hits found	
SEQ ID n°1530	Prot n°PL-2358.1	Contig41	960815	962104	37%	

TABLEAU I

SEQ ID n°1531	Prot n°PL-2359.1	Contig41	962254	963951	58%	Identities = 227/605 (37%), Positives = 334/605 (54%), Gaps = 58/605 (9%) sp P74178 YB78_SYNY3 HYPOTHETICAL 69.1 KD PROTEIN SLL1178 pir S75808 modulation protein - <i>Synechocystis</i> sp. (strain PCC 6803) dbj BAA18267.1 (D90913) nodulation protein [<i>Synechocystis</i> sp.] Length = 615
SEQ ID n°1532	Prot n°PL-236.1	Contig41	397327	398004	55%	Identities = 101/223 (45%), Positives = 140/223 (62%), Gaps = 1/223 (0%) sp Q48806 DLPA_LEGPN DLPA PROTEIN pir S81390 dlpA protein - <i>Legionella pneumophila</i> gb AAA79904.1 (U07940) DlpA [<i>Legionella</i> <i>pneumophila</i>] Length = 615
SEQ ID n°1533	Prot n°PL-2360.1	Contig41	963975	964793	56%	Identities = 91/270 (33%), Positives = 153/270 (55%), Gaps = 11/270 (4%) pir S76729 hypothetical protein - <i>Synechocystis</i> sp. (strain PCC 6803) dbj BAA18641.1 (D90916) hypothetical protein [<i>Synechocystis</i> sp.] Length = 705
SEQ ID n°1534	Prot n°PL-2361.1	Contig41	964775	965965	57%	Identities = 136/403 (33%), Positives = 230/403 (56%), Gaps = 6/403 (1%) dbj BAB08906.1 (AP001518) argininosuccinate synthase (citrulline- <i>aspartate</i> ligase) [Bacillus halodurans] Length = 409
SEQ ID n°1535	Prot n°PL-2362.1	Contig41	965955	966983	53%	Identities = 131/337 (38%), Positives = 199/337 (58%), Gaps = 8/337 (2%) emb CAB89449.1 (AL354048) putative cystathionine beta-synthase [<i>Streptomyces coelicolor</i> A3(2)] Length = 461
SEQ ID n°1536	Prot n°PL-2363.1	Contig41	967770	968654	59%	Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U83995) putative protease [<i>Porphyromonas gingivalis</i>] Length = 300
SEQ ID n°1537	Prot n°PL-2364.1	Contig41	970691	971425	85%	Identities = 208/243 (85%), Positives = 232/243 (94%) sp P39280 YJFH_ECOLI HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE YJFH pir S56405 hypothetical 26.6K protein (vacB- aidB intergenic region) - <i>Escherichia coli</i> gb AAA97076.1 (U14003) ORF_0243 [<i>Escherichia coli</i>] gb AAC77137.1 (AE000490) orf, hypothetical Identities = 609/819 (74%), Positives = 688/819 (83%), Gaps = 7/819 (0%) pir S56404 virulence-associated protein vacB homolog - <i>Escherichia coli</i> gb AAA97075.1 (U14003) vacB gene product [<i>Escherichia coli</i>] gb AAC77136.1 (AE000490) putative enzyme [<i>Escherichia coli</i>] Length
SEQ ID n°1538	Prot n°PL-2365.1	Contig41	971553	974042	82%	Identities = 373/432 (86%), Positives = 400/432 (92%) sp P12283 PJURA_ECOLI ADENYLOSUCCINATE SYNTHETASE (IMP- ASPARTATE LIGASE) (ADSS) (AMPSASE) pir AJECDS adenylosuccinate synthase (EC 6.3.4.4) purA - <i>Escherichia coli</i> gb AAA97073.1 (U14003) adenylosuccinate synthetase [<i>Escherichia coli</i>] gb AAC77134.1 (AE000490) adenylosuccinate synthetase [<i>Escherichia coli</i>]

TABLEAU I

SEQ ID n°1540	Prot n°PL-2367.1	Contig41	976101	977111	80%	<p>Identities = 248/330 (75%), Positives = 277/330 (83%), Gaps = 2/330 (0%) spiP25661 HFLC_ECOLI_HFLC PROTEIN pir C43653 probable integral membrane proteinase (EC 3.4.-.-) hflC - Escherichia coli gb AAC43400.1 (U00005) putative integral membrane protease required for high frequency lysogenization by bacteriophage lambda [Escherichia coli] gb AA97071.1 (U14003) CG Site No. 17520; alternate gene name hflA; putative integral membrane protease required for high frequency lysogenization by bacteriophage lambda [Escherichia coli] gb AAC77132.1 (AE000489) protease specific for phage lambda cII repressor [Escherichia coli] Length = 334 "</p>
SEQ ID n°1541	Prot n°PL-2369.1	Contig41	977117	978337	81%	<p>Identities = 291/410 (70%), Positives = 333/410 (80%), Gaps = 18/410 (3%) spiP25662 HFLK_ECOLI_HFLK PROTEIN pir B43653 probable integral membrane proteinase (EC 3.4.-.-) hflK - Escherichia coli gb AAC43399.1 (U00005) putative integral membrane protein required for high frequency lysogenization by bacteriophage lambda [Escherichia coli] gb AA97070.1 (U14003) CG Site No. 639; alternate gene name hflA; putative integral membrane protease required for high frequency lysogenization by bacteriophage lambda [Escherichia coli] gb AAC77131.1 (AE000489) protease specific for phage lambda cII repressor [Escherichia coli] Length = 419 "</p>
SEQ ID n°1542	Prot n°PL-237.1	Contig41	398004	400187	36%	<p>Identities = 208/373 (55%), Positives = 265/373 (70%), Gaps = 6/373 (1%) spiQ48806 DLPA_LEGPN DLPA PROTEIN pir S61390 dlpA protein - Legionella pneumophila gb AAA79904.1 (U07940) DlpA [Legionella pneumophila] Length = 615 Identities = 347/426 (81%), Positives = 390/426 (91%)</p>
SEQ ID n°1543	Prot n°PL-2370.1	Contig41	978443	979723	90%	<p>spiP25519 HFLX_ECOLI_GTP-BINDING PROTEIN HFLX pir S56398 probable GTP-binding protein hflX - Escherichia coli gb AAC43398.1 (U00005) putative GTPase required for high frequency lysogenization by bacteriophage lambda [Escherichia coli] gb AA97069.1 (U14003) putative GTPase required for high frequency lysogenization by bacteriophage lambda; TTG start codon [Escherichia coli] gb AAC77130.1 (AE000489) GTP - binding subunit of protease specific for</p>

TABLEAU I

SEQ ID n°1544	Prot n°PL-2371.1	Contig41	980239	981180	84%	<p>Identities = 248/313 (79%), Positives = 275/313 (87%)</p> <p>sp P16384 IMIAA_ECOLI TRNA DELTA(2)-ISOPENTENYL PYROPHOSPHATE TRANSFERASE (IPP TRANSFERASE) pir B37318 delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.-) - Escherichia coli gb AA24174.1 (M63655) delta(2)-isopentenyl pyrophosphate transferase [Escherichia coli] gb AAA97067.1 (U14003) rRNA delta(2)-isopentenylpyrophosphate (IPP) transferase [Escherichia coli] gb AAC77128.1 (AE000489) delta(2)-isopentenylpyrophosphate rRNA-adenosine transferase [Escherichia coli] db BAA22627.1 (AB000785) tRNA delta 2-isopentenylpyrophosphate transferase [Shigella flexneri]</p> <p>Identities = 398/633 (62%), Positives = 478/633 (74%), Gaps = 17/633 (2%)</p> <p>sp P14161 MUTL_SALTY DNA MISMATCH REPAIR PROTEIN MUTL pir A33588 mismatch repair protein mutL - Salmonella typhimurium gb AAA27166.1 (M29887) mismatch repair protein [Salmonella typhimurium]</p>
SEQ ID n°1545	Prot n°PL-2372.1	Contig41	981173	983088	75%	
SEQ ID n°1546	Prot n°PL-2373.2	Contig41	983078	984337		
SEQ ID n°1547	Prot n°PL-2374.2	Contig41	985012	986169		
SEQ ID n°1548	Prot n°PL-2375.2	Contig37	489067	490278		
SEQ ID n°1549	Prot n°PL-2376.1	Contig37	485265	487016	44%	<p>Identities = 171/529 (32%), Positives = 260/529 (48%), Gaps = 48/529 (9%)</p> <p>pir B75371 ABC transporter, ATP-binding protein, EF-3 family - Deinococcus radiodurans (strain R1) gb AAF1195.1 AE002007_1 (AE002007) ABC transporter, ATP-binding protein, EF-3 family [Deinococcus radiodurans] Length = 705</p>
SEQ ID n°1550	Prot n°PL-2377.1	Contig37	484023	485114	95%	<p>Identities = 338/363 (93%), Positives = 351/363 (96%)</p> <p>sp P31216 YCHF_ECOLI PROBABLE GTP-BINDING PROTEIN IN TREA-PTH INTERGENIC REGION (ORF-3) pir H64866 probable GTP-binding protein ychF - Escherichia coli gb AAC74287.1 (AE000219) putative GTP-binding protein [Escherichia coli] db BAA36061.1 (D90756) Probable GTP-binding protein in pth 3'region (orf-3) [Escherichia coli] Length = 363</p>
SEQ ID n°1551	Prot n°PL-2378.1	Contig37	480947	482917	8%	<p>Identities = 49/96 (51%), Positives = 59/96 (61%), Gaps = 1/96 (1%)</p> <p>ref NP_050653.1 S. sp Q9T1V0 VPS_BPMU TAIL FIBER PROTEIN (GPS) gb AAF01127.1 AF083977_48 (AF083977) S [Bacteriophage Mu]</p>
SEQ ID n°1552	Prot n°PL-2379.1	Contig37	475363	480543	38%	<p>Identities = 418/1498 (27%), Positives = 864/1498 (43%), Gaps = 159/1498 (10%)</p> <p>pir D64962 probable membrane protein b1978 - Escherichia coli gb AAC75042.1 (AE000289) putative factor [Escherichia coli] Length = 2383</p>
SEQ ID n°1553	Prot n°PL-238.1	Contig41	400166	400930	No Hits found	
SEQ ID n°1554	Prot n°PL-2380.2	Contig37	473061	474563		
SEQ ID n°1555	Prot n°PL-2381.1	Contig37	470974	472503	No Hits found	
SEQ ID n°1556	Prot n°PL-2382.1	Contig37	469089	470675	No Hits found	
SEQ ID n°1557	Prot n°PL-2383.1	Contig37	467151	468758	No Hits found	

TABLEAU I

SEQ ID n°1558	Prot n°PL-2385.2	Contig37	465059	466384	No Hits found	
SEQ ID n°1559	Prot n°PL-2386.1	Contig37	463976	464953		
SEQ ID n°1560	Prot n°PL-2387.1	Contig37	462178	463125	91%	<p>Identities = 289/315 (94%), Positives = 308/315 (98%)</p> <p>sp P08330 KPRS_ECOLI RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE) pir KIECRY ribose-phosphate pyrophosphokinase (EC 2.7.6.1) - Escherichia coli gblAAC74291.1 (AE000219) phosphoribosylpyrophosphate synthetase [Escherichia coli] dbj BAA36065.1 (D90756) Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) (phosphoribosyl pyrophosphate synthetase). [Escherichia coli] Length = 315</p>
SEQ ID n°1561	Prot n°PL-2388.1	Contig37	461224	462114	75%	<p>Identities = 190/279 (68%), Positives = 224/279 (80%) sp P24209 PK_ECOLI ISOPENTENYL MONOPHOSPHATE KINASE (4-CYTIDINE-5'-DIPHOSPHO)-2-C-METHYL-D-ERYTHRITOL KINASE) pir B47706 ychB protein - Escherichia coli gblAAA24434.1 (M77237) ORF2 [Escherichia coli] gblAAC43434.1 (U18555) orf gene product [Escherichia coli] gblAAC74292.1 (AE000219) orf, hypothetical protein [Escherichia coli] dbj BAA36066.1 (D90756) 31k hypothetical protein (5' of prs) [Escherichia coli] gblAAF13867.1 (AF179284) isopentenyl monophosphate kinase [Escherichia coli] emb CAB64963.1 (AJ249325) isopentenyl monophosphate kinase [Escherichia coli] gblAAF29530.1 (AF216300) 4-diphosphocytidyl-2C-methyl-D-erythritol kinase [Escherichia coli] dbj BAA94247.1 (AB037116) 4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase [Escherichia coli] Length = 283</p>
SEQ ID n°1562	Prot n°PL-2389.1	Contig37	460613	461239	68%	<p>Identities = 122/207 (58%), Positives = 152/207 (72%), Gaps = 2/207 (0%) sp P24208 LOLB_ECOLI OUTER MEMBRANE LIPOPROTEIN LOLB PRECURSOR pir A47708 5-aminolevulinate synthase (EC 2.3.1.37) hemM - Escherichia coli gblAAA24433.1 (M77237) ORF1 [Escherichia coli] dbj BAA36067.1 (D90756) 22k hypothetical protein (3' of hema) [Escherichia coli] gblAAC74293.1 (AE000219) an enzyme in main pathway of synthesis of 5-aminolevulinate, possibly glutamyl-tRNA dehydrogenase [Escherichia coli] Length = 207</p>
SEQ ID n°1563	Prot n°PL-239.1	Contig41	400906	401715	36%	<p>Identities = 56/198 (28%), Positives = 98/198 (49%), Gaps = 1/198 (0%) pir B70567 probable mhpE protein - Mycobacterium tuberculosis (strain H37RV) emb CAB08693.1 (Z95390) mhpE [Mycobacterium tuberculosis] Length = 336</p>

TABLEAU I

SEQ ID n°1564	Prot n°PL-2390.1	Contig37	458973	460235	85%	<p>Identities = 320/418 (76%), Positives = 364/418 (86%)</p> <p>sp P13580 HEM1_ECOLI GLUTAMYL-TRNA REDUCTASE (GLUTR) pir J13VECHA glutamyl-tRNA reductase (EC 1.2.1.-) - Escherichia coli gb AA233654.1 (M25323) delta-aminolevulinic synthase (EC 2.3.1.37) [Escherichia coli] dbj BAA36088.1 (D90756) Glutamyl-tRNA reductase (EC 1.2.1.-) (gluTR). [Escherichia coli] gb AAC74294.1 (AE000219) enzyme in alternate path of synthesis of 5-aminolevulinate [Escherichia coli]</p> <p>Identities = 299/360 (83%), Positives = 338/360 (93%) sp P07011 RF1_ECOLI PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1) pir FCECR1 translation releasing factor RF-1 - Escherichia coli dbj BAA36069.1 (D90756) Peptide chain release factor 1 (rf-1). [Escherichia coli] dbj BAA36079.1 (D90757) Peptide chain release factor 1 (rf-1). [Escherichia coli] gb AAC74295.1 (AE000219) peptide chain release factor RF-1 [Escherichia coli] Length = 360</p>
SEQ ID n°1565	Prot n°PL-2391.1	Contig37	457859	458941	92%	
SEQ ID n°1566	Prot n°PL-2392.1	Contig37	457011	457859	73%	<p>Identities = 181/275 (65%), Positives = 214/275 (77%)</p> <p>sp P37186 HEMK_ECOLI HEMK PROTEIN pir J183570 hemK protein (EC 1.3.3.-) - Escherichia coli gb AAC43438.1 (U18555) possible protoporphyrinogen oxidase [Escherichia coli] dbj BAA36070.1 (D90756) Protoporphyrinogen oxidase (EC 1.3.3.4) hemK [Escherichia coli] dbj BAA36080.1 (D90757) Protoporphyrinogen oxidase (EC 1.3.3.4) hemK [Escherichia coli] gb AAC74296.1 (AE000219) possible</p>
SEQ ID n°1567	Prot n°PL-2393.1	Contig37	456218	457027	74%	<p>Identities = 157/269 (58%), Positives = 206/269 (76%)</p> <p>sp P20101 YCHA_ECOLI HYPOTHETICAL 30.8 KDA PROTEIN IN HEMK- KDSA INTERGENIC REGION pir J183572 ychaA protein - Escherichia coli gb AAC43440.1 (U18555) orf1 gene product [Escherichia coli] gb AAC74298.1 (AE000219) orf, hypothetical protein [Escherichia coli] dbj BAA36072.1 (D90756) Hypothetical protein 1 (ksdA 3' region) [Escherichia coli] dbj BAA36082.1 (D90757) Hypothetical protein 1 (ksdA 3' region)</p>

TABLEAU I

SEQ ID n°1568	Prot n°PL-2394.1	Contig37	455208	456082	90%	<p>Identities = 253/284 (89%), Positives = 271/284 (95%)</p> <p>sp P17579 KDSA_ECOLI_2-DEHYDRO-3-DEOXYPHOSPHOCTONATE ALDOLASE (PHOSPHO-2-DEHYDRO-3-DEOXYOCTONATE (3-DEOXY-D-MANNO-OCTULOSONIC ACID 8-PHOSPHATE SYNTHETASE) (KDO-8-PHOSPHATE SYNTHETASE) (KDO 8-P SYNTHASE) p I 183573 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase - Escherichia coli p I SYECOL_2-dehydro-3-deoxyphosphoaldolase (EC 4.1.2.16) - Escherichia coli p I 1D9E A Chain A, Structure Of E. Coli Kdo8p Synthase p I 1D9E B Chain B, Structure Of E. Coli Kdo8p Synthase p I 1D9E C Chain C, Structure Of E. Coli Kdo8p Synthase p I 1D9E D Chain D, Structure Of E. Coli Kdo8p Synthase gb AAC43441.1 (U18555) 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase [Escherichia coli] db JBA38073.1 (D90756) 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase [Escherichia coli] db JBA38083.1 (D90757) 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase [Escherichia coli] db JBA38084.1 (D90756) Hypothetical protein in pth-prsA intergenic region. [Escherichia coli] Length = 550</p>
SEQ ID n°1569	Prot n°PL-2395.1	Contig37	453332	455092	79%	<p>Identities = 386/553 (69%), Positives = 469/553 (84%), Gaps = 4/553 (0%)</p> <p>sp P40877 YCHM_ECOLI_HYPOTHETICAL_58.4 KDA PROTEIN IN PTH-PRSA INTERGENIC REGION p I C64887 probable sulfate transport protein ychM - Escherichia coli gb AAC74290.1 (AE000219) orf, hypothetical protein [Escherichia coli] db JBA38084.1 (D90756) Hypothetical protein in pth-prsA intergenic region. [Escherichia coli] Length = 550</p>
SEQ ID n°1570	Prot n°PL-2396.1	Contig37	451928	452620	45%	<p>Identities = 68/234 (29%), Positives = 106/234 (45%), Gaps = 14/234 (5%)</p> <p>emb CAB83827.1 (AL162753) putative 3-oxoacyl-lacyl-carrier protein reductase [Neisseria meningitidis] Length = 248</p>
SEQ ID n°1571	Prot n°PL-2397.1	Contig37	449582	451333	50%	<p>Identities = 210/596 (35%), Positives = 297/596 (49%), Gaps = 60/596 (10%)</p> <p>sp P74178 YB78_SYNY3_HYPOTHETICAL_69.1 KD PROTEIN SLL1178 p I S75808 nodulation protein - Synecocystis sp. (strain PCC 6803) db JBA18267.1 (D90913) nodulation protein [Synecocystis sp.] Length = 615</p>
SEQ ID n°1572	Prot n°PL-2398.1	Contig37	446557	447999	96%	<p>Identities = 459/480 (95%), Positives = 472/480 (97%) gb AAA27617.1 (M90093) fatty acid reductase [Xenorhabdus luminescens] gb AAG09987.1 (AF251497_5 (AF251497) fatty acid reductase [cloning vector HKBS1] Length = 480</p>
SEQ ID n°1573	Prot n°PL-2399.1	Contig37	445621	446544	95%	<p>Identities = 292/307 (95%), Positives = 298/307 (96%) p I D39853 acyltransferase (EC 2.3.1.-) LuxD - Xenorhabdus luminescens Length = 307</p>
SEQ ID n°1574	Prot n°PL-24.1	Contig41	41824	43414	65%	<p>Identities = 226/478 (47%), Positives = 329/478 (68%), Gaps = 5/478 (1%) gb AAD45415.1 (U65001) salicylaldehyde dehydrogenase [Sphingomonas sp.] Length = 499</p>

TABLEAU I

SEQ ID n°1575	Prot n°PL-240.1	Contig41	401721	403367	29%	Identities = 87/394 (22%), Positives = 164/394 (41%), Gaps = 66/394 (16%) gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae] Length = 552
SEQ ID n°1576	Prot n°PL-2400.1	Contig37	444365	445444	97%	Identities = 349/359 (97%), Positives = 355/359 (98%) spiP19839 LXA1_PHOLU ALKANAL MONOOXYGENASE ALPHA CHAIN (BACTERIAL LUCIFERASE ALPHA CHAIN) pir B35411 alkanal monooxygenase (FMN-linked) [EC 1.14.14.3] alpha chain - Xenorhabdus luminescens gb AAA27619.1 (M90083) luciferase [Xenorhabdus luminescens] gb AAA27623.1 (M57416) luciferase alpha subunit [Xenorhabdus luminescens] gb AAA27626.1 (M55977) luciferase alpha subunit [Xenorhabdus luminescens] gb AAG0985.1 AF251497_3
SEQ ID n°1577	Prot n°PL-2401.1	Contig37	443373	444347	92%	Identities = 306/325 (94%), Positives = 314/325 (96%) monooxygenase (FMN-linked) (EC 1.14.14.3) beta chain - Xenorhabdus luminescens gb AAA27627.1 (M55977) luciferase beta subunit [Xenorhabdus luminescens] Length = 327
SEQ ID n°1578	Prot n°PL-2402.1	Contig37	442199	443311	94%	Identities = 345/370 (93%), Positives = 357/370 (96%) (M90093) luxE [Xenorhabdus luminescens] gb AAG0983.1 AF251497_1 (AF251497) LuxE [cloning vector HKBS1] Length = 370
SEQ ID n°1579	Prot n°PL-2403.1	Contig37	441449	442153	39%	Identities = 58/173 (33%), Positives = 93/173 (53%), Gaps = 22/173 (12%) spiP44217 YE92_HAEIN HYPOTHETICAL PROTEIN HI1492 PRECURSOR pir B64032 hypothetical protein HI1492 - Haemophilus influenzae (strain Rd KW20) gb AAC23144.1 (U32826) H. influenzae predicted coding region HI1492 [Haemophilus influenzae Rd] Length = 168
SEQ ID n°1580	Prot n°PL-2404.1	Contig37	439313	440254	68%	Identities = 174/315 (55%), Positives = 218/315 (68%), Gaps = 1/315 (0%) spiP75913 YCDW_ECOLI PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN PHOH-CSGG INTERGENIC REGION pir JF64845 probable 2-hydroxyacid dehydrogenase ycdW - Escherichia coli gb AAC74117.1 (AE000205) putative dehydrogenase [Escherichia coli] Length = 325
SEQ ID n°1581	Prot n°PL-2405.1	Contig37	438701	439252	68%	Identities = 109/181 (60%), Positives = 139/181 (76%), Gaps = 1/181 (0%) spiP75915 YCDY_ECOLI HYPOTHETICAL 20.7 KDA PROTEIN IN PHOH-CSGG INTERGENIC REGION pir JH64845 ycdY protein - Escherichia coli gb AAC74119.1 (AE000205) putative oxidoreductase component [Escherichia coli] dbj BAA35816.1 (D90740) Hypothetical protein HI1543 [Escherichia coli] dbj BAA35825.1 (D90741) Hypothetical protein HI1543 [Escherichia coli] Length = 184
SEQ ID n°1582	Prot n°PL-2406.1	Contig37	437947	438510	65%	Identities = 100/186 (53%), Positives = 134/186 (71%) spiP09895 YCEB_ECOLI PROTEIN YCEB pir JQCECP5 yceB protein - Escherichia coli emb CAA28156.1 (X04469) URF [Escherichia coli] gb AAC74147.1 (AE000207) orf, hypothetical protein [Escherichia coli] dbj BAA35871.1 (D90743) Hypothetical 20.5 kd protein in pyrC3 region.

TABLEAU I

SEQ ID n°1583	Prot n°PL-2407.1	Contig37	436704	437909	85%	Identities = 292/398 (73%), Positives = 345/398 (86%) permease b1065 - Escherichia coli gb AAC74149.1 (AE000207) orf. hypothetical protein [Escherichia coli] dbj BAA35873.1 (D90743) Hypothetical 44.7 kd protein in glnQ-ansR intergenic region. [Escherichia coli] Length = 412
SEQ ID n°1584	Prot n°PL-2408.1	Contig37	432999	434534	88%	Identities = 411/510 (80%), Positives = 459/510 (89%) sp P37169 MVIN_SALTY VIRULENCE FACTOR MVIN pir S40271 virulence factor mvn - Salmonella typhimurium emb CAA81134.1 (Z26133) mvIB [Salmonella typhimurium] dbj BAA04980.1 (D25292) ORF2 [Salmonella] Identities = 471/577 (81%), Positives = 517/577 (89%), Gaps = 1/577 (0%)
SEQ ID n°1585	Prot n°PL-2409.1	Contig37	430904	432634	89%	sp P11875 SYR_ECOCI ARGINYL-TRNA SYNTHETASE (ARGININE--TRNA LIGASE) (ARGRS) pir SYECRT arginine--trna ligase (EC 6.1.1.19) - Escherichia coli emb CAA33384.1 (X15320) arginyl-trna-synthetase (AA 1- 577) [Escherichia coli] dbj BAA15686.1 (D90829) Arginine--trna ligase (EC 6.1.1.19) [Escherichia coli] dbj BAA15693.1 (D90830) Arginine--trna ligase (EC 6.1.1.19) [Escherichia coli] gb AAC74846.1 (AE000281) arginine trna synthetase [Escherichia coli] Length = 577
SEQ ID n°1586	Prot n°PL-241.1	Contig41	403657	404916	47%	Identities = 122/377 (32%), Positives = 198/377 (52%), Gaps = 2/377 (0%) emb CAB72528.1 (AL139074) putative efflux protein [Campylobacter jejuni] Length = 400
SEQ ID n°1587	Prot n°PL-2410.1	Contig37	429758	430549	32%	Identities = 51/200 (25%), Positives = 87/200 (43%), Gaps = 23/200 (11%) emb CAC11861.1 (AL445065) conserved hypothetical protein [Thermoplasma acidophilum] Length = 220
SEQ ID n°1588	Prot n°PL-2411.1	Contig37	428654	429208	63%	Identities = 116/180 (64%), Positives = 142/180 (78%) membrane protein b1057 - Escherichia coli gb AAC74141.1 (AE000207) putative cytochrome [Escherichia coli] dbj BAA35855.1 (D90742) Cytochrome b561 [Escherichia coli] dbj BAA35866.1 (D90743) Cytochrome b561 [Escherichia coli] Length = 188
SEQ ID n°1589	Prot n°PL-2412.1	Contig37	425835	426398	61%	Identities = 109/189 (57%), Positives = 134/189 (70%), Gaps = 4/189 (2%) sp P52007 YECM_ECOCI HYPOTHETICAL 21.2 KD PROTEIN IN CUTC- ARGS INTERGENIC REGION Length = 188
SEQ ID n°1590	Prot n°PL-2413.2	Contig37	424072	424818		Identities = 242/323 (74%), Positives = 278/323 (85%) sp P76291 YECP_ECOCI HYPOTHETICAL 37.0 KD PROTEIN IN ASPS-BISZ INTERGENIC REGION pir G64949 probable S-adenosylmethionine- dependent methyltransferase yecP - Escherichia coli dbj BAA15681.1 (D90829) ORF_ID:0337#12-similar to [SwissProt Accession Number P44197] [Escherichia coli] gb AAC74941.1 (AE000280) putative enzyme [Escherichia coli] Length = 323
SEQ ID n°1591	Prot n°PL-2414.1	Contig37	422925	423896	85%	

TABLEAU I

SEQ ID n°1592	Prot n°PL-2415.1	Contig37	422170	422928	77%	<p>Identities = 190/242 (78%), Positives = 218/242 (89%)</p> <p>sp P76290 YECO_ECOLI HYPOTHETICAL 27.8 KD PROTEIN IN ASPS-BISZ INTERGENIC REGION pir F84949 probable S-adenosylmethionine-dependent methyltransferase yeco - Escherichia coli dbj BAA15680.1 (D90829) ORF_ID: o337#11 - similar to [SwissProt Accession Number P43985] [Escherichia coli] gb AAC74940.1 (AE000280) orf, hypothetical protein [Escherichia coli] Length = 247</p>
SEQ ID n°1593	Prot n°PL-2416.1	Contig37	419983	420627	No Hits found	<p>Identities = 476/589 (80%), Positives = 522/589 (87%) sp P21889 SYD_ECOLI ASPARTYL-TRNA SYNTHETASE (ASPARTATE-TRNA LIGASE) (ASPRS) pir SYECD aspartate-tRNA ligase (EC 6.1.1.12) - Escherichia coli pdb 1EQRI9 Chain A, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia coli pdb 1EQRI9 Chain B, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia coli pdb 1EQRI9 Chain C, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia coli emb CAA37856.1 (X53863) aspartate-tRNA ligase [Escherichia coli] dbj BAA15677.1 (D90829) Aspartate-tRNA ligase (EC 6.1.1.12) [Escherichia coli] gb AAC74936.1 (AE000280) aspartate tRNA synthetase [Escherichia coli] Length = 590</p>
SEQ ID n°1594	Prot n°PL-2417.1	Contig37	418795	420567	84%	
SEQ ID n°1595	Prot n°PL-2418.1	Contig37	417585	418328	88%	<p>Identities = 207/247 (83%), Positives = 228/247 (91%), Gaps = 1/247 (0%) sp P24237 YECB_ECOLI HYPOTHETICAL 26.4 KD PROTEIN IN RUVC-ASPS INTERGENIC REGION pir C38113 yecC protein - Escherichia coli emb CAA42126.1 (X59551) ORF246 [Escherichia coli] dbj BAA01031.1 (D10165) Orf26 [Escherichia coli] dbj BAA15675.1 (D90829) ORF_ID: o337#5 - similar to [PIR Accession Number C38113] [Escherichia coli] gb AAC74934.1 (AE000280) orf, hypothetical protein [Escherichia coli] Length = 246</p>
SEQ ID n°1596	Prot n°PL-2419.1	Contig37	416128	416745	85%	<p>Identities = 160/205 (78%), Positives = 182/205 (88%), Gaps = 2/205 (0%) sp P08576 RUA_ECOLI HOLLIDAY JUNCTION DNA HELICASE RUVA pir BVECRV ruvA protein - Escherichia coli pdb 1C7Y1A Chain A, E. coli Ruva Holliday Junction Complex pdb 1HJP Holliday Junction Binding Protein Ruva From E. coli pdb 1BDX1A Chain A, E. coli Ruva With Bound Dna Holliday Junction, Alpha Carbons And Phosphate Atoms Only pdb 1BDX1B Chain B, E. coli Ruva With Bound Dna Holliday Junction, Alpha Carbons And Phosphate Atoms Only pdb 1BDX1C Chain C, E. coli Ruva With Bound Dna Holliday Junction, Alpha Carbons And Phosphate Atoms Only pdb 1BDX1D Chain D, E. coli Ruva With Bound Dna Holliday Junction, Alpha Carbons And Phosphate Atoms Only gb AAA24612.1 (M21298) ruvA protein (gtg start) [Escherichia coli] dbj BAA15672.1 (D90829) Ruva protein [Escherichia coli] gb AAC74931.1 (AE000280) Holliday junction helicase subunit B; branch migration; repair [Escherichia coli]</p>

TABLEAU I

SEQ ID n°1597	Prot n°PL-242.1	Contig41	405765	407218	85%	<p>Identities = 379/480 (78%), Positives = 424/480 (87%) pir D665118 pantothenate permease - Escherichia coli gb AAA58061.1 (U18997) pantothenate permease [Escherichia coli] gb AAC76290.1 (AE000404) sodium/pantothenate symporter [Escherichia coli] Length = 485</p> <p>Identities = 277/330 (83%), Positives = 302/330 (90%) spiP08577 RUVB_ECOLI HOLLIDAY JUNCTION DNA HELICASE RUVB pir BVECVB DNA-binding protein ruvB - Escherichia coli emb CAA30120.1 (X07091) ruvB gene product (AA 1 - 336) [Escherichia coli] gb AA24813.1 (M21298) ruvB protein [Escherichia coli] dbj BAA15671.1 (D90829) Holliday junction DNA helicase RuvB. [Escherichia coli] gb AAC74930.1 (AE000280) Holliday junction helicase subunit A; branch migration; repair</p>
SEQ ID n°1598	Prot n°PL-2420.1	Contig37	415104	416111	89%	<p>Identities = 211/258 (81%), Positives = 241/258 (92%) spiP39832 ZNUB_ECOLI HIGH-AFFINITY ZINC UPTAKE SYSTEM MEMBRANE PROTEIN ZNUB pir C64948 probable membrane protein yebL - Escherichia coli dbj BAA15667.1 (D90828) ORF_ID:0336gap#12; similar to [SwissProt Accession Number P39832] [Escherichia coli] dbj BAA15670.1 (D90828) ORF_ID:0336gap#12~similar to [SwissProt Accession Number P39832] [Escherichia coli] gb AAC74928.1 (AE000280) orf, hypothetical protein [Escherichia coli] Length = 261 "</p>
SEQ ID n°1599	Prot n°PL-2421.1	Contig37	414105	414890	90%	<p>Identities = 183/254 (72%), Positives = 213/254 (83%), Gaps = 5/254 (1%) spiP52648 ZNUC_ECOLI HIGH-AFFINITY ZINC UPTAKE SYSTEM ATP- BINDING PROTEIN ZNUC pir B64948 probable ABC transport system ATP- binding protein yebM - Escherichia coli dbj BAA15666.1 (D90828) Sulfate transport ATP-binding protein CysA. [Escherichia coli] gb AAC74928.1 (AE000280) putative ATP-binding component of a transport system [Escherichia coli] Length = 251</p>
SEQ ID n°1600	Prot n°PL-2422.1	Contig37	413311	414108	75%	<p>Identities = 185/315 (58%), Positives = 235/315 (73%), Gaps = 7/315 (2%) spiP39172 ZNUA_ECOLI HIGH-AFFINITY ZINC UPTAKE SYSTEM PROTEIN ZNUA PRECURSOR pir A64948 adhesin homolog yebL precursor - Escherichia coli dbj BAA15665.1 (D90828) 31.1 KD protein in msbB-ruvB intergenic region precursor. [Escherichia coli] gb AAC74927.1 (AE000280) putative adhesin [Escherichia coli] Length = 328</p>
SEQ ID n°1601	Prot n°PL-2423.1	Contig37	412311	413156	71%	<p>Identities = 270/422 (63%), Positives = 317/422 (74%), Gaps = 11/422 (2%) spiP24204 YEBA_ECOLI HYPOTHETICAL 46.7 KD PROTEIN IN MSBB- RUVB INTERGENIC REGION (ORFU) pir H64947 membrane protein yeba - Escherichia coli dbj BAA15664.1 (D90828) Lysoastaphin precursor (EC 3.5.1.-). [Escherichia coli] gb AAC74926.1 (AE000279) orf, hypothetical protein [Escherichia coli] Length = 419</p>
SEQ ID n°1602	Prot n°PL-2424.1	Contig37	410983	412290	72%	

TABLEAU I

SEQ ID n°1603	Prot n°PL-2425.1	Contig37	409863	410831	68%	<p>Identities = 201/310 (64%), Positives = 246/310 (78%)</p> <p>sp P24205 MSBB_ECOLI_LIPID A BIOSYNTHESIS (KDO)2-(LAUROYL)-LIPID IVa ACYLTRANSFERASE pir A42808 (Kdo)2-(lauroyl)-lipid IV4 acyltransferase (EC 2.3.1.-) - Escherichia coli gb AA96706.1 (M87660) originally thought to be a lytic transglycosylase designated Mit [Escherichia coli] gb AA24181.1 (M77039) msbB [Escherichia coli] dbj BAA15663.1 (D90828) Membrane-bound lytic transglycosylase [Escherichia coli] gb AAC74925.1 (AE000279) suppressor of htrB, heat shock protein [Escherichia coli] Length = 323</p>
SEQ ID n°1604	Prot n°PL-2426.1	Contig37	408220	409862	91%	<p>Identities = 417/480 (86%), Positives = 442/480 (91%)</p> <p>sp P21599 KPY2_ECOLI PYRUVATE KINASE II (PK-2) pir S29790 pyruvate kinase (EC 2.7.1.40) A - Escherichia coli gb AA24473.1 (M83703) pyruvate kinase type II [Escherichia coli] dbj BAA15662.1 (D90828) Pyruvate kinase (EC 2.7.1.40) [Escherichia coli] gb AAC74924.1 (AE000279) pyruvate kinase II, glucose stimulated [Escherichia coli] Length = 480</p>
SEQ ID n°1605	Prot n°PL-2427.1	Contig37	406543	407604	26%	<p>Identities = 60/215 (27%), Positives = 94/215 (42%), Gaps = 50/215 (23%)</p> <p>ref NP_049863.1 tail fiber sp P03744 VIG37_BPT4 LONG TAIL FIBER PROTEIN P37 (PROTEIN GP37) (RECEPTOR RECOGNIZING PROTEIN) pir JTLBP74 tail fiber protein gp37 - phage T4 emb CAA24228.1 (V00863) gene 37 [coliphage T4] gb AAA32514.1 (J02509) tail fiber protein 37 [Bacteriophage T4] gb AAD42460.1 (AF158101_47 (AF158101) tail fiber [Bacteriophage T4] Length = 1026</p>
SEQ ID n°1606	Prot n°PL-2428.1	Contig37	405285	406196	41%	<p>Identities = 97/256 (37%), Positives = 127/256 (48%), Gaps = 49/256 (19%)</p> <p>pir S18689 Sc/SvP protein - Escherichia coli plasmid p15B emb CAA44052.1 (X62121) DNA inversion product [Escherichia coli] Length = 753</p>
SEQ ID n°1607	Prot n°PL-2429.1	Contig37	403952	404821	87%	<p>Identities = 222/280 (79%), Positives = 253/280 (90%)</p> <p>sp P46118 YEBK_ECOLI HYPOTHETICAL 32.0 KD PROTEIN IN PYKA-ZWF INTERGENIC REGION pir E64947 yebK protein - Escherichia coli dbj BAA15661.1 (D90828) RpiR protein. [Escherichia coli] gb AAC74923.1 (AE000279) orf, hypothetical protein [Escherichia coli] Length = 289</p>
SEQ ID n°1608	Prot n°PL-243.1	Contig41	407259	408149	84%	<p>Identities = 234/292 (80%), Positives = 255/292 (87%)</p> <p>sp P28637 PRMA_ECOLI RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE pir P949924 ribosomal protein L11 methyltransferase (EC 2.1.1.-) - Escherichia coli gb AAB28769.1 (S67010) ribosomal protein L11 methyltransferase; PrmA [Escherichia coli]</p>
SEQ ID n°1609	Prot n°PL-2430.1	Contig37	402519	403154	No Hits found	<p>Identities = 415/491 (84%), Positives = 445/491 (90%)</p> <p>sp P37986 G6PD_ERWCH GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (G6PD) pir S37053 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Erwinia chrysanthemi emb CAA52858.1 (X74866) glucose-6-phosphate 1-dehydrogenase [Erwinia chrysanthemi] Length = 491</p>
SEQ ID n°1610	Prot n°PL-2431.1	Contig37	402141	403616	87%	

TABLEAU I

SEQ ID n°1611	Prot n°PL-2432.2	Contig37	398641	398563		
SEQ ID n°1612	Prot n°PL-2433.1	Contig37	394762	395457	78%	<p>Identities = 160/231 (69%), Positives = 183/231 (78%), Gaps = 1/231 (0%) sp P76256 YEAZ_ECOLI HYPOTHETICAL 25.2 KD PROTEIN IN FADD-PABB INTERGENIC REGION pir G64941 hypothetical protein b1807 - Escherichia coli (strain K-12) dbj BAA15611.1 (D90824) O-sialoglycoprotein endopeptidase (EC 3.4.24.57) (Glycoprotease). [Escherichia coli] dbj BAA15616.1 (D90825) O-sialoglycoprotein endopeptidase (EC 3.4.24.57) (Glycoprotease). [Escherichia coli] gb AAC74877.1 (AE000275) ori, hypothetical protein [Escherichia coli] Length = 231</p>
SEQ ID n°1613	Prot n°PL-2434.1	Contig37	394100	394714	61%	<p>Identities = 98/176 (55%), Positives = 127/176 (71%), Gaps = 5/176 (2%) pir F64941 md protein - Escherichia coli dbj BAA15610.1 (D90824) Outer membrane protein SLP precursor. [Escherichia coli] dbj BAA15615.1 (D90825) Outer membrane protein SLP precursor. [Escherichia coli] gb AAC74876.1 (AE000275) putative outer membrane protein [Escherichia coli] Length = 193</p>
SEQ ID n°1614	Prot n°PL-2435.1	Contig37	391551	393233	85%	<p>Identities = 430/561 (76%), Positives = 482/561 (85%), Gaps = 1/561 (0%) sp P29212 LCFA_ECOLI LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG- CHAIN ACYL-COA SYNTHETASE) pir S41589 long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) - Escherichia coli emb CAA50321.1 (X70994) acyl- coenzyme A synthetase [Escherichia coli] dbj BAA15609.1 (D90824) Long- chain-fatty-acid--CoA ligase (EC 6.2.1.3) (Long-chain acyl-CoA synthetase) [Escherichia coli] dbj BAA15614.1 (D90825) Long-chain-fatty- acid--CoA ligase (EC 6.2.1.3) (Long-chain acyl-CoA synthetase). [Escherichia coli] gb AAC74875.1 (AE000275) acyl-CoA synthetase, long- chain-fatty-acid--CoA ligase [Escherichia coli] Length = 561</p>
SEQ ID n°1615	Prot n°PL-2436.1	Contig37	390328	391455	77%	<p>Identities = 240/374 (64%), Positives = 293/374 (78%) sp P09155 RND_ECOLI RIBONUCLEASE D (RNASE D) pir JNRECD ribonuclease III (EC 3.1.26.3) md - Escherichia coli emb CAA30098.1 (X07055) ribonuclease D (AA 1-375) (start codon uug) [Escherichia coli] dbj BAA15599.1 (D90823) Ribonuclease D (EC 3.1.13.-) [Escherichia coli] dbj BAA15608.1 (D90824) Ribonuclease D (EC 3.1.13.-) [Escherichia coli] gb AAC74874.1 (AE000274) RNase D, processes rRNA precursor [Escherichia coli] pir 1410308A ribonuclease D [Escherichia coli] Length = 375</p>
SEQ ID n°1616	Prot n°PL-2437.1	Contig37	389102	389914	90%	<p>Identities = 246/270 (91%), Positives = 258/270 (94%) sp P18197 MINI_ECOLI SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND) pir JCCECID cell division inhibitor mind - Escherichia coli gb AAB59082.1 (J03153) MinD protein [Escherichia coli] dbj BAA36009.1 (D90751) Cell division inhibitor MinD. [Escherichia coli] dbj BAA36022.1 (D90752) Cell division inhibitor MinD. [Escherichia coli] gb AAC74259.1 (AE000216) cell division inhibitor, a membrane ATPase, activates minC [Escherichia coli] Length = 270</p>

TABLEAU I

SEQ ID n°1617	Prot n°PL-2438.1	Contig37	388395	389078	78%	Identities = 140/231 (60%), Positives = 178/231 (76%), Gaps = 6/231 (2%) sp P18166 MINC_ECOLI_CELL_DIVISION_INHIBITOR_MINC_pir CEECIC cell division inhibitor minC - Escherichia coli gb AAB59061.1 (J03153) MinC protein [Escherichia coli] db BAA36010.1 (D90751) Cell division inhibitor MinC [Escherichia coli] db BAA36023.1 (D90752) Cell division inhibitor MinC [Escherichia coli] gb AAC74260.1 (AE000216) cell division inhibitor, inhibits fisZ ring formation [Escherichia coli] Length = 231
SEQ ID n°1618	Prot n°PL-2439.1	Contig37	386970	387626	80%	Identities = 155/219 (70%), Positives = 178/219 (80%), Gaps = 1/219 (0%) sp P76004 YCGM_ECOLI_PROTEIN_YCGM_pir A64864 probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase b1180 - Escherichia coli gb AAC74264.1 (AE000216) putative isomerase [Escherichia coli] db BAA36014.1 (D90751) ZK988.3 protein [Escherichia coli] Length = 231
SEQ ID n°1619	Prot n°PL-244.1	Contig41	408412	409398	88%	Identities = 276/320 (86%), Positives = 298/320 (92%) gb AAC77884.1 (AF040379) yndG homolog [Proteus vulgaris] Length = 323
SEQ ID n°1620	Prot n°PL-2440.1	Contig37	385567	386211	No Hits found	
SEQ ID n°1621	Prot n°PL-2441.1	Contig37	384750	385373	No Hits found	
SEQ ID n°1622	Prot n°PL-2442.2	Contig37	382990	383994		
SEQ ID n°1623	Prot n°PL-2443.2	Contig30	90015	90809		
SEQ ID n°1624	Prot n°PL-2444.1	Contig30	88244	89443	40%	Identities = 101/390 (25%), Positives = 163/390 (40%), Gaps = 9/390 (2%) gb AAF84513.1 AE003994_12 (AE003994) hypothetical protein [Xylella fastidiosa] Length = 387
SEQ ID n°1625	Prot n°PL-2445.1	Contig30	87146	87913	46%	Identities = 90/239 (37%), Positives = 118/239 (48%), Gaps = 38/239 (15%) gb AAF84403.1 AE003987_7 (AE003987) hypothetical protein [Xylella fastidiosa] Length = 213
SEQ ID n°1626	Prot n°PL-2446.1	Contig30	86202	87161	43%	Identities = 79/280 (28%), Positives = 138/280 (49%), Gaps = 32/280 (11%) gb AAF84402.1 AE003987_6 (AE003987) hypothetical protein [Xylella fastidiosa] Length = 278
SEQ ID n°1627	Prot n°PL-2448.1	Contig30	83435	85216	12%	Identities = 46/137 (33%), Positives = 72/137 (51%), Gaps = 14/137 (10%) gi 9632875 structural protein P5 gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2] Length = 160
SEQ ID n°1628	Prot n°PL-2449.1	Contig30	80811	82280	53%	Identities = 174/499 (34%), Positives = 265/499 (52%), Gaps = 16/499 (3%) gb AAF84392.1 AE003986_22 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84497.1 AE003993_16 (AE003993) hypothetical protein [Xylella fastidiosa] Length = 498
SEQ ID n°1629	Prot n°PL-245.1	Contig41	410198	411359	64%	Identities = 180/370 (48%), Positives = 256/370 (68%), Gaps = 1/370 (0%) gb AAF96178.1 (AE004366) multidrug resistance protein D [Vibrio cholerae] Length = 379
SEQ ID n°1630	Prot n°PL-2450.1	Contig30	80166	80807	No Hits found	

TABLEAU I

SEQ ID n°1631	Prot n°PL-2451.1	Contig30	75124	76527	48%	Identities = 158/461 (33%), Positives = 240/461 (51%), Gaps = 19/461 (4%) gb AAF84722.1 AE004011_7 (AE004011) coenzyme F390 synthetase [Xylella fastidiosa] Length = 478
SEQ ID n°1632	Prot n°PL-2452.1	Contig30	74180	75127	55%	Identities = 116/304 (38%), Positives = 174/304 (57%), Gaps = 7/304 (2%) sp O67733 ILVE_AQUAE PROBABLE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (BCAT) pf C70463 branched-chain amino acid aminotransferase - Aquifex aeolicus gb AAC07697.1 (AE000762) branched-chain amino acid aminotransferase [Aquifex aeolicus] Length = 94/279 (33%), Positives = 145/279 (51%), Gaps = 20/279 (7%) ref NP_057878.1 crystallin, mu sp O54983 CRYM_MOUSE MU-CRYSTALLIN HOMOLOG gb AAB94770.1 (AF039391) mu-crystallin [Mus musculus] Length = 313
SEQ ID n°1633	Prot n°PL-2453.1	Contig30	72000	72968	44%	Identities = 66/192 (34%), Positives = 108/192 (55%), Gaps = 21/192 (10%) db JBA087689.1 (AB016280) Hypothetical gene [Agrobacterium tumefaciens] Length = 229
SEQ ID n°1634	Prot n°PL-2454.1	Contig30	71224	71931	45%	Identities = 175/347 (50%), Positives = 242/347 (69%), Gaps = 3/347 (0%) gb AAC82660.1 (AF071215) regulator of swarming behavior precursor [Proteus mirabilis] Length = 897
SEQ ID n°1635	Prot n°PL-2455.1	Contig30	69552	70682	64%	Identities = 257/554 (46%), Positives = 378/554 (67%), Gaps = 9/554 (1%) gb AAC82660.1 (AF071215) regulator of swarming behavior precursor [Proteus mirabilis] Length = 897
SEQ ID n°1636	Prot n°PL-2456.1	Contig30	67922	69598	67%	Identities = 167/211 (79%), Positives = 190/211 (89%) gb AAC82661.1 (AF071215) RcsB [Proteus mirabilis] Length = 218
SEQ ID n°1637	Prot n°PL-2457.1	Contig30	67264	67917	78%	Identities = 450/930 (48%), Positives = 637/930 (68%), Gaps = 20/930 (2%) sp P14376 RCSC_ECOLI SENSOR PROTEIN RCSC (CAPSULAR SYNTHESIS REGULATOR COMPONENT C) Length = 933
SEQ ID n°1638	Prot n°PL-2458.1	Contig30	64420	67179	67%	Identities = 765/877 (87%), Positives = 825/877 (93%), Gaps = 2/877 (0%) gb AAB95117.1 (U56906) DNA gyrase [Serratia marcescens] Length = 880
SEQ ID n°1639	Prot n°PL-2459.1	Contig30	61421	64066	93%	Identities = 115/256 (44%), Positives = 165/256 (63%), Gaps = 8/256 (3%) gb AAF96177.1 (AE004366) transcriptional regulator, AraC/XylS family [Vibrio cholerae] Length = 257
SEQ ID n°1640	Prot n°PL-246.1	Contig41	411463	412242	62%	

TABLEAU I

SEQ ID n°1641	Prot n°PL-2460.1	Contig30	60485	61210	88%	<p>Identities = 183/238 (78%), Positives = 210/238 (87%)</p> <p>sp P17993 UBIG_ECOLI_3-DEMETHYLUBIQUINONE-9-3-METHYLTRANSFERASE (3,4-DIHYDROXY-5-HEXAPRENYLBENZOATE METHYLTRANSFERASE) (DHMB-METHYLTRANSFERASE) p ij A47682 3-demethylubiquinone-9 3-O-methyltransferase (EC 2.1.1.64) - Escherichia coli emb CAA68610.1 (Y00544) PufX protein [Escherichia coli] gb AAA24714.1 (M87509) ubiquinone synthesis-related protein [Escherichia coli] gb AAC75292.1 (AE000313) 3-demethylubiquinone-9 3-methyltransferase and 2-octaprenyl-8-hydroxy phenol methylase [Escherichia coli] db BAA16049.1 (D90854) 2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,</p>
SEQ ID n°1642	Prot n°PL-2461.1	Contig30	57825	60122	89%	<p>Identities = 671/763 (87%), Positives = 717/763 (93%), Gaps = 2/763 (0%)</p> <p>sp P00452 IR1_ECOLI_RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 ALPHA CHAIN (RIBONUCLEOTIDE REDUCTASE 1) (B1 PROTEIN) (R1 PROTEIN) p ij RDEC1R ribonucleoside-diphosphate reductase (EC 1.17.4.1) 1 alpha chain - Escherichia coli p db 2R1R A Chain A, Ribonucleotide Reductase R1 Protein With Dtp Occupying The Specificity Site From Escherichia Coli p db 2R1R B Chain B, Ribonucleotide Reductase R1 Protein With Dtp Occupying The Specificity Site From Escherichia Coli p db 2R1R C Chain C, Ribonucleotide Reductase R1 Protein With Dtp Occupying The Specificity Site From Escherichia Coli p db 3R1R A Chain A, Ribonucleotide Reductase R1 Protein With Ampnp Occupying The Activity Site From Escherichia Coli p db 3R1R B Chain B, Ribonucleotide Reductase R1 Protein With Ampnp Occupying The Activity Site From Escherichia Coli p db 3R1R C Chain C, Ribonucleotide</p>
SEQ ID n°1643	Prot n°PL-2462.1	Contig30	56682	57812	93%	<p>Identities = 334/376 (88%), Positives = 358/376 (94%)</p> <p>sp P37427 IR2_SALTY_RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 BETA CHAIN (RIBONUCLEOTIDE REDUCTASE 1) (B2 PROTEIN) (R2 PROTEIN) emb CAA51453.1 (X72948) nrdB [Salmonella typhimurium]</p>
SEQ ID n°1644	Prot n°PL-2463.1	Contig30	55204	55914	No Hits found	
SEQ ID n°1645	Prot n°PL-2464.1	Contig30	53136	54167	37%	<p>Identities = 83/262 (31%), Positives = 129/262 (48%), Gaps = 16/262 (6%)</p> <p>db JBAB07562.1 (AP001520) oxidoreductase [Bacillus halodurans]</p>
SEQ ID n°1646	Prot n°PL-2465.1	Contig30	44800	49947	27%	<p>Identities = 293/1122 (26%), Positives = 475/1122 (42%), Gaps = 172/1122 (15%)</p> <p>gb AAG05850.1 (AE004673_10 (AE004673) hypothetical protein [Pseudomonas aeruginosa] Length = 5627</p>
SEQ ID n°1647	Prot n°PL-2466.1	Contig30	43120	44789	60%	<p>Identities = 242/558 (43%), Positives = 343/558 (61%), Gaps = 13/558 (2%)</p> <p>gb AAC31980.1 (L39897) HecB [Pectobacterium chrysanthemi] Length = 558</p>

TABLEAU I

SEQ ID n°1648	Prot n°PL-2467.1	Contig30	41611	42816	81%	<p>Identities = 281/403 (69%), Positives = 338/403 (83%), Gaps = 2/403 (0%) sp P18199 TYRP_ECOLI_TYROSINE-SPECIFIC TRANSPORT PROTEIN (TYROSINE PERMEASE) pir GRECY tyrosine-specific transport protein - Escherichia coli dbj BAA15730.1 (D90832) Tyrosine-specific transport protein (Tyrosine permease) Escherichia coli gb AAC74977.1 (AE000284) tyrosine-specific transport system [Escherichia coli] Length = 403</p> <p>Identities = 408/481 (84%), Positives = 447/481 (92%) sp P42321 CATA_PROMI_CATALASE pir J458683 catalase (EC 1.11.1.6) - Proteus mirabilis emb CAB93973.1 (A4400964) catalase [Proteus mirabilis] emb CAB93976.1 (A4400965) catalase [Proteus mirabilis] Length = 484</p> <p>Identities = 257/454 (56%), Positives = 323/454 (70%), Gaps = 10/454 (2%) dbj BAA16080.1 (D90856) O-SUCCINYL-BENZOIC ACID-COA LIGASE (EC 6.2.1.26) (OSB-COA SYNTHETASE) (O-SUCCINYL-BENZOATE-COA SYNTHASE) Escherichia coli Length = 450</p> <p>Identities = 141/401 (35%), Positives = 234/401 (58%), Gaps = 20/401 (4%) gb AAC63079.1 (AF035423) putative juvenile hormone esterase [Leptinotarsa decemlineata] Length = 515</p>
SEQ ID n°1649	Prot n°PL-2468.1	Contig30	39294	40739	91%	<p>Identities = 209/318 (65%), Positives = 269/318 (81%), Gaps = 1/318 (0%) dbj BAA16085.1 (D90857) O-SUCCINYL-BENZOATE-COA SYNTHASE (OSB SYNTHASE) (4-(2-CARBOXYPHENYL)- 4-OXYBUTYRIC ACID SYNTHASE) Escherichia coli Length = 329</p>
SEQ ID n°1650	Prot n°PL-2469.1	Contig30	37771	39210	67%	
SEQ ID n°1651	Prot n°PL-247.1	Contig41	412502	413776	55%	<p>Identities = 255/285 (89%), Positives = 272/285 (94%) sp P27290 MENB_ECOLI_NAPHTHOATE SYNTHASE (DIHYDROXYNAPHTHOIC ACID SYNTHETASE) (DHNA SYNTHETASE) pir J42714 naphthoate synthase, DHNA synthase, MenB=menaquinone biosynthesis enzyme/mitochondrial enoyl-CoA hydratase homolog - Escherichia coli pir D64997 naphthoate synthase (EC 4.1.3.36) - Escherichia coli gb AAA23682.1 (M83421) DHNA synthase [Escherichia coli] gb AAC75322.1 (AE000316) dihydroxynaphthoic acid synthetase [Escherichia coli] dbj BAA16086.1 (D90857) naphthoate synthase, DHNA synthase, MenB=menaquinone biosynthesis</p> <p>Identities = 110/237 (46%), Positives = 144/237 (60%), Gaps = 1/237 (0%) dbj BAA16087.1 (D90857) similar to [SwissProt Accession Number P37355]-start codon is not identified yet [Escherichia coli] Length = 270</p>
SEQ ID n°1652	Prot n°PL-2470.1	Contig30	36851	37822	79%	
SEQ ID n°1653	Prot n°PL-2471.1	Contig30	35976	36686	No Hits found	
SEQ ID n°1654	Prot n°PL-2472.1	Contig30	35994	36851	91%	
SEQ ID n°1655	Prot n°PL-2473.1	Contig30	35264	36052	49%	
SEQ ID n°1656	Prot n°PL-2474.1	Contig30	33525	35219	78%	<p>Identities = 377/564 (66%), Positives = 443/564 (77%), Gaps = 8/564 (1%) dbj BAA16089.1 (D90857) 2-SUCCINYL-6-HYDROXY-2, 4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE (SHCHC SYNTHASE) / 2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71) (ALPHA- KETOGLUTARATE DECARBOXYLASE) (KDC) Escherichia</p>

Unknown, similar to insecticidal toxins

TABLEAU I

SEQ ID n°1657	Prot n°PL-2475.1	Contig30	32101	33420	62%	Identities = 215/443 (48%), Positives = 285/443 (63%), Gaps = 16/443 (3%) sp P38051 MENF_ECOLI MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE dbj BAA16092.1 (D90857) MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE (EC 5.4.99.6) [Escherichia coli] dbj BAA16099.1 (D90858) MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE (EC 5.4.99.6) [Escherichia coli] emb CAA90702.1 (Z50849) isochorismate synthase [Escherichia coli] Length = 431
SEQ ID n°1658	Prot n°PL-2476.1	Contig30	29823	31121	42%	Identities = 93/433 (21%), Positives = 184/433 (42%), Gaps = 61/433 (14%) pir T18372 repeat organellar protein - Plasmodium chabaudi gb AAC63403.1 (U43145) repeat organellar protein [Plasmodium chabaudi] Length = 431
SEQ ID n°1659	Prot n°PL-2477.1	Contig30	28715	29794	46%	Identities = 79/368 (21%), Positives = 168/368 (45%), Gaps = 78/368 (21%) gb AAF53604.1 (AE003655) CLIP-190 gene product [alt 1] [Drosophila melanogaster] gb AAF53605.1 (AE003655) CLIP-190 gene product [alt 2] [Drosophila melanogaster] Length = 1690
SEQ ID n°1660	Prot n°PL-2478.1	Contig30	27075	28532	77%	Identities = 325/421 (77%), Positives = 377/421 (89%) sp P33608 NUON_ECOLI NADH DEHYDROGENASE I CHAIN N (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 14) (NUO14) pir B64999 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain N - Escherichia coli gb AAC75336.1 (AE000317) NADH dehydrogenase I chain N [Escherichia coli] dbj BAA16103.1 (D90858) NADH DEHYDROGENASE I CHAIN N (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 14) (NUO14) [Escherichia coli] dbj BAA16104.1 (D90859) NADH DEHYDROGENASE I CHAIN N (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 14) (NUO14) [Escherichia coli] Length = 405/509 (79%) Positives = 456/509 (89%), Gaps = 3/509 (0%)
SEQ ID n°1661	Prot n°PL-2479.1	Contig30	25548	27058	89%	sp P31978 NUOM_ECOLI NADH DEHYDROGENASE I CHAIN M (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 13) (NUO13) pir C64999 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Escherichia coli gb AAC75337.1 (AE000317) NADH dehydrogenase I chain M [Escherichia coli] dbj BAA16105.1 (D90859) NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [Escherichia coli] Length = 509
SEQ ID n°1662	Prot n°PL-248.1	Contig41	415295	415996	84%	Identities = 186/234 (79%), Positives = 211/234 (89%) pir S47673 leucine transport protein livF - Escherichia coli gb AAB18429.1 (U000039) livF [Escherichia coli] gb AAC76479.1 (AE000421) ATP-binding component of leucine transport [Escherichia coli] Length = 241

TABLEAU I

SEQ ID n°1663	Prot n°PL-2480.1	Contig30	23680	25527	87%	<p>Identities = 485/615 (78%), Positives = 543/615 (87%), Gaps = 3/615 (0%) sp P33607 NUOL_ECOLI_NADH_DEHYDROGENASE CHAIN L (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 12) (NUO12) pir D64999 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain L - Escherichia coli gb AAC75338.1 (AE000317) NADH dehydrogenase chain L [Escherichia coli] dbj BAA16106.1 (D90859) NADH dehydrogenase chain nuol [Escherichia coli] Length = 613 Identities = 280/325 (86%), Positives = 310/325 (95%)</p>
SEQ ID n°1664	Prot n°PL-2481.1	Contig30	21292	22269	93%	<p>sp P33603 NUOH_ECOLI_NADH_DEHYDROGENASE CHAIN H (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 8) (NUO8) pir H64999 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain H - Escherichia coli gb AAC75342.1 (AE000317) NADH dehydrogenase chain H [Escherichia coli] dbj BAA16110.1 (D90859) NADH DEHYDROGENASE CHAIN H (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 8) (NUO8) [Escherichia coli] Length = 325</p>
SEQ ID n°1665	Prot n°PL-2482.1	Contig30	18563	21295	85%	<p>sp P33900 NUOG_SALTY_NADH_DEHYDROGENASE CHAIN G (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6) (NUO6) Length = 399/448 (89%) Identities = 417/448 (93%), Gaps = 3/448 (0%) sp P31979 NUOF_ECOLI_NADH_DEHYDROGENASE CHAIN F (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6) (NUO6) pir B65000 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain F - Escherichia coli gb AAC75344.1 (AE000317) NADH dehydrogenase chain F [Escherichia coli] dbj BAA16113.1 (D90859) NADH DEHYDROGENASE CHAIN F (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6) (NUO6) [Escherichia coli] dbj BAA16118.1 (D90860) NADH DEHYDROGENASE CHAIN F (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6) (NUO6) [Escherichia coli] Length = 445</p>
SEQ ID n°1666	Prot n°PL-2483.1	Contig30	17129	18493	90%	<p>Identities = 524/599 (87%), Positives = 562/599 (93%), Gaps = 4/599 (0%) pir D65000 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain C-D - Escherichia coli gb AAC75346.1 (AE000317) NADH dehydrogenase chain C, D [Escherichia coli] Length = 600</p>
SEQ ID n°1667	Prot n°PL-2484.1	Contig30	14782	16581	93%	<p>Identities = 209/224 (93%), Positives = 220/224 (97%) sp O85274 NUOB_ERWCA_NADH_DEHYDROGENASE CHAIN B (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2) (NUO2) gb AAC38641.1 (AF057063) NADH dehydrogenase chain B [Pectobacterium carotovorum subsp. carotovorum] Length = 224</p>
SEQ ID n°1668	Prot n°PL-2485.1	Contig30	13989	14663	93%	<p>Identities = 183/314 (58%), Positives = 239/314 (75%), Gaps = 8/314 (1%) gb AAC38639.1 (AF057063) HexA [Pectobacterium carotovorum subsp. carotovorum] Length = 316</p>
SEQ ID n°1669	Prot n°PL-2486.1	Contig30	11889	12818	76%	

TABLEAU I

SEQ ID n°1670	Prot n°PL-2487.1	Contig30	9865	11080	86%	<p>Identities = 367/404 (90%), Positives = 386/404 (94%)</p> <p>sp P77727 YFBQ_EC01 PROBABLE AMINOTRANSFERASE YFBQ pi JH65000 hypothetical protein b2290 - Escherichia coli (strain K-12) gb AAC75350.1 (AE000318) putative aminotransferase [Escherichia coli] db JBA16127.1 (D90860) ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) [TRANSMINASE A] (ASPART) [Escherichia coli] Length = 405</p>
SEQ ID n°1671	Prot n°PL-2488.1	Contig30	8359	8958	85%	<p>Identities = 151/188 (76%), Positives = 171/188 (86%) pi JAG5001 hypothetical protein b2291 - Escherichia coli (strain K-12) gb AAC75351.1 (AE000318) putative alpha helix protein [Escherichia coli] Length = 199</p>
SEQ ID n°1672	Prot n°PL-2489.1	Contig30	6530	8362	82%	<p>Identities = 444/610 (72%), Positives = 523/610 (84%)</p> <p>sp P77741 YFBS_EC01 HYPOTHETICAL 65.9 KD PROTEIN IN LRHA-ACKA INTERGENIC REGION pi JH65001 hypothetical protein b2292 - Escherichia coli (strain K-12) gb AAC75352.1 (AE000318) putative transport protein [Escherichia coli] db JBA16128.1 (D90860) 46 KD MEMBRANE PROTEIN. [Escherichia coli] Length = 610</p>
SEQ ID n°1673	Prot n°PL-249.1	Contig41	415999	416772	82%	<p>Identities = 207/251 (82%), Positives = 223/251 (88%)</p> <p>sp P30293 LIVG_SALTY HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN LIVG (LIV-I PROTEIN G) pi JH0670 high-affinity branched-chain amino acid transport LIV-I system LivF protein - Salmonella typhimurium db JBA02131.1 (D12589) LivF protein [Salmonella typhimurium] Length = 255</p>
SEQ ID n°1674	Prot n°PL-2490.1	Contig30	4305	5507	88%	<p>Identities = 341/400 (85%), Positives = 372/400 (92%)</p> <p>sp P15048 ACKA_EC01 ACETATE KINASE (ACETOKINASE) pi JKECAA acetate kinase (EC 2.7.2.1) - Escherichia coli gb AAA23406.1 (M22956) acetate kinase (EC 2.7.2.1) [Escherichia coli] gb AAC75356.1 (AE000318) acetate kinase [Escherichia coli] db JBA16135.1 (D90861) acetate kinase (EC 2.7.2.1) [Escherichia coli] Length = 400</p>
SEQ ID n°1675	Prot n°PL-2491.1	Contig30	2092	4233	90%	<p>Identities = 608/712 (85%), Positives = 657/712 (91%), Gaps = 2/712 (0%)</p> <p>pi JX0357 phosphate acetyltransferase (EC 2.3.1.8) - Escherichia coli Length = 714</p>
SEQ ID n°1676	Prot n°PL-2492.1	Contig30	1100	1783	No Hits found	
SEQ ID n°1677	Prot n°PL-2493.1	Contig41	1224455	1225522	20%	<p>Identities = 47/153 (30%), Positives = 74/153 (47%), Gaps = 5/153 (3%)</p> <p>db JBA06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188</p>
SEQ ID n°1678	Prot n°PL-2494.1	Contig41	1222818	1224183	49%	<p>Identities = 114/408 (27%), Positives = 210/408 (50%), Gaps = 15/408 (3%)</p> <p>gb AAF33461.1 (AF233324) 89% identity with E. coli lipopolysaccharide biosynthesis protein (WZXE) (SP-P2783) [Salmonella typhimurium LT2] Length = 416</p>
SEQ ID n°1679	Prot n°PL-2495.1	Contig41	1221806	1222933	74%	<p>Identities = 229/374 (61%), Positives = 285/374 (75%), Gaps = 9/374 (2%)</p> <p>gb AAB81632.1 (AF025396) putative amino transferase [Vibrio anguillarum] Length = 371</p>

TABLEAU I

SEQ ID n°1680	Prot n°PL-2496.1	Contig41	1220478	1221350	82%	<p>Identities = 207/289 (71%), Positives = 253/289 (88%) sp P27831 RFFH_ECOLI_GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (DTDP-GLUCOSE SYNTHASE) GLUCOSE PYROPHOSPHORYLASE) pir JH65182 glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) - Escherichia coli gb AAC76794.1 (AE000455) glucose-1-phosphate thymidyltransferase [Escherichia AE000455]</p>
SEQ ID n°1681	Prot n°PL-2497.1	Contig41	1218731	1219702	52%	<p>Identities = 112/296 (37%), Positives = 169/296 (56%), Gaps = 22/296 (7%) sp P14182 LICB_HAEIN_LICB_PROTEIN pir JC84128 lic-1 operon protein (lcB) homolog - Haemophilus influenzae (strain Rd KW20) gb AAC23188.1 (U32829) lic-1 operon protein (lcB) [Haemophilus influenzae Rd] Length = 292</p>
SEQ ID n°1682	Prot n°PL-2498.1	Contig41	1216459	1218333	73%	<p>Identities = 353/613 (57%), Positives = 459/613 (74%) db BAA85014.1 (AB025970) ORF9P [Plesiomonas shigelloides] gb AAG17416.1 AF285970_10 (AF285970) WbgZ [Plesiomonas shigelloides] Identities = 117/196 (59%), Positives = 156/196 (78%)</p>
SEQ ID n°1683	Prot n°PL-2499.1	Contig41	1215838	1218449	76%	<p>gb AAG17415.1 AF285970_9 (AF285970) WbgY [Plesiomonas shigelloides] Length = 196</p>
SEQ ID n°1684	Prot n°PL-25.1	Contig41	43460	44827	71%	<p>Identities = 272/443 (61%), Positives = 343/443 (77%), Gaps = 3/443 (0%) gb AAG05921.1 AE004681_3 (AE004681) probable sodium:alanine symporter [Pseudomonas aeruginosa] Length = 449</p>
SEQ ID n°1685	Prot n°PL-250.1	Contig41	418769	418046	80%	<p>Identities = 324/425 (76%), Positives = 364/425 (85%) sp P22729 LIVM_ECOLI_HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM PERMEASE PROTEIN LIVM (LIV-I PROTEIN M) pir J547675 leucine transport protein livm - Escherichia coli gb AAB18431.1 (U00039) CG Site No. 18190 [Escherichia coli] gb AAC76481.1 (AE000421) high-affinity branched-chain amino acid transport Identities = 257/380 (67%), Positives = 331/380 (86%)</p>
SEQ ID n°1686	Prot n°PL-2500.1	Contig41	1214680	1215837	84%	<p>gb AAG17414.1 AF285970_8 (AF285970) WbgX [Plesiomonas shigelloides] Length = 384</p>
SEQ ID n°1687	Prot n°PL-2501.1	Contig41	1213644	1214669	53%	<p>Identities = 109/332 (32%), Positives = 183/332 (54%), Gaps = 19/332 (5%) gb AAG17423.1 AF285971_7 (AF285971) WbgW [Shigella sonnei] Length = 331</p>
SEQ ID n°1688	Prot n°PL-2502.1	Contig41	1212251	1213489	61%	<p>Identities = 172/410 (41%), Positives = 259/410 (61%), Gaps = 4/410 (0%) emb CAA07667.1 (AJ007747) putative transferase [Bordetella bronchiseptica] Length = 419</p>
SEQ ID n°1689	Prot n°PL-2503.1	Contig41	1211184	1212254	72%	<p>Identities = 219/352 (62%), Positives = 269/352 (76%) gb AAG06536.1 AE004738_10 (AE004738) probable UDP-N- acetylglucosamine 2-epimerase Wbpl [Pseudomonas aeruginosa]</p>

TABLEAU I

SEQ ID n°1690	Prot n°PL-2504.1	Contig41	1210075	1211178	75%	Identities = 205/367 (55%), Positives = 282/367 (75%), Gaps = 2/367 (0%) gb AAC45862.1 (U50396) WbpH [Pseudomonas aeruginosa] gb AAG06537.1 (AE004738_11) (AE004738) probable glycosyltransferase WbpH [Pseudomonas aeruginosa] Length = 373
SEQ ID n°1691	Prot n°PL-2505.1	Contig41	1208816	1210078	No Hits found	Identities = 57/206 (27%), Positives = 85/206 (40%), Gaps = 39/206 (18%) sp P46555 YKG5_CAEEL HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III pir IT18692 hypothetical protein B0285.5 - Caenorhabditis elegans emb CAA84297.1 (Z34533) cDNA EST yk96a2.5 comes from this gene [Caenorhabditis elegans] Length = 632
SEQ ID n°1692	Prot n°PL-2506.1	Contig41	1207723	1208859	22%	Identities = 102/406 (25%), Positives = 200/406 (49%), Gaps = 27/406 (6%) gb AAC45858.1 (U50396) WbpF [Pseudomonas aeruginosa] gb AAG06541.1 (AE004739_3) (AE004739) O-antigen translocase [Pseudomonas aeruginosa] Length = 411
SEQ ID n°1693	Prot n°PL-2507.1	Contig41	1208504	1207745	48%	Identities = 255/357 (71%), Positives = 301/357 (83%), Gaps = 2/357 (0%) gb AAG06543.1 (AE004739_5) (AE004739) probable aminotransferase WbpE [Pseudomonas aeruginosa] Length = 359
SEQ ID n°1694	Prot n°PL-2508.1	Contig41	1205452	1206522	82%	Identities = 214/316 (67%), Positives = 254/316 (79%) gb AAD45293.1 (AF156256_1) (AF156256) putative dehydrogenase [Vibrio anguillarum] Length = 318
SEQ ID n°1695	Prot n°PL-2509.1	Contig41	1203782	1204831	71%	Identities = 268/308 (87%), Positives = 290/308 (94%) pir IS47676 livH protein - Escherichia coli pir QRECLH leucine transport protein livH - Escherichia coli gb AAB18432.1 (U00039) CG Site No. 552 [Escherichia coli] gb AAC76482.1 (AE000421) high-affinity branched-chain amino acid transport system; membrane component [Escherichia coli] Length = 308 *
SEQ ID n°1696	Prot n°PL-251.1	Contig41	418043	418869	87%	Identities = 326/436 (74%), Positives = 372/436 (84%) gb AAC45852.1 (U50396) WbpA [Pseudomonas aeruginosa] gb AAG06547.1 (AE004739_9) (AE004739) probable UDP-glucose/GDP-mannose dehydrogenase WbpA [Pseudomonas aeruginosa] Length = 436
SEQ ID n°1697	Prot n°PL-2510.1	Contig41	1202457	1203767	82%	Identities = 365/456 (80%), Positives = 409/456 (89%) sp P08336 CPXA_ECOLI SENSOR PROTEIN CPXA pir S40855 chemotaxis protein cpxA (EC 2.7.3.-) - Escherichia coli gb AAB03044.1 (L19201) CG Site No. 908 [Escherichia coli] gb AAC76893.1 (AE000466) probable sensor protein (histidine protein kinase), acting on arcA [Escherichia coli] Identities = 203/232 (87%), Positives = 218/232 (92%), Gaps = 1/232 (0%)
SEQ ID n°1698	Prot n°PL-2511.1	Contig41	1200685	1202055	87%	sp P16244 CPXR_ECOLI TRANSCRIPTIONAL REGULATORY PROTEIN CPXR pir I53679 transcription factor - Escherichia coli pir C65197 transcription regulator cpxR - Escherichia coli (strain K-12) gb AAC38868.1 (L14579) transcription factor [Escherichia coli] gb AAC76894.1 (AE000466) transcriptional regulator in 2-component system [Escherichia coli] pir I2004283A membrane sensor regulator [Escherichia coli] Length =
SEQ ID n°1699	Prot n°PL-2512.1	Contig41	1199993	1200688	92%	

TABLEAU I

SEQ ID n°1700	Prot n°PL-2513.1	Contig41	1191199	1192005	48%	Identities = 94/214 (43%), Positives = 131/214 (60%), Gaps = 10/214 (4%) gb AAF5083.1 (AE004269) CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase-related protein [Vibrio cholerae] Length = 252
SEQ ID n°1701	Prot n°PL-2514.1	Contig41	1190565	1191233	56%	Identities = 92/188 (48%), Positives = 127/188 (66%), Gaps = 4/188 (2%) gb AAG05925.1 (AE004681) probable acyltransferase [Pseudomonas aeruginosa] Length = 209
SEQ ID n°1702	Prot n°PL-2515.1	Contig41	1189624	1190568	72%	Identities = 179/311 (57%), Positives = 238/311 (75%), Gaps = 1/311 (0%) gb AAG05924.1 (AE004681) probable phosphatidate cytidyltransferase [Pseudomonas aeruginosa] Length = 311
SEQ ID n°1703	Prot n°PL-2516.1	Contig41	1188271	1189242	86%	Identities = 272/319 (85%), Positives = 298/319 (93%) gb AAD16179.1 (AF098509) phosphofructokinase [Enterobacter cloacae] Length = 320
SEQ ID n°1704	Prot n°PL-2517.1	Contig41	1187104	1188099	82%	Identities = 255/328 (77%), Positives = 291/328 (87%), Gaps = 1/328 (0%) pir S40860 periplasmic sulphate binding protein - Escherichia coli pir BYEC sulfate binding protein precursor, periplasmic - Escherichia coli gb AAB03049.1 (L19201) periplasmic sulphate binding protein [Escherichia coli] gb AAC76899.1 (AE000466) periplasmic sulfate-binding protein [Escherichia coli] Length = 329
SEQ ID n°1705	Prot n°PL-2518.1	Contig41	1186284	1187051	85%	Identities = 214/255 (83%), Positives = 232/255 (90%) sp Q9Z6B9 TPIS_ENTCL TRIOSEPHOSPHATE ISOMERASE (TIM) gb AAD16183.1 (AF098509) triose phosphate isomerase [Enterobacter] Length = 255
SEQ ID n°1706	Prot n°PL-2519.1	Contig41	1185529	1186149	53%	Identities = 79/169 (46%), Positives = 111/169 (64%), Gaps = 1/169 (0%) sp P32160 YIQ_ECOLI HYPOTHETICAL 21.8 KD PROTEIN IN TPIA-FPR INTERGENIC REGION PRECURSOR pir S40863 hypothetical 21.8K protein (tpia 3'region) precursor - Escherichia coli gb AAB03052.1 (L19201) ORF_f199 [Escherichia coli] gb AAC76902.1 (AE000466) orf, hypothetical protein [Escherichia coli] Length = 199
SEQ ID n°1707	Prot n°PL-252.1	Contig41	419031	420143	82%	Identities = 268/364 (73%), Positives = 316/364 (86%) pir BLECL leucine-specific binding protein precursor - Escherichia coli gb AAB18433.1 (U00039) CG Site No. 550 [Escherichia coli] gb AAC76483.1 (AE000421) high-affinity leucine-specific transport system; periplasmic binding protein [Escherichia coli] Length = 369
SEQ ID n°1708	Prot n°PL-2520.1	Contig41	1184296	1185042	84%	Identities = 180/248 (72%), Positives = 212/248 (84%) sp P28861 FENR_ECOLI FERREDOXIN-NADP REDUCTASE (FNR) (FLAVODOXIN REDUCTASE) (FLXR) (FLDR) (METHYL VIOLOGEN RESISTANCE PROTEIN A) (DA1) pir S40867 ferredoxin-NADP+ reductase (EC 1.18.1.2) - Escherichia coli gb AA23805.1 (L04757) ferredoxin NADP+ reductase [Escherichia coli] gb AAB03066.1 (L19201) ORF_f248 [Escherichia coli] gb AAC76806.1 (AE000467) ferredoxin-NADP reductase [Escherichia coli]

TABLEAU I

SEQ ID n°1708	Prot n°PL-2521.1	Contig41	1182364	1183887	89%	<p>Identities = 420/503 (83%), Positives = 463/503 (91%), Gaps = 1/503 (0%) sp P08859 GLPK_ECOLI GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) pir KIEGGL glycerol kinase (EC 2.7.1.30) - Escherichia coli gb AA23913.1 (M18393) ATP:glycerol 3-phosphotransferase (EC 2.7.1.30) [Escherichia coli] gb AA03058.1 (L19201) glycerol kinase [Escherichia coli] gb AAC76908.1 (AE000467) glycerol kinase [Escherichia coli] Length = 502</p> <p>Identities = 184/272 (67%), Positives = 229/272 (83%), Gaps = 2/272 (0%) sp P31140 GLPF_SHIFL GLYCEROL UPTAKE FACILITATOR PROTEIN Length = 281</p>
SEQ ID n°1710	Prot n°PL-2522.1	Contig41	1181503	1182333	80%	<p>Identities = 196/300 (65%), Positives = 230/300 (76%) sp P32166 MENA_ECOLI 1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE (DHNA-OCTAPRENYLTRANSFERASE) pir S40873 menaquinone biosynthesis protein mena - Escherichia coli gb AA03062.1 (L19201) ORF_308 [Escherichia coli] gb AA01207.1 (U56082) 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Escherichia coli] gb AAC76912.1 (AE000467)</p> <p>Identities = 393/443 (88%), Positives = 420/443 (94%) sp P32168 HSLU_ECOLI HEAT SHOCK PROTEIN HSLU pir JT0761 heat shock protein hslU - Escherichia coli gb AA03063.1 (L19201) matches PS00017: ATP_GTP_A; similar to Pasteurella haemolytica hypoph. protein ORF1; heat shock induced [Escherichia coli] gb AAC76913.1 (AE000467) heat shock protein hslVU, ATPase subunit, homologous to chaperones [Escherichia coli] Length = 443 "</p>
SEQ ID n°1712	Prot n°PL-2524.1	Contig41	1177891	1179222	91%	<p>Identities = 141/320 (44%), Positives = 184/320 (57%), Gaps = 46/320 (14%) sp P29131 FTSN_ECOLI CELL DIVISION PROTEIN FTSN pir AA7122 cell division protein FtsN - Escherichia coli gb AA23814.1 (L14281) cell division protein [Escherichia coli] Length = 319</p>
SEQ ID n°1713	Prot n°PL-2525.1	Contig41	1176398	1177225	66%	<p>Identities = 222/337 (65%), Positives = 269/337 (78%) sp P06964 CYTR_ECOLI TRANSCRIPTIONAL REPRESSOR CYTR pir JPECCY cyr transcription repressor cytr - Escherichia coli gb AA03066.1 (L19201) CG Site No. 887 [Escherichia coli] emb CAA27318.1 (X03683) put. Cyt repressor (aa 1-341) [Escherichia coli] gb AAC76916.1 (AE000467) regulator for deo operon, udp, cdd, tsx, nupC, Length = 502/732 (68%), Positives = 597/732 (80%), Gaps = 2/732 (0%)</p>
SEQ ID n°1715	Prot n°PL-2527.1	Contig41	1172754	1174973	76%	<p>Identities = 135/505 (26%), Positives = 597/732 (80%), Gaps = 2/732 (0%) pir J35505 primosomal replication factor Y - Escherichia coli gb AA03067.1 (L19201) primosomal protein replication factor [Escherichia coli] gb AAC76917.1 (AE000467) primosomal protein N (= factor Y) (putative helicase) [Escherichia coli] Length = 732</p>

TABLEAU I

SEQ ID n°1716	Prot n°PL-2528.1	Contig41	1170457	1171629	84%	<p>Identities = 289/385 (75%), Positives = 334/385 (86%)</p> <p>sp P00935 METB_ECOLI_CYSTATHIONINE GAMMA-SYNTHASE (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) pir SYECCG O-succinylhomoserine (thiol)-lyase (EC 4.2.99.9) - Escherichia coli</p> <p>gb AA24167.1 (K01547) cystathionine gamma-synthase [Escherichia coli]</p> <p>gb AAB03071.1 (L19201) cystathionine gamma-synthase [Escherichia coli]</p> <p>gb AAC76921.1 (AE000468) cystathionine gamma-synthase [Escherichia coli]</p> <p>Identities = 638/808 (78%), Positives = 711/808 (87%)</p> <p>sp P00562 AK2H_ECOLI_BIFUNCTIONAL ASPARTOKINASE/HOMOSERINE DEHYDROGENASE II (AKII-HDI) [INCLUDES: ASPARTOKINASE II; HOMOSERINE DEHYDROGENASE II] pir DEECK2 metL bifunctional enzyme - Escherichia coli gb AAB03072.1 (L19201) aspartokinase II/homoserine dehydrogenase II [Escherichia coli] gb AAC76922.1 (AE000468) aspartokinase II and homoserine dehydrogenase II [Escherichia coli] Length = 810</p>
SEQ ID n°1717	Prot n°PL-2529.1	Contig41	1168019	1170460	86%	<p>Identities = 228/377 (60%), Positives = 291/377 (76%)</p> <p>sp P42100 YXAA_BACSU_HYPOTHETICAL 39.4 KDA PROTEIN IN GNTR-HTPG INTERGENIC REGION pir A70071 conserved hypothetical protein yxas - Bacillus subtilis db BAA21580.1 (AB005554) homologs are found in E. coli and H. influenzae; see SWISS_PROT ACC#: P42100 [Bacillus subtilis] emb CAB16041.1 (Z99124) similar to hypothetical proteins [Bacillus subtilis] emb CAB16041.1 (Z99124) similar to hypothetical proteins [Bacillus subtilis] emb CAB16041.1 (Z99124) similar to hypothetical proteins [Bacillus subtilis] emb CAB16041.1 (Z99124) similar to hypothetical proteins [Bacillus subtilis]</p> <p>Identities = 250/294 (85%), Positives = 277/294 (94%) pir S03169 5,10-methylenetetrahydrofolate reductase (FADH2) (EC 1.7.99.5) - Salmonella typhimurium Length = 298</p>
SEQ ID n°1718	Prot n°PL-2530.1	Contig41	1166790	1167674	87%	
SEQ ID n°1720	Prot n°PL-2531.2	Contig41	1164372	1165331		
SEQ ID n°1721	Prot n°PL-2532.2	Contig41	1163744	1164386		
SEQ ID n°1722	Prot n°PL-2533.1	Contig41	1162410	1163372	No Hits found	
SEQ ID n°1723	Prot n°PL-2534.1	Contig41	1158186	1160822	84%	<p>Identities = 672/883 (76%), Positives = 760/883 (85%) Gaps = 5/883 (0%)</p> <p>sp P00864 CAPP_ECOLI_PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) (PEPC) pir QYEC phosphoenolpyruvate carboxylase (EC 4.1.1.31) - Escherichia coli pdb 1FIY Three-Dimensional Structure Of Phosphoenolpyruvate Carboxylase From Escherichia Coli At 2.8 A Resolution emb CAA29332.1 (X05903) PEP carboxylase (AA 1-883) [Escherichia coli] gb AAC43062.1 (U00006) phosphoenolpyruvate carboxylase [Escherichia coli] gb AAC76938.1 (AE000469) phosphoenolpyruvate carboxylase [Escherichia coli] pir 1005219A carboxylase, phosphoenolpyruvate [Escherichia coli] Length = 883</p>

TABLEAU I

SEQ ID n°1724	Prot n°PL-2535.1	Contig41	1158748	1157903	85%	<p>Identities = 276/378 (73%), Positives = 333/378 (88%)</p> <p>spIP23908IARGE_ECOLI ACETYLORNITHINE DEACETYLASE (ACETYLORNITHINASE) (AO) (N-ACETYLORNITHINASE) (NAO) pir B42377 acetylornithine deacetylase (EC 3.5.1.16) - Escherichia coli emb CAA44625.1 (X62807) acetylornithine deacetylase subunit a2 [Escherichia coli] emb CAA39076.1 (X55417) N-acetylornithinase [Escherichia coli] gb AAC43063.1 (U00006) acetylornithine deacetylase [Escherichia coli] gb AAC76939.1 (AE000470) acetylornithine deacetylase</p> <p>Identities = 241/334 (72%), Positives = 280/334 (83%)</p>
SEQ ID n°1725	Prot n°PL-2536.1	Contig41	1155639	1156843	82%	<p>spIP11448IARGC_ECOLI N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (AGPR) (N-ACETYL-GLUTAMATE SEMIALDEHYDE DEHYDROGENASE) (NAGSA DEHYDROGENASE) pir RDECEP N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) - Escherichia coli gb AA23477.1 (M21446) argC (EC 1.2.1.38) [Escherichia coli] gb AAC43084.1 (U00006) N-acetyl-gamma-glutamyl-phosphate reductase [Escherichia coli] gb AAC76940.1 (AE000470) N-acetyl-gamma-glutamyl-phosphate reductase [Escherichia coli] Length =</p> <p>Identities = 191/257 (74%), Positives = 226/257 (87%)</p>
SEQ ID n°1726	Prot n°PL-2537.1	Contig41	1154840	1155613	85%	<p>spIP11445IARGB_ECOLI ACETYLGLUTAMATE KINASE (NAG KINASE) (AGK) (N-ACETYL-L-GLUTAMATE 5-PHOSPHOTRANSFERASE) pir KIECAE acetylglutamate kinase (EC 2.7.2.8) - Escherichia coli gb AA23478.1 (M21446) argB (EC 2.7.2.8) [Escherichia coli] gb AAC43085.1 (U00006) acetylglutamate kinase [Escherichia coli] gb AAC76941.1 (AE000470) acetylglutamate kinase [Escherichia coli] Identities = 287/405 (73%), Positives = 348/405 (85%), Gaps = 1/405 (0%)</p>
SEQ ID n°1727	Prot n°PL-2538.1	Contig41	1153557	1154771	81%	<p>gb AAF95783.1 (AE004330) argininosuccinate synthase [Vibrio cholerae] Length = 404</p> <p>Identities = 384/456 (84%), Positives = 411/456 (89%)</p>
SEQ ID n°1728	Prot n°PL-2539.1	Contig41	1152025	1153404	83%	<p>spIP11447IARLY_ECOLI ARGININOSUCCINATE LYASE (ARGINOSUCCINASE) (ASAL) pir C65203 argininosuccinate lyase (EC 4.3.2.1) - Escherichia coli gb AAC43088.1 (U00006) argininosuccinate lyase [Escherichia coli] gb AAC76942.1 (AE000470) argininosuccinate lyase</p> <p>Identities = 251/285 (88%), Positives = 271/285 (95%)</p>
SEQ ID n°1729	Prot n°PL-254.1	Contig41	422145	423002	94%	<p>spIP50508IRP32_ENTCL RNA POLYMERASE SIGMA-32 FACTOR pir S60165 transcription initiation factor sigma 32 - Enterobacter cloacae dbj BA009440.1 (D50829) sigma-32 homolog [Enterobacter cloacae] Identities = 250/296 (84%), Positives = 269/296 (90%)</p>
SEQ ID n°1730	Prot n°PL-2540.1	Contig41	1150840	1151745	84%	<p>spIP71318IOXYR_ERWCA HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR gb AAC72241.1 (U74302) oxidative stress transcriptional regulator [Pectobacterium carotovorum] Length = 302</p>

TABLEAU I

SEQ ID n°1731	Prot n°PL-2541.1	Contig41	1149451	1150848	84%	<p>Identities = 368/444 (82%), Positives = 401/444 (89%) sp P27306 UDHA_ECOLI UNKNOWN DEHYDROGENASE A_pir E65203 probable dehydrogenase (EC 1.8.1.-) udha - Escherichia coli gb AAC76844.1 (AE000470) putative oxidoreductase [Escherichia coli] Length = 444</p> <p>Identities = 277/358 (77%), Positives = 314/358 (87%) sp P23003 TRNA_ECOLI TRNA (URACIL-5-METHYLTRANSFERASE (TRNA(M-5-U54)-METHYLTRANSFERASE) (RUMT) pir J37321 RNA (uracil- 5-methyltransferase (EC 2.1.1.35) - Escherichia coli gb AAA24691.1 (M57568) m-5-U54 transfer RNA methyltransferase [Escherichia coli] gb AAC43071.1 (U00006) rRNA (uracil-5-methyltransferase [Escherichia coli] gb AAC76947.1 (AE000470) rRNA (uracil-5-methyltransferase [Escherichia coli] Length = 366</p>
SEQ ID n°1732	Prot n°PL-2542.1	Contig41	1146877	1147977	79%	
SEQ ID n°1733	Prot n°PL-2543.1	Contig41	1144834	1146693	73%	<p>Identities = 371/618 (60%), Positives = 467/618 (75%), Gaps = 8/618 (1%) sp P06129 BTUB_ECOLI VITAMIN B12 RECEPTOR PRECURSOR pir QRECBT vitamin b12 receptor precursor - Escherichia coli (strain K-12) gb AAC43072.1 (U00006) CG Site No. 946 [Escherichia coli] gb AAC76948.1 (AE000471) outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23 [Escherichia coli] Length = 614</p> <p>Identities = 198/288 (68%), Positives = 231/288 (79%), Gaps = 4/288 (1%) pir J41187 glutamate racemase (EC 5.1.1.3) - Escherichia coli emb CAA23637.1 (V00347) unidentified reading frame [Escherichia coli] emb CAA23638.1 (V00348) unidentified reading frame I [Escherichia coli] gb AAA23677.1 (L14556) glutamate synthase [Escherichia coli] gb AAC43073.1 (U00006) glutamate synthase [Escherichia coli] gb AAC76949.1 (AE000471) glutamate racemase, required for biosynthesis of D-glutamate and peptidoglycan [Escherichia coli] Length = 289</p>
SEQ ID n°1734	Prot n°PL-2544.1	Contig41	1144026	1144889	77%	
SEQ ID n°1735	Prot n°PL-2545.2	Contig34	113355	115319		
SEQ ID n°1736	Prot n°PL-2546.1	Contig34	112430	113044	43%	<p>Identities = 51/220 (23%), Positives = 89/220 (40%), Gaps = 39/220 (17%) pir T41309 hypothetical T/N-rich protein - fission yeast (Schizosaccharomyces pombe) emb CAA18304.1 (AL022245) hypothetical T/N-rich protein [Schizosaccharomyces pombe] Length = 658</p>
SEQ ID n°1737	Prot n°PL-2547.1	Contig34	112059	113291	23%	<p>Identities = 51/217 (23%), Positives = 96/217 (43%), Gaps = 46/217 (21%) pir JQ1866 hypothetical 87.1K protein - bovine adenovirus 3 Length =</p>
SEQ ID n°1738	Prot n°PL-2548.1	Contig34	108608	111964	No Hits found	
SEQ ID n°1739	Prot n°PL-2549.1	Contig34	105888	108614	No Hits found	
SEQ ID n°1740	Prot n°PL-255.1	Contig41	423439	424440	77%	<p>Identities = 207/301 (68%), Positives = 258/301 (84%) sp P10122 FTSX_ECOLI CELL DIVISION PROTEIN FTSX_pir CECFX cell division protein ftsX - Escherichia coli emb CAA27986.1 (X04398) ORF 3 (AA 1-352); 38 kD (put. ftsX) [Escherichia coli] gb AAB18437.1 (U00039) CG Site No. 19298 [Escherichia coli] gb AAC76487.1 (AE000422) cell division membrane protein [Escherichia coli] Length = 352 "</p>

TABLEAU I

SEQ ID n°1741	Prot n°PL-2550.1	Contig34	103306	104946	12%	Identities = 45/171 (26%), Positives = 71/171 (41%), Gaps = 18/171 (10%) gb AAF94573.1 (AE004220) vgrG protein [Vibrio cholerae] Length =
SEQ ID n°1742	Prot n°PL-2551.1	Contig34	102638	103348	No Hits found	
SEQ ID n°1743	Prot n°PL-2552.1	Contig34	100708	102030	31%	Identities = 79/285 (27%), Positives = 137/285 (47%), Gaps = 16/285 (5%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°1744	Prot n°PL-2553.1	Contig34	99212	100747	21%	Identities = 74/183 (40%), Positives = 110/183 (59%), Gaps = 1/183 (0%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°1745	Prot n°PL-2554.1	Contig34	98220	99302	28%	Identities = 77/202 (38%), Positives = 116/202 (57%), Gaps = 2/202 (0%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°1746	Prot n°PL-2555.1	Contig34	96042	96968	77%	Identities = 188/313 (60%), Positives = 246/313 (78%), Gaps = 5/313 (1%) sp P37415 YTL2_SALTY HYPOTHETICAL 35.3 KD PROTEIN NEAR TLPA OPERON pir S41385 hypothetical yadD homolog - Salmonella typhimurium emb CAA82634.1 (Z29513) 30 kDa protein similar to E. coli yadD and yhgA [Salmonella typhimurium] Length = 313
SEQ ID n°1747	Prot n°PL-2556.1	Contig34	94541	95614	No Hits found	
SEQ ID n°1748	Prot n°PL-2557.1	Contig34	93556	94566	No Hits found	
SEQ ID n°1749	Prot n°PL-2558.1	Contig34	92302	93018	No Hits found	
SEQ ID n°1750	Prot n°PL-2559.1	Contig34	90208	92301	23%	Identities = 117/263 (44%), Positives = 164/263 (61%), Gaps = 11/263 (4%) emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)] Length = 690
SEQ ID n°1751	Prot n°PL-256.1	Contig41	424406	425071	89%	sp P10115 FTSE_ECOLI CELL DIVISION ATP-BINDING PROTEIN FTSE pir ICECFE cell division ATP-binding protein ftsE - Escherichia coli emb CAA27985.1 (X04398) ORF 2 (AA 1-222); 25 kD (put. ftsE) [Escherichia coli] gb AAB18438.1 (U00039) CG Site No. 736 [Escherichia coli] gb AAC76488.1 (AE000422) ATP-binding component of a membrane-associated complex involved in cell division [Escherichia coli]
SEQ ID n°1752	Prot n°PL-2560.1	Contig34	88498	90207	No Hits found	
SEQ ID n°1753	Prot n°PL-2561.1	Contig34	87404	88471	38%	Identities = 80/362 (22%), Positives = 137/362 (37%), Gaps = 71/362 (19%) pir C48399 ABC-type transport protein ydbA.2 - Escherichia coli Length = 2020
SEQ ID n°1754	Prot n°PL-2562.1	Contig34	84379	87297	No Hits found	
SEQ ID n°1755	Prot n°PL-2563.1	Contig34	81690	84425	No Hits found	
SEQ ID n°1756	Prot n°PL-2564.1	Contig34	79134	80774	38%	Identities = 127/579 (21%), Positives = 210/579 (35%), Gaps = 88/579 (15%) emb CAB77340.1 (AL160331) hypothetical protein SCD8A.19c [Streptomyces coelicolor A3(2)] Length = 643

TABLEAU I

SEQ ID n°1757	Prot n°PL-2566.1	Contig34	76598	77836	33%	Identities = 78/276 (28%), Positives = 139/276 (50%), Gaps = 11/276 (3%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°1758	Prot n°PL-2567.1	Contig34	75220	76805	22%	Identities = 73/183 (39%), Positives = 110/183 (59%), Gaps = 1/183 (0%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°1759	Prot n°PL-2568.1	Contig34	73913	75208	28%	Identities = 86/237 (36%), Positives = 125/237 (52%), Gaps = 2/237 (0%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°1760	Prot n°PL-2569.1	Contig34	71593	72570	No Hits found	Identities = 318/497 (63%), Positives = 369/497 (73%), Gaps = 73/497 (14%) sp P10121 FTSY_ECOLI_CELL_DIVISION PROTEIN FTSY_pir CEECFY cell division protein ftsY - Escherichia coli emb CAA27984.1 (X04398) ORF 1 (AA 1-497); 48 kD (put. ftsY) [Escherichia coli] gb AAB18439.1 (U00039) CG Site No. 18295 [Escherichia coli] gb AAC76489.1 (AE000422) cell division membrane protein [Escherichia coli] Length = 497 "
SEQ ID n°1761	Prot n°PL-2570.1	Contig34	70484	71431	No Hits found	
SEQ ID n°1762	Prot n°PL-2571.1	Contig34	69495	70421	No Hits found	Identities = 114/259 (44%), Positives = 157/259 (60%), Gaps = 3/259 (1%) emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)] Length = 690
SEQ ID n°1763	Prot n°PL-2572.1	Contig34	67419	69494	22%	Identities = 32/129 (24%), Positives = 63/129 (48%), Gaps = 9/129 (6%) ref NP_065040.1 AMV258 gb AAG02964.1 AF250284_258 (AF250284) AMV258 [Amsacta moorei entomopoxvirus] Length = 826
SEQ ID n°1764	Prot n°PL-2573.1	Contig34	65847	67418	12%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°1765	Prot n°PL-2574.1	Contig34	64610	65677	21%	Identities = 47/163 (28%), Positives = 87/163 (52%), Gaps = 13/163 (7%) pir JQ1866 hypothetical 87.1K protein - bovine adenovirus 3 Length =
SEQ ID n°1766	Prot n°PL-2575.1	Contig34	63637	64602	27%	
SEQ ID n°1767	Prot n°PL-2576.1	Contig34	60541	63450	No Hits found	
SEQ ID n°1768	Prot n°PL-2577.1	Contig34	57806	60547	No Hits found	Identities = 46/171 (26%), Positives = 72/171 (41%), Gaps = 18/171 (10%) gb AAF94573.1 (AE004220) vgrG protein [Vibrio cholerae] Length =
SEQ ID n°1769	Prot n°PL-2578.1	Contig34	55191	56831	13%	Identities = 128/188 (68%), Positives = 152/188 (80%) sp P10120 YHHF_ECOLI_PROTEIN YHHF_pir QCECX3 hypothetical 21.7K protein (ftsY-nikA intergenic region) - Escherichia coli emb CAA27983.1 (X04398) ORF 4 (AA 1-198); 20 kD [Escherichia coli] gb AAB18440.1 (U00039) CG Site No. 18301 [Escherichia coli] gb AAC76490.1 (AE000422) orf, hypothetical protein [Escherichia coli]
SEQ ID n°1770	Prot n°PL-2579.1	Contig34	426512	427096	74%	

TABLEAU I

SEQ ID n°1772	Prot n°PL-2580.1	Contig34	52671	53915	33%	Identities = 77/284 (27%), Positives = 137/284 (48%), Gaps = 14/284 (4%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°1773	Prot n°PL-2581.1	Contig34	51066	52661	20%	Identities = 73/182 (40%), Positives = 109/182 (59%), Gaps = 1/182 (0%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°1774	Prot n°PL-2582.1	Contig34	50089	51165	29%	Identities = 74/202 (36%), Positives = 114/202 (55%), Gaps = 2/202 (0%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°1775	Prot n°PL-2583.1	Contig34	47536	48558	66%	Identities = 167/341 (48%), Positives = 231/341 (66%), Gaps = 32/341 (9%) gb AAAF81206.1 (AF247502) Y12 [Salmonella dublin] Length = 316
SEQ ID n°1776	Prot n°PL-2584.1	Contig34	46020	47042	41%	Identities = 104/256 (40%), Positives = 149/256 (57%), Gaps = 9/256 (3%) gb AAG09644.1 (AF135182) SepC [Serratia entomophila] Length = 973
SEQ ID n°1777	Prot n°PL-2585.1	Contig34	45049	45900	No Hits found	
SEQ ID n°1778	Prot n°PL-2586.2	Contig34	43233	44135		
SEQ ID n°1779	Prot n°PL-2587.1	Contig29	52030	52809	79%	Identities = 166/250 (66%), Positives = 206/250 (82%), gb AAAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558
SEQ ID n°1780	Prot n°PL-2588.1	Contig29	44873	50743	78%	Identities = 127/1962 (65%), Positives = 1541/1962 (78%), Gaps = 33/1962 (1%) gb AAAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558
SEQ ID n°1781	Prot n°PL-2589.1	Contig29	40006	40890	No Hits found	
SEQ ID n°1782	Prot n°PL-259.1	Contig41	427672	428298	69%	Identities = 113/208 (54%), Positives = 147/208 (70%) spiP37616 YHNN_ECOLI_HYPOTHETICAL_23.8_KD_PROTEIN_IN_FTSY-NIKA INTERGENIC REGION (O208) pir S47687 hypothetical protein o208 - Escherichia coli gb AAB18443.1 (U00039) No definition line found [Escherichia coli] gb AAC76493.1 (AE000422) putative enzyme [Escherichia coli] gb AAD21057.1 (AF119150) RtxA protein [Vibrio cholerae] Length = 768/1137 (67%), Positives = 910/1137 (79%), Gaps = 33/1137 (2%) gb AAD21057.1 (AF119150) RtxA protein [Vibrio cholerae] Length = 79/277 (28%), Positives = 126/277 (44%), Gaps = 40/277 (14%)
SEQ ID n°1783	Prot n°PL-2590.1	Contig29	39691	44889	52%	Identities = 768/1137 (67%), Positives = 910/1137 (79%), Gaps = 33/1137 (2%) gb AAD21057.1 (AF119150) RtxA protein [Vibrio cholerae] Length = 79/277 (28%), Positives = 126/277 (44%), Gaps = 40/277 (14%)
SEQ ID n°1784	Prot n°PL-2592.1	Contig29	36165	36968	47%	pir A47283 calphoton - fruit fly (Drosophila melanogaster) gb AA28420.1 (L05080) calphoton [Drosophila melanogaster] Length = 873
SEQ ID n°1785	Prot n°PL-2593.1	Contig29	28061	39079	41%	Identities = 1226/1963 (62%), Positives = 1529/1963 (77%), Gaps = 34/1963 (1%) gb AAAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558
SEQ ID n°1786	Prot n°PL-2594.1	Contig29	26618	27271	69%	Identities = 124/222 (55%), Positives = 154/222 (68%), Gaps = 18/222 (8%) gb AAAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558
SEQ ID n°1787	Prot n°PL-2595.1	Contig29	24398	25159	38%	Identities = 76/281 (27%), Positives = 97/281 (34%), Gaps = 37/281 (13%) gb AAA59875.1 (M74027) mucin [Homo sapiens] Length = 573

TABLEAU I

SEQ ID n°1788	Prot n°PL-2597.1	Contig29	16237	26727	38%	Identities = 1062/1737 (61%), Positives = 1332/1737 (76%), Gaps = 17/1737 (0%) gb AAAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558
SEQ ID n°1789	Prot n°PL-2598.1	Contig29	3245	15472	34%	Identities = 1143/1892 (60%), Positives = 1409/1892 (74%), Gaps = 85/1892 (4%) gb AAAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558
SEQ ID n°1790	Prot n°PL-2598.1	Contig29	2161	3045	59%	Identities = 126/284 (44%), Positives = 188/284 (66%), Gaps = 4/284 (1%) gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300
SEQ ID n°1791	Prot n°PL-26.1	Contig41	45567	47159	62%	Identities = 235/559 (42%), Positives = 336/559 (60%), Gaps = 32/559 (5%) emb CAB81024.1 (AL161576) putative protein [Arabidopsis thaliana] Length = 569
SEQ ID n°1792	Prot n°PL-260.1	Contig41	428443	430728	76%	Identities = 503/689 (73%), Positives = 586/689 (85%), Gaps = 8/689 (1%) emb CAA04762.1 (AJ001437) putative P-type cation-translocating membrane ATPase [Proteus mirabilis] Length = 692
SEQ ID n°1793	Prot n°PL-2600.2	Contig34	167523	188095		Identities = 87/394 (22%), Positives = 164/394 (41%), Gaps = 66/394 (16%) gb AAG00942.1 (AF272977) transposase [Mycoplasma hyopneumoniae] Length = 552
SEQ ID n°1794	Prot n°PL-2601.1	Contig34	170008	171654	29%	Identities = 56/237 (23%), Positives = 107/237 (45%), Gaps = 51/237 (21%) gb AAG07705.1 (AE004848) hypothetical protein [Pseudomonas aeruginosa] Length = 245
SEQ ID n°1795	Prot n°PL-2602.1	Contig34	171731	172501	39%	Identities = 355/430 (82%), Positives = 398/430 (92%), Gaps = 1/430 (0%) sp P09156 SYS_ECOLI SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SRRS) pir YSEC serine--trna ligase (EC 6.1.1.1) - Escherichia coli emb CAA28673.1 (X05017) seryl-trna synthetase [Escherichia coli] dbj BAA35625.1 (D90727) Serine-trna ligase (EC 6.1.1.1) [Escherichia coli] gb AAC73979.1 (AE000191) serine trna synthetase; also charges selenocysteine tRNA with serine [Escherichia coli] Length = 430 "
SEQ ID n°1796	Prot n°PL-2603.1	Contig34	172597	173886	90%	Identities = 391/447 (87%), Positives = 415/447 (92%) sp P45526 YCAJ_ECOLI HYPOTHETICAL 49.6 KDA PROTEIN IN LOLA-SERS INTERGENIC REGION pir C84828 ycaJ protein - Escherichia coli gb AAC73978.1 (AE000191) putative polynucleotide enzyme [Escherichia coli] dbj BAA35617.1 (D90726) Hypothetical protein HI1590 [Escherichia coli] dbj BAA35624.1 (D90727) Hypothetical protein HI1590 [Escherichia coli] Identities = 134/203 (66%), Positives = 161/203 (79%)
SEQ ID n°1797	Prot n°PL-2604.1	Contig34	174118	175461	92%	
SEQ ID n°1798	Prot n°PL-2605.1	Contig34	175469	176080	74%	sp P39178 LOLA_ECOLI OUTER-MEMBRANE LIPOPROTEINS CARRIER PROTEIN PRECURSOR (P20) Length = 203

TABLEAU I

SEQ ID n°1798	Prot n°PL-2606.1	Contig34	176299	179760	57%	<p>Identities = 566/954 (59%), Positives = 663/954 (69%), Gaps = 66/954 (6%) sp P46889 FTSK_ECOLI_CELL_DIVISION_PROTEIN_FTSK_pir A64828 cell division protein ftsK - Escherichia coli dbj BAA35615.1 (D90726) Cell division protein FtsK. [Escherichia coli] dbj BAA35622.1 (D90727) Cell division protein FtsK. [Escherichia coli] gb AAC73976.1 (AE000191) cell division protein [Escherichia coli] Length = 1329</p>
SEQ ID n°1800	Prot n°PL-2607.1	Contig34	180857	181816	88%	<p>Identities = 267/318 (83%), Positives = 287/318 (89%), Gaps = 1/318 (0%) sp P09625 TRXB_ECOLI_THIOREDOXIN_REDUCTASE (TRXR) pir RDCT thioresoxin reductase (NADPH) (EC 1.6.4.5) - Escherichia coli gb AAA24697.1 (J03762) thioresoxin reductase [Escherichia coli] dbj BAA35613.1 (D90726) Thioresoxin reductase (NADPH) (EC 1.6.4.5) [Escherichia coli] dbj BAA35620.1 (D90727) Thioresoxin reductase (NADPH) (EC 1.6.4.5) [Escherichia coli] gb AAC73974.1 (AE000190) thioresoxin reductase [Escherichia coli] Length = 321</p>
SEQ ID n°1801	Prot n°PL-2608.1	Contig34	181951	183720	82%	<p>Identities = 433/589 (73%), Positives = 502/589 (84%), Gaps = 1/589 (0%) sp Q52402 AARD_PROT_TRANSPORT_ATP-BINDING_PROTEIN_AARD_pir S70900 ABC-type transport protein aarD - Providencia stuartii gb AAB18930.1 (U30383) AarD [Providencia stuartii] Length = 588 Identities = 375/572 (65%), Positives = 452/572 (78%), Gaps = 2/572 (0%) sp P23886 CYDC_ECOLI_TRANSPORT_ATP-BINDING_PROTEIN_CYDC_pir B36888 ABC-type transport protein cydC - Escherichia coli gb AAA03230.1 (L10383) putative [Escherichia coli] dbj BAA35611.1 (D90726) Probable transport protein mdh [Escherichia coli] gb AAC73972.1 (AE000190) ATP-binding component of cytochrome-related transport [Escherichia coli] Length = 573</p>
SEQ ID n°1803	Prot n°PL-261.1	Contig41	431317	431991	70%	<p>Identities = 150/200 (75%), Positives = 172/200 (86%) sp P37619 YHQQ_ECOLI_HYPOTHETICAL_25.3_KD_PROTEIN_IN_FTSY-NIKA_INTERGENIC_REGION (O21) pir S47690 hypothetical 25.3K protein (ftsY-nika intergenic region) - Escherichia coli gb AAB18446.1 (U00039) No definition line found [Escherichia coli] gb AAC76496.1 (AE000423) orf, hypothetical protein [Escherichia coli] Length = 221 Identities = 129/229 (56%), Positives = 167/229 (72%), Gaps = 1/229 (0%) sp P23885 LPTP_ECOLI_LEUCYL-PHENYLALANYL-TRNA-PROTEIN_TRANSFERASE_pir A36888 leucyl, phenylalanyl-tRNA--protein transferase (EC 2.3.2.-) - Escherichia coli gb AAA03231.1 (L10383) Leu/Phe-tRNA-protein transferase [Escherichia coli] gb AAC36910.1 (M63145) orf 2 [Escherichia coli] dbj BAA35610.1 (D90726) Leucyltransferase (EC 2.3.2.6) [Escherichia coli] gb AAC73971.1 (AE000190) leucyl, phenylalanyl-tRNA-protein transferase [Escherichia coli] Length = 234</p>
SEQ ID n°1804	Prot n°PL-2610.1	Contig34	185475	186170	71%	

TABLEAU I

SEQ ID n°1806	Prot n°PL-2611.1	Contig34	186645	188921	89%	<p>Identities = 628/755 (83%), Positives = 685/755 (90%), Gaps = 1/755 (0%)</p> <p>sp P15716 CLPA_ECOLI ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA pir J5UECCA endopeptidase Clp ATP-binding chain A - Escherichia coli dbj BAA35601.1 (D90725) ATP-dependent Clp protease ATP-binding subunit ClpA. [Escherichia coli] gb AAC73969.1 (AE000190) ATP-binding component of serine protease [Escherichia coli]</p> <p>Length = 758</p>
SEQ ID n°1808	Prot n°PL-2612.2	Contig34	188919	191862		<p>Identities = 212/362 (58%), Positives = 272/362 (74%), Gaps = 1/362 (0%)</p> <p>sp P75830 YBJE_ECOLI HYPOTHETICAL 41.7 KDA PROTEIN IN AQPZ-CSPD INTERGENIC REGION dbj BAA35597.1 (D90725) MtC protein [Escherichia coli] Length = 371</p>
SEQ ID n°1807	Prot n°PL-2613.1	Contig34	191862	192974	73%	<p>Identities = 189/301 (62%), Positives = 234/301 (78%), Gaps = 1/301 (0%)</p> <p>sp P75826 YBJE_ECOLI HYPOTHETICAL 34.4 KD PROTEIN IN POXB-AQPZ INTERGENIC REGION pir J584826 probable membrane protein ybjE - Escherichia coli gb AAC73961.1 (AE000189) putative surface protein [Escherichia coli] Length = 315</p>
SEQ ID n°1808	Prot n°PL-2614.1	Contig34	193295	194194	76%	<p>Identities = 187/242 (77%), Positives = 211/242 (86%)</p> <p>sp P30858 ARTP_ECOLI ARGININE TRANSPORT ATP-BINDING PROTEIN ARTP pir J584824 arginine transport protein artP - Escherichia coli dbj BAA35578.1 (D90724) Periplasmic transport system protein artP. [Escherichia coli] gb AAC73951.1 (AE000188) ATP-binding component of 3rd arginine transport system [Escherichia coli]</p>
SEQ ID n°1809	Prot n°PL-2615.1	Contig34	194498	195226	86%	<p>Identities = 168/245 (68%), Positives = 205/245 (83%), Gaps = 2/245 (0%)</p> <p>sp P30859 ARTI_ECOLI ARGinine-BINDING PERIPLASMIC PROTEIN 1 PRECURSOR pir J584824 arginine-binding periplasmic protein 1 precursor - Escherichia coli dbj BAA35577.1 (D90724) Arginine binding protein artI [Escherichia coli] gb AAC73950.1 (AE000188) arginine 3rd transport system periplasmic binding protein [Escherichia coli] Length = 243</p>
SEQ ID n°1810	Prot n°PL-2616.1	Contig34	195246	195980	82%	<p>Identities = 176/235 (74%), Positives = 207/235 (87%)</p> <p>sp P30861 ARTQ_ECOLI ARGinine TRANSPORT SYSTEM PERMEASE PROTEIN ARTQ pir J584824 arginine transport system permease protein artQ - Escherichia coli dbj BAA35576.1 (D90724) Arginine transport system protein artQ. [Escherichia coli] gb AAC73949.1 (AE000188) arginine 3rd transport system permease protein [Escherichia coli] Length = 159/222 (71%), Positives = 193/222 (86%)</p>
SEQ ID n°1811	Prot n°PL-2617.1	Contig34	195995	196711	84%	<p>Identities = 159/222 (71%), Positives = 193/222 (86%)</p> <p>sp P30862 ARTM_ECOLI ARGinine TRANSPORT SYSTEM PERMEASE PROTEIN ARTM pir J584824 arginine transport system permease protein artM - Escherichia coli dbj BAA35575.1 (D90724) Arginine transport system protein artM. [Escherichia coli] gb AAC73948.1 (AE000188) arginine 3rd transport system permease protein [Escherichia coli] Length = 159/222 (71%), Positives = 193/222 (86%)</p>
SEQ ID n°1812	Prot n°PL-2618.1	Contig34	196708	197379	84%	<p>Identities = 159/222 (71%), Positives = 193/222 (86%)</p> <p>sp P30862 ARTM_ECOLI ARGinine TRANSPORT SYSTEM PERMEASE PROTEIN ARTM pir J584824 arginine transport system permease protein artM - Escherichia coli dbj BAA35575.1 (D90724) Arginine transport system protein artM. [Escherichia coli] gb AAC73948.1 (AE000188) arginine 3rd transport system permease protein [Escherichia coli] Length = 159/222 (71%), Positives = 193/222 (86%)</p>

TABLEAU I

SEQ ID n°1813	Prot n°PL-2619.2	Contig34	197433	198566			Identities = 126/284 (44%), Positives = 188/284 (65%), Gaps = 4/284 (1%) gb AAC26598.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300
SEQ ID n°1814	Prot n°PL-262.1	Contig41	432288	433172	59%		Identities = 103/201 (51%), Positives = 139/201 (68%), Gaps = 5/201 (2%) (AF020809) putative permease Mig-13 [Salmonella typhimurium] Length = 202
SEQ ID n°1815	Prot n°PL-2620.1	Contig34	200497	201105	66%		Identities = 335/433 (77%), Positives = 386/433 (88%), Gaps = 5/433 (1%) sp P36569 SDAC_ECOLI SERINE TRANSPORTER pir IS45633 serine transport protein sdaC - Escherichia coli gb AAA50169.1 (U01233) putative serine transporter [Escherichia coli] gb AAB40446.1 (U28581) putative serine transporter [Escherichia coli] gb AAC75838.1 (AE000363) probable serine transporter [Escherichia coli] Length = 429
SEQ ID n°1816	Prot n°PL-2621.1	Contig34	202012	203310	87%		
SEQ ID n°1817	Prot n°PL-2622.1	Contig34	203388	204221	No Hits found		
SEQ ID n°1818	Prot n°PL-2623.1	Contig34	207263	208168	No Hits found		
SEQ ID n°1819	Prot n°PL-2624.1	Contig34	208385	208590	77%		Identities = 267/374 (71%), Positives = 312/374 (83%), Gaps = 1/374 (0%) sp P08506 DACC_ECOLI PENICILLIN-BINDING PROTEIN 6 PRECURSOR (D- ALANYL-D-ALANINE CARBOXYPEPTIDASE) (PBP-6) pir G64821 serine- PEPTIDASE) (DD-CARBOXYPEPTIDASE) (PBP-6) pir G64821 serine- type D-Ala-D-Ala carboxypeptidase (EC 3.4.16.4) dacC precursor - Escherichia coli dbj BAA35542.1 (D90722) Penicillin-binding protein 6 precursor. [Escherichia coli] gb AAC73926.1 (AE000186) D-alanyl-D-alanine carboxypeptidase; penicillin-binding protein 6 [Escherichia coli] Length = 400 "
SEQ ID n°1820	Prot n°PL-2625.1	Contig34	210021	210641	64%		Identities = 111/206 (53%), Positives = 142/206 (68%) gb AAG06201.1 AE004708_7 (AE004708) probable glutathione S-transferase [Pseudomonas aeruginosa] Length = 206
SEQ ID n°1821	Prot n°PL-2626.1	Contig34	210648	211475	66%		Identities = 165/274 (60%), Positives = 198/274 (72%), Gaps = 1/274 (0%) sp P76370 YEEZ_ECOLI PROTEIN YEEZ PRECURSOR pir G64966 hypothetical protein b2016 - Escherichia coli gb AAC75077.1 (AE000293) putative enzyme of sugar metabolism [Escherichia coli] Length = 274
SEQ ID n°1822	Prot n°PL-2627.1	Contig34	211904	212815	90%		Identities = 261/299 (87%), Positives = 274/299 (91%) sp P10366 HIS1_ECOLI ATP PHOSPHORIBOSYLTRANSFERASE pir I56436 ATP phosphoribosyltransferase - Escherichia coli pir XREC ATP phosphoribosyltransferase (EC 2.4.2.17) - Escherichia coli emb CAA45224.1 (X63697) ATP-phosphoribosyl transferase [Escherichia coli] gb AAA19742.1 (U02070) ATP phosphoribosyltransferase [Escherichia coli] dbj BAA15850.1 (D90840) ATP phosphoribosyltransferase (EC 2.4.2.17) [Escherichia coli] gb AAC75080.1 (AE000293) ATP phosphoribosyltransferase [Escherichia coli] Length = 299

TABLEAU I

SEQ ID n°1823	Prot n°PL-2628.1	Contig34	212822	215245	43%	<p>Identities = 308/428 (71%), Positives = 353/428 (81%)</p> <p>sp P10370 HISX_SALTY HISTIDINOL DEHYDROGENASE (HDH) pir DDEEBHT histidinol dehydrogenase (EC 1.1.1.23) - Salmonella typhimurium emb CAA31823.1 (X13464) hisD ORF (AA 1-434) [Salmonella typhimurium] gb AAA88615.1 (J01804) histidinol dehydrogenase [Salmonella typhimurium] gb AAAT73023.1 (M64753) histidinol dehydrogenase [unidentified cloning vector] gb AAAT73024.1 (M64754) histidinol dehydrogenase [unidentified vector] identities = 285/356 (80%), Positives = 309/356 (86%) pir DWECHB hisB bifunctional enzyme - Escherichia coli gb AAC75083.1 (AE000293) imidazoleglycerol-phosphate dehydratase and histidinol-phosphate phosphatase [Escherichia coli] Length = 356</p>
SEQ ID n°1824	Prot n°PL-2629.1	Contig34	215242	216312	84%	<p>Identities = 214/365 (58%), Positives = 280/365 (76%), Gaps = 2/365 (0%)</p> <p>sp P45511 GLDA_CITFR GLYCEROL DEHYDROGENASE (GLDH) gb AAB48844.1 (U09771) glycerol dehydrogenase [Citrobacter freundii] Length = 365</p>
SEQ ID n°1825	Prot n°PL-263.1	Contig41	434799	435899	72%	<p>Identities = 132/201 (65%), Positives = 158/201 (77%), Gaps = 5/201 (2%)</p> <p>sp P10375 HIS5_ECOLI AMIDOTRANSFERASE HIS5 pir XQECHH imidazole glycerol phosphate synthase (EC 2.4.2.-) chain hisH - Escherichia coli emb CAA31815.1 (X13462) hisH ORF (AA 1-196) [Escherichia coli] dbj BAA15854.1 (D90840) Amidotransferase HisH (EC 2.4.2.-) [Escherichia coli] dbj BAA15862.1 (D90841) Amidotransferase HisH (EC 2.4.2.-) [Escherichia coli] gb AAC75084.1 (AE000293) glutamine amidotransferase subunit of heterodimer with HisF = imidazole glycerol phosphate synthase holoenzyme [Escherichia coli] dbj BAA77742.1 (AB008676) aminotransferase [Escherichia coli] Length = 196</p>
SEQ ID n°1826	Prot n°PL-2630.1	Contig34	216309	216917	69%	<p>Identities = 166/245 (67%), Positives = 205/245 (82%) dbj BAA77741.1 (AB008676) phosphoribosylformimino-5 aminimidazole carboxamide ribotide isomerase [Escherichia coli] Length = 245</p>
SEQ ID n°1827	Prot n°PL-2631.1	Contig34	216923	217660	77%	<p>Identities = 215/258 (83%), Positives = 239/258 (92%)</p> <p>sp P10374 HIS6_SALTY HISF PROTEIN (CYCLASE) pir OYEBHF cyclase hisF - Salmonella typhimurium emb CAA31828.1 (X13464) hisF ORF (AA 1-258) [Salmonella typhimurium] Length = 258</p>
SEQ ID n°1828	Prot n°PL-2632.1	Contig34	217642	218418	89%	<p>Identities = 150/201 (74%), Positives = 175/201 (86%) dbj BAA77739.1 (AB008676) phosphoribosyl-AMP cyclohydrolase [Escherichia coli] Length = 203</p>
SEQ ID n°1829	Prot n°PL-2633.1	Contig34	218412	219017	81%	<p>Identities = 255/381 (66%), Positives = 306/381 (79%)</p> <p>sp P37686 ADH2_ECOLI PROBABLE ALCOHOL DEHYDROGENASE pir S47810 probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli gb AAB18566.1 (U00039) No definition line found [Escherichia coli] gb AAC76613.1 (AE000436) putative oxidoreductase [Escherichia coli]</p>
SEQ ID n°1830	Prot n°PL-2634.1	Contig34	219299	220450	78%	

TABLEAU I

SEQ ID n°1831	Prot n°PL-2635.1	Contig34	221973	222599	44%	<p>Identities = 56/202 (27%), Positives = 92/202 (44%), Gaps = 11/202 (5%) sp P54657 CAD1_DICDI CALCIUM-DEPENDENT CELL ADHESION MOLECULE-1 (DDCAD-1) (GP24) gb AAC47135.1 (U49650) dictyostelium discoideum calcium-dependent cell adhesion molecule-1 DdCAD-1 [Dictyostelium discoideum] Length = 213</p>
SEQ ID n°1832	Prot n°PL-2636.1	Contig34	223249	224655	89%	<p>Identities = 405/469 (86%), Positives = 434/469 (92%), Gaps = 2/469 (0%) sp P14062 BPGD_SALTY 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING pir S04397 phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - Salmonella typhimurium emb CAA33877.1 (X15651) 6-phosphogluconate dehydrogenase (AA 1-468) [Salmonella enterica] gb AAA27137.1 (M64332) 6-phosphogluconate dehydrogenase [Salmonella typhimurium] Length = 468</p>
SEQ ID n°1833	Prot n°PL-2637.1	Contig34	224901	226472	83%	<p>Identities = 357/526 (67%), Positives = 444/526 (83%), Gaps = 2/526 (0%) sp P76389 YEGH_ECOLI HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION Length = 527</p>
SEQ ID n°1834	Prot n°PL-2638.1	Contig34	226963	228795	61%	<p>Identities = 255/610 (41%), Positives = 386/610 (62%), Gaps = 7/610 (1%) sp P28248 ASMA_ECOLI ASMA PROTEIN PRECURSOR pir G64972 yegA protein precursor - Escherichia coli db BAA15917.1 (D90844) ORF_ID: o355#3; similar to [SwissProt Accession Number P28248] [Escherichia coli] gb AAC75125.1 (AE000296) suppressor of ompF assembly mutants [Escherichia coli] Length = 617</p>
SEQ ID n°1835	Prot n°PL-2639.1	Contig34	228854	229435	79%	<p>Identities = 186/193 (96%), Positives = 178/193 (92%) sp P28248 DCD_ECOLI DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (DCTP DEAMINASE) pir A42940 dCTP deaminase (EC 3.5.4.13) - Escherichia coli gb AAA23869.1 (M90069) deoxycytidine triphosphate deaminase [Escherichia coli] db BAA15918.1 (D90844) Deoxycytidine triphosphate deaminase (EC 3.5.4.13) (DCTP deaminase) [Escherichia coli] db BAA15923.1 (D90845) Deoxycytidine triphosphate deaminase (EC 3.5.4.13) (DCTP deaminase) [Escherichia coli] gb AAC75126.1 (AE000296) 2'-deoxycytidine 5'-triphosphate deaminase [Escherichia coli] Length = 193</p>
SEQ ID n°1836	Prot n°PL-264.1	Contig41	436668	437852	30%	<p>Identities = 73/189 (38%), Positives = 120/189 (62%), Gaps = 1/189 (0%) gb AAF83821.1 AE0003938_12 (AE0003938) hemolysin-type calcium binding protein [Xylella fastidiosa] Length = 1636</p>
SEQ ID n°1837	Prot n°PL-2640.1	Contig34	229489	230130	78%	<p>Identities = 168/213 (78%), Positives = 188/213 (87%) pir A64973 uridine kinase (EC 2.7.1.48) - Escherichia coli gb AAC75127.1 (AE000296) uridine/cytidine kinase [Escherichia coli] Length = 231</p>
SEQ ID n°1838	Prot n°PL-2641.1	Contig34	230388	231524	85%	<p>Identities = 282/374 (75%), Positives = 323/374 (85%), Gaps = 1/374 (0%) sp P21590 MRP_ECOLI MRP PROTEIN pir H64978 probable ATPase mrp - Escherichia coli gb AAA60527.1 (U00007) mrp [Escherichia coli] gb AAC75174.1 (AE000300) putative ATPase [Escherichia coli] pir 2014253F ATPase [Escherichia coli] Length = 379</p>

TABLEAU I

SEQ ID n°1839	Prot n°PL-2643.1	Contig34	231762	233789	89%	Identities = 568/678 (82%), Positives = 622/678 (91%), Gaps = 2/678 (0%) gb AA60526.1 (U00007) methionyl-tRNA synthetase [Escherichia coli] prf 2014253G Met-tRNA synthetase [Escherichia coli] Length = 680
SEQ ID n°1840	Prot n°PL-2644.1	Contig34	235112	235771	No Hits found	Identities = 168/227 (73%), Positives = 205/227 (90%) spiP33373 YOHK_ECOLI HYPOTHETICAL 24.5 KD PROTEIN IN PBPG-CDD INTERGENIC REGION prf G64982 yohK protein - Escherichia coli (strain K-12) gb AAC75203.1 (AE000303) putative serotonin transporter [Escherichia coli] Identities = 175/290 (60%), Positives = 204/290 (70%), Gaps = 1/290 (0%) spiP13652 CDD_ECOLI CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA) prf F64982 cytidine deaminase (EC 3.5.4.5) - Escherichia coli pdb 1CTT Cytidine Deaminase (Cda) (E.C.3.5.4.5) Complexed With 3,4-Dihydrozebularine (Dhz) pdb 1AF2 A Chain A, Crystal Structure Of Cytidine Deaminase Complexed With Uridine pdb 1ALN Crystal Structure Of Cytidine Deaminase Complexed With 3-Deazacytidine pdb 1CTU Cytidine Deaminase (Cda) (E.C.3.5.4.5) Complexed With 3,4 Hydrated Pyrimidine-2-One Riboside (Zeb) gb AA23542.1 (M60916) cytidine deaminase [Escherichia coli] gb AA60533.1 (U00007) cytidine deaminase [Escherichia coli] gb AAC75204.1 (AE000303) cytidine/deoxycytidine deaminase [Escherichia coli] prf 2014253BU cytidine deaminase [Escherichia coli] Length = 294
SEQ ID n°1842	Prot n°PL-2646.1	Contig34	237209	238093	62%	Identities = 429/569 (75%), Positives = 489/569 (85%) spiP26616 MAO1_ECOLI NAD-DEPENDENT MALIC ENZYME (NAD-ME) prf B64901 malate dehydrogenase (oxaloacetate-decarboxylating) (EC 1.1.1.38), NAD-linked - Escherichia coli db BAA15127.1 (D90788) SfcA protein (fragment) [Escherichia coli] db BAA15136.1 (D90789) SfcA protein (fragment) [Escherichia coli] db BAA15146.1 (D90790) SfcA protein (fragment) [Escherichia coli] gb AAC74552.1 (AE000245) NAD-linked malate dehydrogenase (malic enzyme) [Escherichia coli] Length = 574
SEQ ID n°1843	Prot n°PL-2647.1	Contig34	238344	240041	77%	Identities = 168/239 (70%), Positives = 201/239 (83%) spiP33017 SANA_ECOLI SANA PROTEIN prf G64982 sanA protein - Escherichia coli (strain K-12) gb AAC75205.1 (AE000303) vancomycin sensitivity [Escherichia coli] Length = 239
SEQ ID n°1844	Prot n°PL-2648.1	Contig34	240308	241048	80%	Identities = 181/372 (48%), Positives = 244/372 (64%), Gaps = 1/372 (0%) spiP25747 YEIB_ECOLI HYPOTHETICAL 43.4 KD PROTEIN IN GALS-FOLE INTERGENIC REGION prf G64983 hypothetical 43.4 kD protein in galS-fole intergenic region - Escherichia coli gb AA60506.1 (U00007) yeiB [Escherichia coli] gb AAC75213.1 (AE000304) orf, hypothetical protein [Escherichia coli] prf 2014253AW yeiB gene [Escherichia coli] Length = 385
SEQ ID n°1845	Prot n°PL-2649.1	Contig34	241020	242168	62%	

TABLEAU I

SEQ ID n°1846	Prot n°PL-265.1	Contig41	439187	440539	91%	<p>sp P08194 GLPT_ECOLI GLYCEROL-3-PHOSPHATE TRANSPORTER (G-3-P TRANSPORTER) (G-3-P PERMEASE) pir JNECGT glycerol-3-phosphate transport protein - Escherichia coli emb CAA68598.1 (Y00536) glycerol-3-phosphatase transporter (AA 1 - 452, gtpT) [Escherichia coli] gb AAC75300.1 (AE000314) sn-glycerol-3-phosphate permease [Escherichia coli] db JBA16059.1 (D90855) glycerol-3-phosphate transport protein [Escherichia coli] sp P27511 GCH1_ECOLI GTP CYCLOHYDROLASE I (GTP-CH-I) pir JH64983 GTP cyclohydrolase I (EC 3.5.4.16) - Escherichia coli emb CAA45365.1 (X63910) GTP cyclohydrolase I [Escherichia coli] gb AAA60535.1 (U00007) GTP cyclohydrolase I [Escherichia coli] gb AAC75214.1 (AE000304) GTP cyclohydrolase I [Escherichia coli] pr J2014253AX GTP cyclohydrolase I [Escherichia coli] Length = 222</p> <p>Identities = 190/220 (86%), Positives = 196/220 (88%), Gaps = 2/220 (0%)</p>
SEQ ID n°1847	Prot n°PL-2650.1	Contig34	242190	242849	85%	<p>sp P12281 MOEA_ECOLI MOLYBDOPROTEIN BIOSYNTHESIS MOEA PROTEIN pir J32352 molybdopterin biosynthesis protein moeA - Escherichia coli gb AAA23579.1 (M21151) chIE protein [Escherichia coli] db BAA35515.1 (D90720) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] db JBA35522.1 (D90721) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] gb AAC73914.1 </p> <p>Identities = 171/245 (69%), Positives = 199/245 (80%)</p>
SEQ ID n°1848	Prot n°PL-2651.1	Contig34	243043	244221	55%	<p>sp P12281 MOEA_ECOLI MOLYBDOPROTEIN BIOSYNTHESIS MOEA PROTEIN pir J32352 molybdopterin biosynthesis protein moeA - Escherichia coli gb AAA23579.1 (M21151) chIE protein [Escherichia coli] db BAA35515.1 (D90720) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] db JBA35522.1 (D90721) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] gb AAC73914.1 </p> <p>Identities = 163/363 (44%), Positives = 218/363 (59%), Gaps = 4/363 (1%)</p>
SEQ ID n°1849	Prot n°PL-2652.1	Contig34	244715	245461	53%	<p>sp P12281 MOEA_ECOLI MOLYBDOPROTEIN BIOSYNTHESIS MOEA PROTEIN pir J32352 molybdopterin biosynthesis protein moeA - Escherichia coli gb AAA23579.1 (M21151) chIE protein [Escherichia coli] db BAA35515.1 (D90720) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] db JBA35522.1 (D90721) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] gb AAC73914.1 </p> <p>Identities = 105/248 (42%), Positives = 145/248 (58%), Gaps = 9/248 (3%)</p>
SEQ ID n°1850	Prot n°PL-2653.1	Contig34	245683	246924	77%	<p>sp P12281 MOEA_ECOLI MOLYBDOPROTEIN BIOSYNTHESIS MOEA PROTEIN pir J32352 molybdopterin biosynthesis protein moeA - Escherichia coli gb AAA23579.1 (M21151) chIE protein [Escherichia coli] db BAA35515.1 (D90720) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] db JBA35522.1 (D90721) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] gb AAC73914.1 </p> <p>Identities = 268/404 (66%), Positives = 325/404 (80%)</p>
SEQ ID n°1851	Prot n°PL-2654.1	Contig34	246924	247676	78%	<p>sp P12281 MOEA_ECOLI MOLYBDOPROTEIN BIOSYNTHESIS MOEA PROTEIN pir J32352 molybdopterin biosynthesis protein moeA - Escherichia coli gb AAA23579.1 (M21151) chIE protein [Escherichia coli] db BAA35515.1 (D90720) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] db JBA35522.1 (D90721) Molybdopterin biosynthesis MoeA protein. [Escherichia coli] gb AAC73914.1 </p> <p>Identities = 171/245 (69%), Positives = 199/245 (80%)</p>
SEQ ID n°1852	Prot n°PL-2655.2	Contig34	247775	249130	No Hits found	
SEQ ID n°1853	Prot n°PL-2658.1	Contig33	203904	204899	No Hits found	
SEQ ID n°1854	Prot n°PL-2659.1	Contig33	202071	202967	No Hits found	

TABLEAU I

SEQ ID n°1856	Prot n°PL-266.1	Contig41	440719	441795	84%	<p>Identities = 259/358 (72%), Positives = 307/358 (85%), Gaps = 4/358 (1%) spiP09394 GLPQ_ECOLI_GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE, PERIPLASMIC PRECURSOR (GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE) pir S15945 glycerophosphodiester phosphodiesterase (EC 3.1.4.46) precursor, periplasmic - Escherichia coli emb CAA40223.1 (X56907) glycerophosphocholine phosphodiesterase [Escherichia coli] gb AAC75299.1 (AE000314) glycerophosphodiester phosphodiesterase, periplasmic [Escherichia coli] dbj BAA16058.1 (D90855) glycerophosphodiester phosphodiesterase (EC 3.1.4.46) precursor, periplasmic [Escherichia coli] prf 1712315A glycerophosphoryl diester esterase [Escherichia coli] Length = 358</p>	Unknown, similar to toxins
SEQ ID n°1856	Prot n°PL-2660.1	Contig33	200544	209468	46%	<p>Identities = 964/3204 (30%), Positives = 1398/3204 (43%), Gaps = 539/3204 (16%) gb AAF84995.1 AE004032_14 (AE004032) hemagglutinin-like secreted protein [Xylella fastidiosa] Length = 3442</p>	
SEQ ID n°1857	Prot n°PL-2661.1	Contig33	198870	200534	56%	<p>Identities = 236/546 (43%), Positives = 323/546 (58%), Gaps = 26/546 (4%) gb AAF85347.1 AE004062_2 (AE004062) outer membrane hemolysin activator protein [Xylella fastidiosa] Length = 597</p>	
SEQ ID n°1858	Prot n°PL-2662.1	Contig33	196486	197286	49%	<p>Identities = 96/281 (34%), Positives = 137/281 (48%), Gaps = 28/281 (9%) pir G75120 hypothetical protein PAB0518 - Pyrococcus abyssi (strain Orsay) emb CAB49680.1 (A248285) hypothetical protein [Pyrococcus abyssi] Length = 272</p>	
SEQ ID n°1859	Prot n°PL-2663.1	Contig33	190214	195274	72%	<p>Identities = 951/1658 (57%), Positives = 1218/1658 (73%), Gaps = 22/1658 (1%) pir G65028 hypothetical protein b2520 - Escherichia coli (strain K-12) gb AAC75573.1 (AE000338) orf, hypothetical protein [Escherichia coli] Length = 1653</p>	
SEQ ID n°1860	Prot n°PL-2664.1	Contig33	187836	190235	72%	<p>Identities = 463/759 (61%), Positives = 582/759 (76%), Gaps = 8/759 (1%) spiP76577 PBPC_ECOLI_BIFUNCTIONAL PENICILLIN-BINDING PROTEIN 1C PRECURSOR (PBP-1C) pir F65028 hypothetical protein b2519 - Escherichia coli (strain K-12) gb AAC75572.1 (AE000338) putative peptidoglycan enzyme [Escherichia coli] gb AAB48052.1 (U88571) bifunctional penicillin-binding protein 1C [Escherichia coli] Identities = 323/379 (85%), Positives = 351/379 (92%)</p>	
SEQ ID n°1861	Prot n°PL-2666.1	Contig33	185830	186966	86%	<p>spiP36979 YFGB_ECOLI_HYPOTHETICAL 43.1 KD PROTEIN IN NDK-GCPE INTERGENIC REGION pir D66028 hypothetical 43.1 kD protein in ndk-gcpe intergenic region - Escherichia coli (strain K-12) gb AAA21359.1 (U02965) unknown [Escherichia coli] gb AAC75570.1 (AE000338) orf, hypothetical protein [Escherichia coli] dbj BAA16404.1 (D90881) similar to [SwissProt Accession Number P36979] [Escherichia coli] dbj BAA16408.1 (D90882) similar to [SwissProt Accession Number P36979]</p>	

TABLEAU I

SEQ ID n°1862	Prot n°PL-2667.1	Contig33	184150	185190	59%	Identities = 172/348 (49%), Positives = 221/348 (63%), Gaps = 17/348 (4%) sp P27434 YFGA_ECOLI_HYPOTHETICAL 36.2 KD PROTEIN IN NDK-GCPE INTERGENIC REGION pir J065028 hypothetical 36.2K protein (ndk-gcpe intergenic region) - Escherichia coli gbl AAC75569.1 (AE000338) putative membrane protein [Escherichia coli] dbj BAA16403.1 (D90881) similar to [SwissProt Accession Number P27434] [Escherichia coli] Length = 337
SEQ ID n°1863	Prot n°PL-2668.1	Contig33	182955	184076	84%	Identities = 326/362 (90%), Positives = 353/362 (97%) sp P72241 GCPE_PROST GCPE PROTEIN HOMOLOG gbl AAB51469.1 (U67933) AarC [Providencia stuartii] Length = 365
SEQ ID n°1884	Prot n°PL-2669.1	Contig33	181559	182838	86%	Identities = 328/424 (77%), Positives = 369/424 (86%), Gaps = 1/424 (0%) sp P04804 SYH_ECOLI_HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS) pir J065027 histidine-tRNA ligase (EC 6.1.1.21) - Escherichia coli pdb 1KMMIC Chain C, Histidyl-Trna Synthetase Complexed With Histidyl-Adenylate pdb 1KMNIA Chain A, Histidyl-Trna Synthetase Complexed With Histidyl-Adenylate pdb 1KMNIC Chain C, Histidyl-Trna Synthetase Complexed With Histidinol And Atp pdb 1KMNIA Chain A, Histidyl-Trna Synthetase Complexed With Histidinol And Atp pdb 1KMMIB Chain B, Histidyl-Trna Synthetase Complexed With Histidyl-Adenylate pdb 1KMMID Chain D, Histidyl-Trna Synthetase Complexed With Histidyl-Adenylate pdb 1KMNIB Chain B, Histidyl-Trna Synthetase Complexed With Histidinol And Atp pdb 1KMNID Chain D, Histidyl-Trna Synthetase Complexed With Histidinol And Atp gbl AAA03226.1 (M11843) histidine-tRNA synthetase [Escherichia coli] gbl AAC75567.1 (AE000337) histidine-tRNA synthetase [Escherichia coli] dbj BAA16401.1 (D90880) histidine-tRNA synthetase [Escherichia coli] gbl AAC75566.1 (AE000488) putative lysyl-tRNA synthetase [Escherichia coli] Length = 335
SEQ ID n°1865	Prot n°PL-267.1	Contig41	441845	442855	83%	Identities = 262/329 (78%), Positives = 283/328 (86%) pir J065027 histidine-tRNA synthetase (EC 6.1.1.6) genX - Escherichia coli gbl AAA97054.1 (U14003) lysyl-tRNA synthetase analog [Escherichia coli] gbl AAC77115.1 (AE000488) putative lysyl-tRNA synthetase [Escherichia coli] Length = 335
SEQ ID n°1866	Prot n°PL-2670.1	Contig33	180927	181547	66%	Identities = 98/205 (47%), Positives = 142/205 (68%) sp P76576 YFGM_ECOLI_HYPOTHETICAL 22.2 KD PROTEIN IN XSEA-HISS INTERGENIC REGION pir J065027 hypothetical protein b2513 - Escherichia coli (strain K-12) gbl AAC75566.1 (AE000337) orf, hypothetical protein [Escherichia coli] Length = 206
SEQ ID n°1867	Prot n°PL-2671.1	Contig33	179740	180912	80%	Identities = 270/393 (68%), Positives = 323/393 (81%), Gaps = 4/393 (1%) sp P7774 YFGL_ECOLI_HYPOTHETICAL 41.9 KD PROTEIN IN XSEA-HISS INTERGENIC REGION pir J065027 hypothetical protein b2512 - Escherichia coli (strain K-12) gbl AAC75565.1 (AE000337) putative dehydrogenase [Escherichia coli] dbj BAA16398.1 (D90880) SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-) Length = 392

TABLEAU I

SEQ ID n°1866	Prot n°PL-2672.1	Contig33	177968	179449	89%	<p>Identities = 408/494 (82%), Positives = 446/494 (89%), Gaps = 4/494 (0%) sp P77254 YFGK_ECOLI_HYPOTHETICAL GTP-BINDING PROTEIN IN XSEA- HISS INTERGENIC REGION pir JF65027 probable GTPase/GTP-binding protein b2511 - Escherichia coli (strain K-12) gb AAC75564.1 (AE000337) putative GTP-binding factor [Escherichia coli] dbj BAA16397.1 (D90880) similar to [SwissProt Accession Number P44536] [Escherichia coli] Length = 503</p>	Unknown, similar to toxins
SEQ ID n°1868	Prot n°PL-2673.1	Contig33	176368	177465	64%	<p>Identities = 182/344 (52%), Positives = 245/344 (70%), Gaps = 9/344 (2%) sp Q98132 PRT1_ERWCA EXTRACELLULAR METALLOPROTEASE PRECURSOR pir J441048 extracellular metalloproteinase (EC 3.4.24.-) precursor - Erwinia carotovora subsp. carotovora gb AA24868.1 (M36851) extracellular protease (prt) [Pectobacterium carotovorum] Length = 347</p>	
SEQ ID n°1870	Prot n°PL-2674.1	Contig33	175227	176135	81%	<p>Identities = 213/299 (71%), Positives = 255/299 (85%), Gaps = 2/299 (0%) sp P33771 HEM6_SALTY COPROPORPHYRINOGEN III OXIDASE, AEROBIC (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) pir B53302 coproporphyrinogen oxidase (EC 1.3.3.3) - Salmonella typhimurium gb AA27139.1 (L19503) oxygen-dependent coproporphyrinogen III oxidase [Salmonella typhimurium] Length Identities = 93/193 (48%), Positives = 127/193 (65%), Gaps = 2/193 (1%)</p>	
SEQ ID n°1871	Prot n°PL-2675.1	Contig33	173334	173915	60%	<p>pir G65017 hypothetical protein b2432 - Escherichia coli (strain K-12) gb AAC75485.1 (AE000330) orf, hypothetical protein [Escherichia coli] Length = 191</p>	
SEQ ID n°1872	Prot n°PL-2676.1	Contig33	171944	172981	79%	<p>Identities = 234/324 (72%), Positives = 275/324 (84%) sp P16700 CYSP_ECOLI_THIOSULFATE-BINDING PROTEIN PRECURSOR pir JUGECT thiosulfate-binding protein cysP precursor - Escherichia coli gb AAA23636.1 (M32101) thiosulfate binding protein [Escherichia coli] gb AAC75478.1 (AE000330) thiosulfate binding protein [Escherichia coli] dbj BAA16299.1 (D90871) thiosulfate-binding protein cysP precursor [Escherichia coli] dbj BAA16308.1 (D90872) thiosulfate-binding protein cysP precursor [Escherichia coli] Length = 338</p>	
SEQ ID n°1873	Prot n°PL-2677.1	Contig33	171111	171944	91%	<p>Identities = 228/277 (82%), Positives = 255/277 (91%) sp P16701 CYST_ECOLI_SULFATE TRANSPORT SYSTEM PERMEASE PROTEIN CYST pir JQRECST sulfate/thiosulfate transport protein cysT - Escherichia coli gb AAA23637.1 (M32101) cysT [Escherichia coli] gb AAC75477.1 (AE000330) sulfate, thiosulfate transport system permease T protein [Escherichia coli] dbj BAA16298.1 (D90871) SULFATE TRANSPORT SYSTEM PERMEASE PROTEIN CYST. [Escherichia coli] dbj BAA16307.1 (D90872) SULFATE TRANSPORT SYSTEM PERMEASE PROTEIN CYST. [Escherichia coli] Length = 277</p>	

TABLEAU I

SEQ ID n°1874	Prot n°PL-2678.1	Contig33	170266	171111	84%	<p>Identities = 208/279 (74%), Positives = 242/279 (86%)</p> <p>spjP16702(CYSW_ECOLI SULFATE TRANSPORT SYSTEM PERMEASE PROTEIN CYSW gb AA23638.1 (M32101) sulfate permease [Escherichia coli] dbj BAA16287.1 (D90871) sulfate/thiosulfate transport protein cysW [Escherichia coli] dbj BAA16306.1 (D90872) sulfate/thiosulfate transport protein cysW [Escherichia coli] Length = 291</p>
SEQ ID n°1876	Prot n°PL-2679.1	Contig33	169163	170251	82%	<p>Identities = 260/366 (71%), Positives = 302/366 (82%), Gaps = 5/366 (1%)</p> <p>spjP16676(CYSA_ECOLI SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA pir QRECSA sulfate transport ATP-binding protein cysA - Escherichia coli gb AAC75475.1 (AE000329) ATP-binding component of sulfate permease A protein; chromate resistance [Escherichia coli] dbj BAA16296.1 (D90871) sulfate/thiosulfate transport protein cysA [Escherichia coli] dbj BAA16305.1 (D90872) sulfate/thiosulfate transport protein cysA [Escherichia coli] Length = 365 "</p>
SEQ ID n°1878	Prot n°PL-2681.1	Contig41	444085	445152	21%	<p>Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%)</p> <p>dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188</p>
SEQ ID n°1877	Prot n°PL-2680.2	Contig33	168143	169024		
SEQ ID n°1878	Prot n°PL-2681.1	Contig27	69034	69726	44%	<p>Identities = 61/191 (31%), Positives = 102/191 (52%), Gaps = 8/191 (4%)</p> <p>gb AAD50485.1 (AF172324) WbnA [Escherichia coli] Length = 306</p>
SEQ ID n°1878	Prot n°PL-2682.1	Contig27	67915	69033	38%	<p>Identities = 81/322 (25%), Positives = 144/322 (44%), Gaps = 34/322 (10%)</p> <p>gb AAD50480.1 (AF172324) WbnE [Escherichia coli] Length = 392</p>
SEQ ID n°1880	Prot n°PL-2683.1	Contig27	66010	67038	62%	<p>Identities = 161/340 (47%), Positives = 224/340 (65%), Gaps = 4/340 (1%)</p> <p>emb CAB73849.1 (AL139078) putative sugar kinase [Campylobacter jejuni] Length = 339</p>
SEQ ID n°1881	Prot n°PL-2684.1	Contig27	65432	66022	72%	<p>Identities = 110/195 (56%), Positives = 146/195 (74%), Gaps = 2/195 (1%)</p> <p>emb CAB73848.1 (AL139078) putative phosphoheptose isomerase [Campylobacter jejuni] Length = 201</p>
SEQ ID n°1882	Prot n°PL-2685.1	Contig27	64751	65428	62%	<p>Identities = 89/218 (40%), Positives = 142/218 (64%), Gaps = 6/218 (2%)</p> <p>emb CAB73847.1 (AL139078) putative sugar-phosphate nucleotidyltransferase [Campylobacter jejuni] Length = 221</p>
SEQ ID n°1883	Prot n°PL-2686.1	Contig27	60774	61955	32%	<p>Identities = 71/281 (25%), Positives = 128/281 (45%), Gaps = 19/281 (6%)</p> <p>gb AAF30875.1 (AE002142) methionyl-tRNA formyltransferase [Ureaplasma urealyticum] Length = 305</p>
SEQ ID n°1884	Prot n°PL-2687.1	Contig27	59551	60573	79%	<p>Identities = 227/337 (67%), Positives = 272/337 (80%)</p> <p>gb AAB39336.1 (U76617) UDP-glucose-4-epimerase [Pasteurella multocida] Length = 338</p>
SEQ ID n°1885	Prot n°PL-2688.1	Contig27	58240	58959	No Hits found	

TABLEAU I

SEQ ID n°1886	Prot n°PL-2688.1	Contig27	56287	57021	33%	Identities = 46/196 (23%), Positives = 81/196 (40%), Gaps = 20/196 (10%) pir C64572 conserved hypothetical protein HP0419 - Helicobacter pylori (strain 26695) gb AAD07484.1 (AE000557) conserved hypothetical protein [Helicobacter pylori 26695] Length = 261
SEQ ID n°1887	Prot n°PL-2689.1	Contig41	446049	447845	91%	Identities = 520/598 (86%), Positives = 551/598 (91%) sp P20922 FRDA_PROVU FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT pir IRDEBFV fumarate reductase (EC 1.3.99.1) flavoprotein - Proteus vulgaris emb CAA29501.1 (X06144) frdA (AA 1-598) [Proteus vulgaris] Length = 598
SEQ ID n°1888	Prot n°PL-2690.1	Contig27	55241	56062	88%	Identities = 228/273 (83%), Positives = 255/273 (92%) ... sp P05796 CYSE_ECOLI SERINE ACETYLTRANSFERASE (SAT) pir XYECSA serine O-acetyltransferase (EC 2.3.1.30) - Escherichia coli gb AAA23648.1 (M15745) serine acetyltransferase [Escherichia coli] gb AAA23659.1 (M34333) 33 Kd protein (cysE) [Escherichia coli] gb AAB18584.1 (U00039) serine acetyltransferase [Escherichia coli] gb AAC76631.1 (AE000438) serine acetyltransferase [Escherichia coli] Length = 289/329 (81%), Positives = 298/329 (90%)
SEQ ID n°1889	Prot n°PL-2691.1	Contig27	54175	55197	86%	sp P37606 GPDA_ECOLI GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+] pir S47829 glycerol-3-phosphate dehydrogenase (NAD+) (EC 1.1.1.8) - Escherichia coli gb AAB18585.1 (U00039) L-glycerol 3-phosphate dehydrogenase [Escherichia coli] gb AAC76632.1 (AE000439) glycerol-3-phosphate dehydrogenase (NAD+) [Escherichia coli] Length = 242/389 (62%), Positives = 315/389 (80%), Gaps = 4/389 (1%)
SEQ ID n°1890	Prot n°PL-2692.1	Contig27	51336	52661	71%	Identities = 242/389 (62%), Positives = 315/389 (80%), Gaps = 4/389 (1%) sp P37690 YIBP_ECOLI HYPOTHETICAL 46.6 KD PROTEIN IN SECB-TDH INTERGENIC REGION Length = 419
SEQ ID n°1891	Prot n°PL-2693.1	Contig27	50531	51199	61%	Identities = 142/226 (62%), Positives = 169/226 (73%), Gaps = 13/226 (5%) sp P37691 YIBQ_ECOLI HYPOTHETICAL 30.7 KD PROTEIN IN SECB-TDH INTERGENIC REGION pir S47835 hypothetical 30.7K protein (secb-tdh intergenic region) - Escherichia coli gb AAB18591.1 (U00039) No definition line found [Escherichia coli] gb AAC76638.1 (AE000439) ori, hypothetical protein [Escherichia coli] Length = 277
SEQ ID n°1892	Prot n°PL-2694.1	Contig27	48122	49198	42%	Identities = 77/352 (21%), Positives = 151/352 (42%), Gaps = 40/352 (11%) gb AAF95171.1 (AE004276) 3-oxoacyl-(acyl-carrier-protein) synthase III [Vibrio cholerae] Length = 316
SEQ ID n°1893	Prot n°PL-2695.1	Contig27	46808	47833	95%	Identities = 313/341 (91%), Positives = 331/341 (96%) sp P07813 TDH_ECOLI THREONINE 3-DEHYDROGENASE pir DEECTH L-threonine 3-dehydrogenase (EC 1.1.1.103) - Escherichia coli emb CAA29884.1 (X06690) tdh gene [Escherichia coli] gb AAB18593.1 (U00039) threonine dehydrogenase [Escherichia coli] gb AAC76640.1 (AE000439) threonine dehydrogenase [Escherichia coli] Length = 341

TABLEAU I

SEQ ID n°1894	Prot n°PL-2696.1	Contig27	45602	46798	90%	Identities = 336/398 (84%), Positives = 362/398 (90%) sp P07912 KBL_ECOLI 2-AMINO-3-KETO BUTYRATE COENZYME A LIGASE (AKB LIGASE) (GLYCINE ACETYLTRANSFERASE) pir XUECGA glycine C-acetyltransferase (EC 2.3.1.29) - Escherichia coli gb AAB18594.1 (U00039) glycine acetyltransferase [Escherichia coli] gb AAC76841.1 (AE000439) 2-amino-3-ketobutyrate CoA ligase (glycine acetyltransferase)
SEQ ID n°1895	Prot n°PL-2697.1	Contig27	44429	45367	79%	Identities = 251/311 (80%), Positives = 279/311 (89%), Gaps = 2/311 (0%) sp P17963 RFAD_ECOLI ADP-L-GLYCERO-D-MANNO-HEPTOSE-6-EPIMERASE (ADP-GLYCEROMANNO-HEPTOSE 6-EPIMERASE) pir JU0298 ADP-L-glycero-D-mannoheptose-6-epimerase (EC 5.1.3.-) - Escherichia coli emb CAA38384.1 (X54492) acidic 34,893Da HtrM protein [Escherichia coli] gb AAA24525.1 (M33577) rfaD protein [Escherichia coli] gb AAB18598.1 (U00039) ADP-L-Glycero-D-mannoheptose-6-epimerase [Escherichia coli] gb AAC76843.1 (AE000440) ADP-L-glycero-D-mannoheptose-6-epimerase [Escherichia coli] Length = 310
SEQ ID n°1896	Prot n°PL-2698.1	Contig27	43369	44418	83%	Identities = 257/351 (73%), Positives = 303/351 (86%), Gaps = 2/351 (0%) gb AAD37762.1 AF146532_2 (AF146532) heptosyl II transferase Waaf [Klebsiella pneumoniae] Length = 352
SEQ ID n°1897	Prot n°PL-2699.1	Contig27	42404	43369	72%	Identities = 211/316 (66%), Positives = 256/316 (80%) sp P24173 RFAC_ECOLI LIPOPOLYSACCHARIDE HEPTOSYLTRANSFERASE-1 pir JA0619 heptosyltransferase (EC 2.4.99.-) Escherichia coli emb CAA44391.1 (X62530) rfa-2 [Escherichia coli] gb AAB18598.1 (U00039) alternate gene name rfa2 [Escherichia coli] gb AAC76845.1 (AE000440) heptosyl transferase I; lipopolysaccharide core biosynthesis [Escherichia coli] Length = 319 "
SEQ ID n°1898	Prot n°PL-27.1	Contig41	47204	48061	66%	Identities = 142/283 (50%), Positives = 194/283 (68%), Gaps = 3/283 (1%) emb CAA21352.1 (AL031866) ORF29, len: 295 aa, probable tellurite resistance protein (tehB), highly similar to many, eg. P25397 TEHB_ECOLI (197 aa). 61.3% identity in 191 aa overlap Fasta scores: opt: 792, E0: 0 or U32807_6 Haemophilus influenzae (286 a a) 58.2% ide> Length = 295
SEQ ID n°1899	Prot n°PL-270.1	Contig41	447838	448572	84%	Identities = 209/242 (86%), Positives = 229/242 (94%) sp P20821 FRDB_PROVU FUMARATE REDUCTASE IRON-SULFUR PROTEIN pir RDEBIV fumarate reductase (EC 1.3.99.1) iron-sulfur protein - Proteus vulgaris emb CAA29502.1 (X06144) frdB (AA 1-245) [Proteus vulgaris] Length = 245
SEQ ID n°1900	Prot n°PL-2700.1	Contig27	41254	42279	No Hits found	
SEQ ID n°1901	Prot n°PL-2701.1	Contig27	39949	41052	60%	Identities = 171/364 (46%), Positives = 240/364 (64%), Gaps = 1/364 (0%) gb AAD28802.1 (U52844) putative glycosyltransferase [Serratia marcescens] Length = 366

TABLEAU I

SEQ ID n°1902	Prot n°PL-2702.1	Contig27	38822	39952	80%	Identities = 262/374 (70%), Positives = 312/374 (83%) gb AAD28801.1 (U52844) putative glycosyltransferase [Serratia marcescens] Length = 133/344 (56%), Positives = 253/344 (73%) Gaps = 1/344 (0%)
SEQ ID n°1903	Prot n°PL-2703.1	Contig27	37632	38825	63%	gb AAD37767.1 AF146532_7 (AF146532) putative heptosyl III transferase WaaQ [Klebsiella pneumoniae] Length = 358
SEQ ID n°1904	Prot n°PL-2704.1	Contig27	36255	37532	83%	Identities = 347/425 (81%), Positives = 378/425 (88%) gb AAC44432.1 (U52844) 3-deoxy-manno-octulosonic acid transferase [Serratia marcescens] Length = 425
SEQ ID n°1905	Prot n°PL-2705.1	Contig27	35481	36254	75%	Identities = 174/248 (70%), Positives = 196/248 (78%) sp Q54435 KDTX_SERMA LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS GLYCOSYL TRANSFERASE KDTX gb AAC44433.1 (U52844) glucosyl transferase [Serratia marcescens] Length = 257
SEQ ID n°1906	Prot n°PL-2706.1	Contig27	34111	34920	82%	Identities = 204/268 (76%), Positives = 228/268 (84%) sp P05523 FPG_ECOLI FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE) pir IDGECFP formamidopyrimidine-DNA glycosidase (EC 3.2.2.23) - Escherichia coli emb CAA29431.1 (X06036) Fapy-DNA glycosylase (AA 1 - 269) [Escherichia coli] gb AAB18612.1 (U00039) formamidopyrimidine-DNA glycosylase [Escherichia coli] gb AAC76859.1 (AE000441) formamidopyrimidine DNA glycosylase [Escherichia coli]
SEQ ID n°1907	Prot n°PL-2707.1	Contig27	32774	34000	57%	Identities = 163/382 (41%), Positives = 244/382 (61%), Gaps = 6/392 (1%) sp P26471 RFAL_SALTY O-ANTIGEN LIGASE pir B41317 O-antigen ligase complex protein rfaL - Salmonella typhimurium gb AAA27206.1 (M73826) O-antigen ligase [Salmonella typhimurium] Length = 404
SEQ ID n°1908	Prot n°PL-2708.1	Contig27	31562	32740	31%	Identities = 71/300 (23%), Positives = 125/300 (41%), Gaps = 46/300 (15%) emb CAB58324.1 (AL121855) hypothetical protein SCF62.09 [Streptomyces coelicolor A3(2)] Length = 407
SEQ ID n°1909	Prot n°PL-2709.1	Contig27	30442	31584	33%	Identities = 80/240 (33%), Positives = 126/240 (52%), Gaps = 12/240 (5%) pir F71196 hypothetical protein PH1844 - Pyrococcus horikoshii db BAA30865.1 (AP000007) 381aa long hypothetical protein [Pyrococcus horikoshii] Length = 381
SEQ ID n°1910	Prot n°PL-271.1	Contig41	449554	450438	59%	Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300
SEQ ID n°1911	Prot n°PL-2710.1	Contig27	29448	30485	39%	Identities = 74/293 (25%), Positives = 135/293 (45%), Gaps = 31/293 (10%) gb AAD37767.1 AF146532_7 (AF146532) putative heptosyl III transferase WaaQ [Klebsiella pneumoniae] Length = 358
SEQ ID n°1912	Prot n°PL-2711.1	Contig27	28136	29275	44%	Identities = 101/345 (29%), Positives = 168/345 (48%), Gaps = 22/345 (6%) gb AAF84279.1 AE003977.2 (AE003977) conserved hypothetical protein [Xylella fastidiosa] Length = 376
SEQ ID n°1913	Prot n°PL-2712.1	Contig27	26567	27328	68%	Identities = 124/215 (57%), Positives = 173/215 (79%) sp P25531 RADC_ECOLI DNA REPAIR PROTEIN RADC Length = 222

TABLEAU I

SEQ ID n°1914	Prot n°PL-2713.1	Contig27	25220	26503	78%	<p>Identities = 300/424 (70%), Positives = 349/424 (81%), Gaps = 6/424 (1%) sp P24285 DFP_ECOLI_DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN pir A65165 pantothenate metabolism flavoprotein dfp - Escherichia coli (strain K-12) gb AAC76663.1 (AE000441) flavoprotein affecting synthesis of DNA and pantothenate metabolism [Escherichia coli] Length = 161/203 (79%), Positives = 188/203 (92%), Gaps = 1/203 (0%)</p>
SEQ ID n°1916	Prot n°PL-2714.1	Contig27	23944	24543	81%	<p>Identities = 161/203 (79%), Positives = 188/203 (92%), Gaps = 1/203 (0%) pir C65165 tk protein - Escherichia coli gb AA61994.1 (L10328) 23 kD protein [Escherichia coli] gb AAC76665.1 (AE000441) putative transcriptional regulator [Escherichia coli] Length = 212</p>
SEQ ID n°1916	Prot n°PL-2715.1	Contig27	23243	23884	82%	<p>Identities = 176/213 (82%), Positives = 193/213 (89%) sp P08870 PYRE_SALTY_ORYZATE PHOSPHORIBOSYLTRANSFERASE (OPRT) (OPRTASE) pir S32801 orotate phosphoribosyltransferase (EC 2.4.2.10) - Salmonella typhimurium pdj 10PR Mol_id: 1; Molecule: Orotate Phosphoribosyltransferase; Chain: Null; Synonym: Optase; Ec: 2.4.2.10; Engineered: Yes emb CAA79607.1 (Z19547) orotate phosphoribosyltransferase [Salmonella typhimurium] Length = 213 "</p>
SEQ ID n°1917	Prot n°PL-2716.1	Contig27	22430	23158	87%	<p>Identities = 198/236 (83%), Positives = 218/236 (91%) sp P03842 RNPH_ECOLI_RIBONUCLEASE PH (RNASE PH) (TRNA NUCLEOTIDYLTRANSFERASE) Length = 238</p>
SEQ ID n°1918	Prot n°PL-2717.1	Contig27	21440	22303	83%	<p>Identities = 238/287 (82%), Positives = 258/287 (88%) sp P23839 YICC_ECOLI_PROTEIN YICC pir F65165 33.2 kD protein in dinD- rph intergenic region (orf x) - Escherichia coli (strain K-12) gb AAA61997.1 (L10328) o287 [Escherichia coli] gb AAC76668.1 (AE000441) putative alpha helix protein [Escherichia coli] Length = 287</p>
SEQ ID n°1919	Prot n°PL-2718.1	Contig27	18215	19396	51%	<p>Identities = 118/400 (29%), Positives = 207/400 (51%), Gaps = 15/400 (3%) gb AAB70880.1 (U68703) reverse transcriptase [Escherichia coli] Length = 408</p>
SEQ ID n°1920	Prot n°PL-2719.1	Contig27	16031	16984	No Hits found	<p>Identities = 237/341 (69%), Positives = 291/341 (84%) sp P39280 YJEK_ECOLI_HYPOTHETICAL 38.7 KD PROTEIN IN MOPA-EFP INTERGENIC REGION pir S56374 hypothetical 38.7K protein (mopa-efp intergenic region) - Escherichia coli gb AAA97045.1 (U14003) ORF_1342 [Escherichia coli] gb AAC77106.1 (AE000487) orf, hypothetical protein [Escherichia coli] Length = 342</p>
SEQ ID n°1922	Prot n°PL-2720.1	Contig27	14399	15340	68%	<p>Identities = 186/314 (59%), Positives = 229/314 (72%), Gaps = 3/314 (0%) emb CAB84863.1 (AL162756) hypothetical protein [Neisseria meningitidis] Length = 375</p>
SEQ ID n°1923	Prot n°PL-2721.1	Contig27	12678	13916	52%	<p>Identities = 124/394 (31%), Positives = 215/394 (54%), Gaps = 12/394 (3%) emb CAA63510.1 (X92946) macrolide efflux protein [Lactococcus lactis] Length = 418</p>

TABLEAU I

SEQ ID n°1924	Prot n°PL-2722.1	Contig27	11719	12551	51%	Identities = 116/298 (38%), Positives = 160/298 (52%), Gaps = 8/298 (2%) sp P76419 YEGV_ECOLI_HYPOTHETICAL_SUGAR_KINASE_IN_FBAB-THID INTERGENIC_REGION_pir C64977_hypothetical_protein_b2100 - Escherichia coli (strain K-12) gb AAC75161.1 (AE000299) putative kinase [Escherichia coli] Length = 321
SEQ ID n°1925	Prot n°PL-2723.1	Contig27	10353	11243	38%	Identities = 75/239 (31%), Positives = 113/239 (46%), Gaps = 9/239 (3%) emb CAB67714.1 (AJ271405) putative transferase enzyme [Streptomyces rochei] Length = 250
SEQ ID n°1926	Prot n°PL-2724.1	Contig27	9354	10241	73%	Identities = 185/262 (70%), Positives = 218/262 (82%), Gaps = 3/262 (1%) sp P32177 FDHD_ECOLI_FDHD_PROTEIN_pir S40839_fdhd_protein - Escherichia coli gb AAB03028.1 (L19201) similar to Wolinella succinogenes Fdhd [Escherichia coli] gb AAC76877.1 (AE000465) affects formate dehydrogenase-N [Escherichia coli] Length = 277
SEQ ID n°1927	Prot n°PL-2725.1	Contig27	8626	9213	91%	Identities = 175/195 (89%), Positives = 186/195 (94%) gb AAD13456.1 (AE000484) formate dehydrogenase-O, major subunit [Escherichia coli] Length = 1016
SEQ ID n°1928	Prot n°PL-2726.1	Contig27	6166	8625	91%	Identities = 696/820 (84%), Positives = 750/820 (90%), Gaps = 1/820 (0%) gb AAD13456.1 (AE000484) formate dehydrogenase-O, major subunit [Escherichia coli] Length = 1016
SEQ ID n°1929	Prot n°PL-2727.1	Contig27	5226	6155	86%	Identities = 246/301 (81%), Positives = 273/301 (89%), Gaps = 1/301 (0%) sp P32175 FDOH_ECOLI_FORMATE_DEHYDROGENASE-O_IRON-SULFUR SUBUNIT (FORMATE DEHYDROGENASE-O BETA SUBUNIT) (FDH-Z BETA SUBUNIT) (AEROBIC FORMATE DEHYDROGENASE IRON- SULFUR SUBUNIT) pir S40837_formate_dehydrogenase (EC 1.2.1.2) O (aerobic) beta chain - Escherichia coli gb AAB03026.1 (L19201) formate dehydrogenase-O beta subunit [Escherichia coli] gb AAD13455.1 (AE000484) formate dehydrogenase-O, iron-sulfur subunit [Escherichia coli] Length = 300
SEQ ID n°1930	Prot n°PL-2728.1	Contig27	4588	5229	74%	Identities = 140/207 (67%), Positives = 164/207 (78%) sp P32174 FDOH_ECOLI_FORMATE_DEHYDROGENASE_CYTOCHROME B556(FDO) SUBUNIT (FORMATE DEHYDROGENASE-O GAMMA SUBUNIT) (FDH-Z GAMMA SUBUNIT) (AEROBIC FORMATE DEHYDROGENASE CYTOCHROME B556 SUBUNIT) pir S40836_formate dehydrogenase (EC 1.2.1.2) O (aerobic) gamma chain - Escherichia coli gb AAB03025.1 (L19201) formate dehydrogenase-O gamma subunit [Escherichia coli] gb AAD13454.1 (AE000464) formate dehydrogenase, cytochrome B556 (FDO) subunit [Escherichia coli] Length = 211
SEQ ID n°1931	Prot n°PL-2729.1	Contig27	2991	4187	31%	Identities = 70/218 (32%), Positives = 126/218 (57%), Gaps = 18/218 (8%) gb AAF18691.1 AC010795_6 (AC010795) caffeic O-methyltransferase, putative, 68744-70102 [Arabidopsis thaliana] Length = 381 "

TABLEAU I

SEQ ID n°1932	Prot n°PL-273.1	Contig41	453988	454896	67%	gb AAG06512.1 AE004736_9 (AE004736) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 303
SEQ ID n°1933	Prot n°PL-2730.2	Contig27	1281	2270		
SEQ ID n°1934	Prot n°PL-2731.1	Contig40	63833	64735	91%	sp O52399 ICIA_EDWIC CHROMOSOME INITIATION INHIBITOR (ORIC REPLICATION INHIBITOR) gb AAB92569.1 (AF037440) Inhibitor of chromosome initiation [Edwardsiella ictaluri] Length = 297
SEQ ID n°1935	Prot n°PL-2732.1	Contig40	63114	63836	68%	sp P11668 YGGG_ECOLI HYPOTHETICAL 26.8 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 6) (F246) pir A65077 hypothetical 26.6K protein (sbm-fba intergenic region) - Escherichia coli gb AAA69089.1 (U28377) ORF_f246; alternate name yggE; orf6 of X14436 [Escherichia coli] gb AAC75959.1 (AE000375) putative actin [Escherichia coli] Length = 248 "
SEQ ID n°1936	Prot n°PL-2733.1	Contig40	62377	63000	68%	sp P11667 YGGG_ECOLI HYPOTHETICAL 23.2 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 5) pir IQEC5A hypothetical 23K protein (sbm- fba intergenic region) - Escherichia coli gb AA69090.1 (U28377) ORF_f211; alternate name yggA; orf5 of X14436 [Escherichia coli] gb AAC75960.1 (AE000375) orf, hypothetical protein [Escherichia coli] emb CAC09317.1 (AX030085) unnamed protein product [Escherichia coli] Length = 94/335 (28%), Positives = 157/335 (46%), Gaps = 24/335 (7%)
SEQ ID n°1937	Prot n°PL-2734.1	Contig40	60161	61498	35%	pir D64903 hypothetical protein b1497 - Escherichia coli gb AAC74570.1 (AE000247) putative enzyme [Escherichia coli] Length = 390
SEQ ID n°1938	Prot n°PL-2735.1	Contig40	58332	59204	79%	sp O52401 YGGG_EDWIC HYPOTHETICAL 30.6 KDA PROTEIN IN ICIA-FBA INTERGENIC REGION gb AAB92571.1 (AF037440) putative 30.6 kDa protein [Edwardsiella ictaluri] Length = 286
SEQ ID n°1939	Prot n°PL-2736.1	Contig40	53636	56233	93%	sp P36883 ACO2_ECOLI ACONITATE HYDRATASE 2 (CITRATE HYDRO- LYASE 2) (ACONITASE 2) pir JF64734 aconitate hydratase (EC 4.2.1.3) 2 - Escherichia coli gb AAC73229.1 (AE000121) aconitate hydratase B [Escherichia coli] Length = 865
SEQ ID n°1940	Prot n°PL-2737.1	Contig40	52024	53181	No Hits found	
SEQ ID n°1941	Prot n°PL-2738.1	Contig40	51733	53163	95%	Identities = 444/475 (93%), Positives = 458/475 (95%) emb CAA24742.1 (V01498) coding sequence of gene lpd [Escherichia coli] Length = 475
SEQ ID n°1942	Prot n°PL-2739.1	Contig40	49928	50767	No Hits found	

TABLEAU I

SEQ ID n°1943	Prot n°PL-274.1	Contig41	455543	457189	94%	<p>sp P48217 CH60_SALT160_KD_CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) gb AAA85277.1 (U01039) GroEL [Salmonella typhimurium] Length = 490/548 (89%), Positives = 521/548 (94%)</p> <p>dbj BAA94286.1 (AB033231) groEL [Salmonella typhimurium] Length = 490/548 (89%), Positives = 521/548 (94%)</p> <p>sp P06989 ODP2_ECOLI DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX (E2) p j XECDDP dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - Escherichia coli emb CAA24741.1 (V01498) acf [Escherichia coli] dbj BAA05573.1 (D26562) dihydrolipoamide acetyltransferase (E2 component of pyruvate dehydrogenase complex) [Escherichia coli] gb AAC73226.1 (AE000120) pyruvate dehydrogenase (dihydrolipoacetyltransferase component) [Escherichia coli] Length = 630</p>
SEQ ID n°1944	Prot n°PL-2740.1	Contig40	48931	51529	85%	<p>sp P06989 ODP1_ECOLI PYRUVATE DEHYDROGENASE E1 COMPONENT p j DEECPV pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) - Escherichia coli gb AAC73225.1 (AE000120) pyruvate dehydrogenase (decarboxylase component) [Escherichia coli] Length = 887</p>
SEQ ID n°1945	Prot n°PL-2741.1	Contig40	47253	49916	93%	<p>sp P06989 ODP1_ECOLI PYRUVATE DEHYDROGENASE E1 COMPONENT p j DEECPV pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) - Escherichia coli gb AAC73225.1 (AE000120) pyruvate dehydrogenase (decarboxylase component) [Escherichia coli] Length = 887</p>
SEQ ID n°1946	Prot n°PL-2742.1	Contig40	46299	47063	87%	<p>sp P06989 ODP1_ECOLI PYRUVATE DEHYDROGENASE E1 COMPONENT p j DEECPV pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) - Escherichia coli gb AAC73225.1 (AE000120) pyruvate dehydrogenase (decarboxylase component) [Escherichia coli] Length = 887</p>
SEQ ID n°1947	Prot n°PL-2743.1	Contig40	41319	42116	46%	<p>sp P75856 YCBR_ECOLI HYPOTHETICAL 25.4 KDA FIMBRIAL CHAPERONE IN PEPP-PYRD INTERGENIC REGION PRECURSOR p j B64834 probable fimbrial chaperone ycbR precursor - Escherichia coli gb AAC74025.1 (AE000196) putative chaperone [Escherichia coli] dbj BAA35694.1 (D90732) Periplasmic chaperone fccC protein [Escherichia coli] Length = 121/300 (40%), Positives = 169/300 (56%), Gaps = 16/300 (5%)</p>
SEQ ID n°1948	Prot n°PL-2744.1	Contig40	39776	40765	51%	<p>sp P30130 FIMD_ECOLI OUTER MEMBRANE USHER PROTEIN FIMD PRECURSOR p j S66542 outer membrane usher protein fimD precursor - Escherichia coli gb AAA97213.1 (U14003) CG Site No. 18349 [Escherichia coli] gb AAC77273.1 (AE000502) outer membrane protein; export and assembly of type 1 fimbriae, interrupted [Escherichia coli] Length = 161/284 (56%), Positives = 214/284 (74%) emb CAB89836.1 (AJ242516) AmpE protein [Salmonella typhimurium] Length = 284</p>
SEQ ID n°1949	Prot n°PL-2745.1	Contig40	38363	39207	70%	<p>sp P30130 FIMD_ECOLI OUTER MEMBRANE USHER PROTEIN FIMD PRECURSOR p j S66542 outer membrane usher protein fimD precursor - Escherichia coli gb AAA97213.1 (U14003) CG Site No. 18349 [Escherichia coli] gb AAC77273.1 (AE000502) outer membrane protein; export and assembly of type 1 fimbriae, interrupted [Escherichia coli] Length = 161/284 (56%), Positives = 214/284 (74%) emb CAB89836.1 (AJ242516) AmpE protein [Salmonella typhimurium] Length = 284</p>
SEQ ID n°1950	Prot n°PL-2746.1	Contig40	36967	37857	77%	<p>emb CAB89834.1 (AJ242516) NadC protein [Salmonella typhimurium] Length = 311</p>

TABLEAU I

SEQ ID n°1951	Prot n°PL-2747.1	Contig40	34737	36146	59%	Identities = 222/464 (47%), Positives = 294/464 (62%), Gaps = 20/464 (4%) sp P36845 HOFB_ECOLI PROTEIN TRANSPORT PROTEIN HOFB pir JG64733 protein transport protein hofB - Escherichia coli gb AAC73218.1 (AE000119) putative integral membrane protein involved in biogenesis of fimbriae, protein transport, DNA uptake [Escherichia coli]
SEQ ID n°1952	Prot n°PL-2748.1	Contig40	33535	34734	51%	Identities = 138/395 (34%), Positives = 228/395 (56%), Gaps = 4/395 (1%) sp P36646 HOFB_ECOLI PROTEIN TRANSPORT PROTEIN HOFB pir JG64733 protein transport protein hofC - Escherichia coli gb AAC73217.1 (AE000119) putative integral membrane protein involved in biogenesis of fimbriae, protein transport, DNA uptake [Escherichia coli]
SEQ ID n°1953	Prot n°PL-2749.1	Contig40	32820	33443	64%	Identities = 115/197 (58%), Positives = 148/197 (74%) sp P36679 YACE_ECOLI 22.6 KDA PROTEIN IN MUTT-GUAC INTERGENIC REGION pir JG64732 yaeE protein - Escherichia coli (strain K-12) gb AAC73214.1 (AE000119) putative DNA repair protein [Escherichia coli]
SEQ ID n°1954	Prot n°PL-275.1	Contig41	458596	460020	91%	Identities = 405/475 (85%), Positives = 444/475 (93%) sp P33109 ASPA_SERMA ASPARTATE AMMONIA-LYASE (ASPARTASE) pir JG0784 aspartate ammonia-lyase (EC 4.3.1.1) - Serratia marcescens db JBA02518.1 (D13252) aspartase [Serratia marcescens] Length =
SEQ ID n°1955	Prot n°PL-2750.1	Contig40	32075	32827	69%	Identities = 148/243 (60%), Positives = 181/243 (73%) sp P36680 YACF_ECOLI HYPOTHETICAL 28.3 KD PROTEIN IN MUTT- GUAC INTERGENIC REGION pir JG64732 hypothetical protein in mutt-guac intergenic region - Escherichia coli (strain K-12) gb AAC73213.1 (AE000119) orf, hypothetical protein [Escherichia coli] Length = 247
SEQ ID n°1956	Prot n°PL-2751.1	Contig40	28584	31295	93%	Identities = 806/903 (89%), Positives = 850/903 (93%), Gaps = 2/903 (0%) sp P10408 SECA_ECOLI PREPROTEIN TRANSLOCASE SECA SUBUNIT pir JBVECCA preprotein translocase secA - Escherichia coli gb AAC73209.1 (AE000119) preprotein translocase; secretion protein [Escherichia coli] Length = 901
SEQ ID n°1957	Prot n°PL-2752.1	Contig40	27416	28066	39%	Identities = 57/163 (34%), Positives = 85/163 (51%), Gaps = 13/163 (7%) gb AA095538.1 (AE004310) hypothetical protein [Vibrio cholerae] Length = 157
SEQ ID n°1958	Prot n°PL-2753.1	Contig40	26356	27288	93%	Identities = 273/305 (89%), Positives = 286/305 (96%) sp P07652 LPXC_ECOLI UDP-3-O-[3-HYDROXYMYRISTOYL] N- ACETYLGLUCOSAMINE DEACETYLASE (ENVA PROTEIN) pir JBVECEA UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (EC 3.5.1.-) - Escherichia coli emb CAA38873.1 (X55034) EnvA protein [Escherichia coli] gb AA483849.1 (M19211) ell permeability-cell separation protein [Escherichia coli] db JBA01361.1 (D10483) envA protein [Escherichia coli] gb AAC73207.1 (AE000119) UDP-3-O-acyl N- acetylglucosamine deacetylase; lipid A biosynthesis [Escherichia coli]

TABLEAU I

SEQ ID n°1958	Prot n°PL-2754.1	Contig40	25112	26272	83%	<p>Identities = 356/386 (92%), Positives = 369/386 (95%), Gaps = 3/386 (0%) pir CEECZ cell division protein ftsZ - Escherichia coli gb AAC73206.1 (AE000119) cell division; forms circumferential ring; tubulin-like GTP-binding protein and GTPase [Escherichia coli] Length = 383 "</p>	
SEQ ID n°1960	Prot n°PL-2755.1	Contig40	23793	25049	94%	<p>Identities = 394/420 (91%), Positives = 405/420 (96%), Gaps = 2/420 (0%) sp P06137 FTSA_ECOLI CELL DIVISION PROTEIN FtsA pir CEECA cell division protein ftsA - Escherichia coli emb CAA38871.1 (X55034) FtsA protein [Escherichia coli] emb CAA26590.1 (X02821) ftsA protein [Escherichia coli] dbj BAA01359.1 (D10483) cell division protein ftsA [Escherichia coli] gb AAC73205.1 (AE000118) ATP-binding cell division protein, septation process, complexes with FtsZ, associated with junctions of inner and outer membranes [Escherichia coli] Length = 420 "</p>	
SEQ ID n°1961	Prot n°PL-2756.1	Contig40	22945	23751	74%	<p>Identities = 174/261 (66%), Positives = 207/261 (78%), Gaps = 5/261 (1%) sp P06136 FTSQ_ECOLI CELL DIVISION PROTEIN FtsQ pir CEECQ cell division protein ftsQ - Escherichia coli emb CAA38870.1 (X55034) FtsQ protein [Escherichia coli] emb CAA26589.1 (X02821) put. ftsA protein [Escherichia coli] gb AAA23816.1 (K02668) ftsQ protein [Escherichia coli] dbj BAA01358.1 (D10483) cell division protein ftsQ [Escherichia coli] gb AAC73204.1 (AE000118) cell division protein; ingrowth of wall at septum [Escherichia coli] Length = 276 "</p>	
SEQ ID n°1962	Prot n°PL-2757.1	Contig40	22023	22943	82%	<p>Identities = 215/307 (70%), Positives = 257/307 (83%), Gaps = 2/307 (0%) sp P07862 DDL B_ECOLI D-ALANINE-D-ALANINE LIGASE B (D-ALANYLALANINE SYNTHETASE) (D-ALA-D-ALA LIGASE) pir CECDL D-alanine-D-alanine ligase (EC 6.3.2.4) B - Escherichia coli pdb 110V Complex Of D-Ala:d-Ala Ligase With Adp And A Phosphoryl Phosphonate pdb 2DLN Mol_id: 1; Molecule: D-Alanine-D-Alanine Ligase; Chain: Null; Ec: 6.3.2.4 emb CAA38869.1 (X55034) D-Ala:D-Ala ligase (Ddl) [Escherichia coli] gb AAA23672.1 (M14029) ddl cell wall enzyme [Escherichia coli] dbj BAA01357.1 (D10483) D-alanine-D-alanine ligase [Escherichia coli] gb AAC73203.1 (AE000118) D-alanine-D-alanine ligase B, affects cell division [Escherichia coli] Length = 306 "</p>	

TABLEAU I

SEQ ID n°1963	Prot n°PL-2758.1	Contig40	20555	22030	84%	<p>Identities = 406/490 (82%), Positives = 439/490 (88%)</p> <p>sp P17952 MURC_ECOLI_UDP-N-ACETYLMURAMATE-ALANINE LIGASE (UDP-N-ACETYLMURAMOYL-L-ALANINE SYNTHETASE) pir JCEECAM_UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) - Escherichia coli emb CAA38868.1 (X55034) UDP-N-acetylmuramate-alanine ligase [Escherichia coli] emb CAA38868.1 (X52644) (UDP-N-acetylmuramate: L-alanine ligase) (AA 1-491) [Escherichia coli] dbj BAA01356.1 (D10483) UDP-N-acetylmuramate-alanine ligase [Escherichia coli] gb AAC73202.1 (AE000118) L-alanine adding enzyme, UDP-N-acetylmuramate:alanine ligase [Escherichia coli] prf 1808265A murC gene [Escherichia coli] ----Length = 491</p>
SEQ ID n°1964	Prot n°PL-2759.1	Contig40	19432	20499	83%	<p>Identities = 267/346 (77%), Positives = 310/346 (89%) pdb 1F0K A Chain A, The 1.9 Angstrom Crystal Structure Of E. Coli Murg pdb 1F0K B Chain B, The 1.9 Angstrom Crystal Structure Of E. Coli Murg Length = 364</p> <p>Identities = 363/433 (83%), Positives = 399/433 (91%)</p> <p>sp P04539 DCUA_ECOLI_ANAEROBIC C4-DICARBOXYLATE TRANSPORTER DCUA pir [S56366 dicarboxylate membrane-transporter protein A - Escherichia coli pir QQEC94 dicarboxylate membrane-transporter protein A - Escherichia coli emb CAA56259.1 (X79887) dicarboxylate membrane-transporter protein [Escherichia coli] gb AAA97037.1 (U14003) genA gene product [Escherichia coli] gb AAB30213.1 GenA=integral inner-membrane protein involved in anaerobic dicarboxylic acid transport [Escherichia coli, K12, Peptide, 433 aa] gb AAC77098.1 (AE000486) anaerobic dicarboxylate transport [Escherichia</p>
SEQ ID n°1965	Prot n°PL-276.1	Contig41	460161	461462	90%	<p>Identities = 314/402 (78%), Positives = 358/402 (88%), Gaps = 7/402 (1%)</p> <p>sp P18457 FTSW_ECOLI_CELL_DIVISION PROTEIN FTSW pir JCECFW cell division protein ftsW - Escherichia coli emb CAA38866.1 (X55034) FtsW protein [Escherichia coli] gb AAA83859.1 (M30807) cell division protein [Escherichia coli] dbj BAA01354.1 (D10483) cell division protein ftsW [Escherichia coli] gb AAC73200.1 (AE000118) cell division; membrane protein involved in shape determination [Escherichia coli] Length</p>
SEQ ID n°1966	Prot n°PL-2760.1	Contig40	18239	19435	87%	

TABLEAU I

SEQ ID n°1967	Prot n°PL-2761.1	Contig40	16932	18242	76%	<p>Identities = 318/438 (72%), Positives = 360/438 (81%), Gaps = 2/438 (0%) sp P14900 MURD_ECOLI_UDP-N-ACETYL-MURAMOYL-L-ALANYL-D-GLUTAMATE LIGASE (UDP-N-ACETYL-MURAMOYL-L-ALANYL-D-GLUTAMATE SYNTHETASE) (D-GLUTAMIC ACID ADDING ENZYME) [EC 6.3.2.9] pir JCEECME_UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9) [Escherichia coli emb CAA38865.1] (X55034) UDP-MurNac-L-Ala-D-Glu (MurD) (AA 1-438) [Escherichia coli emb CAA35933.1] (X51584) murD gene product (AA 1-438) [Escherichia coli dbj BAA01353.1] (D10483) UDP-N-acetylmuramoylalanine-D-glutamate ligase [Escherichia coli] gb AAC73198.1 (AE000118) UDP-N-acetylmuramoylalanine-D-glutamate ligase [Escherichia coli] Length = 438</p>
SEQ ID n°1968	Prot n°PL-2762.1	Contig40	15847	16929	90%	<p>Identities = 325/360 (90%), Positives = 341/360 (94%) sp P15876 MRAY_ECOLI_PHOSPHO-N-ACETYL-MURAMOYL-PENTAPEPTIDE-TRANSFERASE (UDP-MURNAC-PENTAPEPTIDE PHOSPHOTRANSFERASE) pir J08395 phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) mray - Escherichia coli emb CAA38864.1 (X55034) Miray protein (AA 1-360) [Escherichia coli] emb CAA35932.1 (X51584) ORF-Y (AA 1-360) [Escherichia coli] dbj BAA01352.1 (D10483) Phospho-N-Acetylmuramoyl-Pentapeptide-Transferase [Escherichia coli] gb AAC73198.1 (AE000118) phospho-N-acetylmuramoyl-pentapeptide transferase? [Escherichia coli]</p>
SEQ ID n°1969	Prot n°PL-2763.1	Contig40	14474	15853	73%	<p>Identities = 286/459 (64%), Positives = 359/459 (77%), Gaps = 7/459 (1%) sp P11880 MURF_ECOLI_UDP-N-ACETYL-MURAMOYL-ALANYL-D-GLUTAMYL-2, 6-DIAMINOPIMELATE-D-ALANYL-D-ALANYL LIGASE (UDP-MURNAC-PENTAPEPTIDE SYNTHETASE) (D-ALANYL-D-ALANINE-ADDING ENZYME) pir J64730 UDP-N-acetylmuramoylanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli gb AAC44657.1 (U67891) UDP-MurNac Tripeptide:D-Ala-D-Ala-Adding enzyme [Escherichia coli] gb AAC73197.1 (AE000118) D-alanine:D-alanine-adding enzyme [Escherichia coli] Identities = 388/495 (74%), Positives = 414/495 (83%) pir J540595 UDP-N-acetylmuramoylanyl-D-glutamate-2,6-diaminopimelate ligase (EC 6.3.2.13) murE - Escherichia coli Length = 495</p>
SEQ ID n°1970	Prot n°PL-2764.1	Contig40	12990	14477	82%	<p>Identities = 466/566 (79%), Positives = 526/566 (89%), Gaps = 1/566 (0%) sp P04286 PBP3_ECOLI_PENICILLIN-BINDING PROTEIN 3 PRECURSOR (PBP-3) pir JZPEC3 penicillin-binding protein 3 precursor - Escherichia coli emb CAA38861.1 (X55034) Pbp3 protein [Escherichia coli] gb AAA24300.1 (K00137) penicillin-binding protein 3 [Escherichia coli] dbj BAA01349.1 (D10483) penicillin-binding protein 3 precursor [Escherichia coli] gb AAC73195.1 (AE000118) septum formation; penicillin-binding protein 3; peptidoglycan synthetase [Escherichia coli] Length = 568</p>
SEQ ID n°1971	Prot n°PL-2765.1	Contig40	11237	13003	89%	

TABLEAU I

SEQ ID n°1972	Prot n°PL-2766.1	Contig40	9947	10891	82%	<p>Identities = 240/309 (77%), Positives = 276/309 (88%) pir JQCECT yabC protein - Escherichia coli dbj BAA01348.1 (D10483) ORF [Escherichia coli] Length = 346</p>
SEQ ID n°1973	Prot n°PL-2767.1	Contig40	7847	8854	90%	<p>Identities = 284/333 (85%), Positives = 313/333 (93%) sp P21830 FRUR_SALTY FRUCTOSE REPRESSOR (CATABOLITE REPRESSOR/ACTIVATOR) pir S15941 PEP-fructosephosphotransferase system repressor - Salmonella typhimurium emb CAA39103.1 (X55456) PEP-fructose phosphotransferase system repressor [Salmonella typhimurium] gb AAF65176.1 AF117227_1 (AF117227) FruR [Salmonella typhimurium] pir 1712316F fruR gene [Salmonella typhimurium] Identities = 459/595 (77%), Positives = 518/595 (86%), Gaps = 1/595 (0%) pir YCEC3 acetolactate synthase (EC 4.1.3.18) III large chain - Escherichia coli gb AAC73188.1 (AE000118) acetolactate synthase III, valine sensitive, large subunit [Escherichia coli] Length = 604</p>
SEQ ID n°1974	Prot n°PL-2768.1	Contig40	5538	7265	86%	<p>Identities = 69/148 (46%), Positives = 105/148 (70%), Gaps = 3/148 (2%) sp P55126 FRPA_NEIMC IRON-REGULATED PROTEIN FRPA pir A47058 Fe-regulated RTX cytotoxin homolog FrpA - Neisseria meningitidis gb AAA25454.1 (L06302) iron-regulated protein [Neisseria meningitidis] Identities = 344/571 (60%), Positives = 424/571 (74%), Gaps = 10/571 (1%) pir S56364 Inner membrane copper tolerance protein cyzC - Escherichia coli gb AA97035.1 (U14003) cyzC gene product [Escherichia coli] gb AAC77096.1 (AE000486) thiol:disulfide interchange protein; copper tolerance [Escherichia coli] Length = 565 "</p>
SEQ ID n°1975	Prot n°PL-2769.1	Contig40	2847	4148	24%	<p>Identities = 44/122 (36%), Positives = 88/122 (64%), Gaps = 5/122 (4%) pir G71856 hypothetical protein jhp1045 - Helicobacter pylori (strain J99) gb AAD06623.1 (AE001532) putative [Helicobacter pylori J99] Length = 256</p>
SEQ ID n°1976	Prot n°PL-2770.1	Contig40	2211	2846	31%	<p>Identities = 238/367 (61%), Positives = 304/367 (78%) gb AAF85626.1 (AE004318) long-chain-fatty-acid--CoA ligase, putative [Vibrio cholerae] Length = 801</p>
SEQ ID n°1977	Prot n°PL-2771.1	Contig40	1	1164	78%	
SEQ ID n°1978	Prot n°PL-2772.1	Contig28	20453	21937		
SEQ ID n°1979	Prot n°PL-2773.1	Contig28	23123	23761	50%	<p>Identities = 73/210 (34%), Positives = 109/210 (51%), Gaps = 22/210 (10%) gb AAD43465.1 AF113606_1 (AF113606) UspA1 [Moraxella catarrhalis] Length = 863</p>
SEQ ID n°1980	Prot n°PL-2774.1	Contig28	25247	25951	68%	<p>Identities = 127/210 (60%), Positives = 156/210 (73%) sp P25924 CYSG_SALTY SIROHEME SYNTHASE [INCLUDES: UROPORPHYRIN-III C-METHYLTRANSFERASE (UROGEN III METHYLASE) (SUMT) (UROPORPHYRINOGEN III METHYLASE) (UROM); PRECORRIN-2 OXIDASE; FERROCHELATASE] gb AA27041.1 (M64606) cysG [Salmonella typhimurium] Length = 457</p>

TABLEAU I

SEQ ID n°1982	Prot n°PL-2775.1	Contig28	25932	26837	65%	Identities = 163/292 (55%), Positives = 213/292 (72%) gb AAD39022.1 (AF026270) Pdux [Salmonella enterica serovar Typhimurium] Length = 300
SEQ ID n°1983	Prot n°PL-2776.1	Contig28	26785	27861	69%	Identities = 197/350 (56%), Positives = 250/350 (71%), Gaps = 1/350 (0%) gb AAC79515.1 (U90826) CobD [Salmonella typhimurium] Length = 300
SEQ ID n°1984	Prot n°PL-2777.1	Contig28	27890	28675	62%	Identities = 122/253 (48%), Positives = 178/253 (70%), Gaps = 4/253 (1%) gb AAC18603.1 (AF067123) uroporphyrin-III C-methyltransferase [Lactobacillus reuteri] Length = 256
SEQ ID n°1985	Prot n°PL-2778.1	Contig28	28988	30415	75%	Identities = 316/475 (66%), Positives = 371/475 (77%), Gaps = 8/475 (1%) sp Q9ZFV2 EUTA_SALTY ETHANOLAMINE UTILIZATION PROTEIN EUTA gb AAC78122.1 (AF093749) putative chaperonin [Salmonella typhimurium] Length = 467
SEQ ID n°1986	Prot n°PL-2779.1	Contig28	30428	31789	93%	Identities = 401/453 (88%), Positives = 427/453 (93%) sp P19635 EUTB_ECOLI ETHANOLAMINE AMMONIA-LYASE HEAVY CHAIN dbj BAA16323.1 (D90873) ETHANOLAMINE AMMONIA-LYASE HEAVY CHAIN (EC 4.3.1.7) (FRAGMENT). [Escherichia coli] dbj BAA16329.1 (D90874) ETHANOLAMINE AMMONIA-LYASE HEAVY CHAIN (EC 4.3.1.7) (FRAGMENT). [Escherichia coli] Length = 453
SEQ ID n°1987	Prot n°PL-278.1	Contig41	463371	483984	72%	Identities = 110/195 (56%), Positives = 148/195 (75%), Gaps = 1/195 (0%) pir S56363 divalent cation tolerance protein cutA3, inner membrane - Escherichia coli gb AAAG7034.1 (U14003) yidC gene product [Escherichia coli] emb CAA85376.1 (Z36905) 199 residue polypeptide [Escherichia coli] gb AAC77095.1 (AE000486) orf, hypothetical protein [Escherichia coli] Length = 199
SEQ ID n°1988	Prot n°PL-2780.1	Contig28	31806	32666	80%	Identities = 200/264 (75%), Positives = 232/264 (87%), Gaps = 3/264 (1%) sp P19265 EUTC_SALTY ETHANOLAMINE AMMONIA-LYASE LIGHT CHAIN gb AAC78124.1 (AF093749) ethanolamine ammonia lyase small subunit [Salmonella typhimurium] Length = 298
SEQ ID n°1989	Prot n°PL-2781.1	Contig28	32760	33434	No Hits found	
SEQ ID n°1990	Prot n°PL-2782.1	Contig28	35712	36611	No Hits found	
SEQ ID n°1991	Prot n°PL-2783.1	Contig28	38064	39146	68%	Identities = 230/350 (65%), Positives = 288/350 (81%), Gaps = 2/350 (0%) sp P36562 COBT_ECOLI NICOTINATE-NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (NN:DBI PRT) (N1-ALPHA-PHOSPHORIBOSYLTRANSFERASE) pir F64963 nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21) - Escherichia coli dbj BAA15808.1 (D90837) Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21) (NN:DBI PRT) (N1-alpha-Phosphoribosyltransferase). [Escherichia coli] gb AAC75052.1 (AE000291) nicotinate-nucleotide dimethylbenzimidazole-P phosphoribosyl transferase [Escherichia coli] Length = 359

TABLEAU I

SEQ ID n°1992	Prot n°PL-2784.1	Contig28	39118	39735	65%	<p>Identities = 105/203 (51%), Positives = 138/203 (67%) sp P39701 COBC_SALTY ALPHA-RIBAZOLE-5-PHOSPHATE PHOSPHATASE Length = 234</p>
SEQ ID n°1993	Prot n°PL-2785.1	Contig28	41186	41932	76%	<p>Identities = 152/245 (62%), Positives = 190/245 (77%), Gaps = 4/245 (1%) sp Q05802 COBS_SALTY COBALAMIN [5-PHOSPHATE] SYNTHASE gb AA27270.1 (L12006) cobalamin synthase [Salmonella typhimurium] Length = 247</p>
SEQ ID n°1994	Prot n°PL-2786.1	Contig28	42471	44012	76%	<p>Identities = 341/508 (67%), Positives = 404/508 (79%), Gaps = 4/508 (0%) sp Q05597 CBIP_SALTY COBYRIC ACID SYNTHASE gb AA27268.1 (L12006) cobyrilic acid synthase [Salmonella typhimurium] Length = 506</p>
SEQ ID n°1995	Prot n°PL-2787.1	Contig28	44199	44912	73%	<p>Identities = 165/233 (70%), Positives = 194/233 (82%) sp Q05593 CBIL_SALTY PRECORRIN-2 C20-METHYLTRANSFERASE (S-ADENOSYL-L-METHIONINE-PRECORRIN-2 METHYLTRANSFERASE) (SP2MT) gb AA27263.1 (L12006) S-adenosyl-methionine: precorrin-2 methyltransferase [Salmonella typhimurium] Length = 237</p>
SEQ ID n°1996	Prot n°PL-2788.1	Contig28	44912	45706	73%	<p>Identities = 170/262 (64%), Positives = 202/262 (76%) sp Q05592 CBIK_SALTY CBIK PROTEIN pdb 1QGO A Chain A, Anaerobic Cobalt Chelatase In Cobalamin Biosynthesis From Salmonella Typhimurium gb AA27262.1 (L12006) putative [Salmonella typhimurium]</p>
SEQ ID n°1997	Prot n°PL-2789.1	Contig28	45720	46505	67%	<p>Identities = 141/259 (54%), Positives = 177/259 (67%), Gaps = 2/259 (0%) sp Q05591 CBIJ_SALTY PRECORRIN-6X REDUCTASE gb AA27261.1 (L12006) GTG start; putative [Salmonella typhimurium] Length = 263 "</p>
SEQ ID n°1998	Prot n°PL-279.1	Contig41	465023	465856	No Hits found	
SEQ ID n°1999	Prot n°PL-2790.1	Contig28	46502	47227	83%	<p>Identities = 190/241 (78%), Positives = 220/241 (90%) sp Q05580 CBIH_SALTY PRECORRIN-3B C17-METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE) (PRECORRIN-3 METHYLASE) gb AA27260.1 (L12006) precorrin methylase [Salmonella Typhimurium] Identities = 229/350 (65%), Positives = 268/350 (76%)</p>
SEQ ID n°2000	Prot n°PL-2791.1	Contig28	47221	48282	71%	<p>sp Q05631 CBIG_SALTY CBIK PROTEIN gb AA27259.1 (L12006) putative [Salmonella typhimurium] Length = 351</p>
SEQ ID n°2001	Prot n°PL-2792.1	Contig28	48263	49036	86%	<p>Identities = 207/257 (80%), Positives = 229/257 (88%) sp Q05630 CBIF_SALTY PRECORRIN-4 C11-METHYLTRANSFERASE (PRECORRIN-3 METHYLASE) gb AA27258.1 (L12006) precorrin methylase [Salmonella typhimurium] Length = 257</p>
SEQ ID n°2002	Prot n°PL-2793.1	Contig28	49588	50190	65%	<p>Identities = 106/201 (52%), Positives = 136/201 (66%), Gaps = 1/201 (0%) sp Q05629 CBIE_SALTY PRECORRIN-6Y C5,15-METHYLTRANSFERASE [DECARBOXYLATING] (PRECORRIN-6 METHYLTRANSFERASE) (PRECORRIN-6Y METHYLASE) gb AA27256.1 (L12006) precorrin methylase [Salmonella typhimurium] Length = 201</p>

TABLEAU I

SEQ ID n°2003	Prot n°PL-2794.1	Contig28	50187	51323	81%	sp Q05628 CBID_SALTY CBID PROTEIN gb AA27255.1 (L12006) putative [Salmonella typhimurium] Length = 379	Identities = 282/369 (76%), Positives = 323/369 (87%)
SEQ ID n°2004	Prot n°PL-2795.1	Contig28	51320	51952	65%	sp Q05601 CBIC_SALTY PRECORRIN-8X METHYLMUTASE (PRECORRIN ISOMERASE) gb AAA27254.1 (L12006) precorrin isomerase [Salmonella typhimurium] Length = 210	Identities = 146/210 (69%), Positives = 166/210 (78%), Gaps = 1/210 (0%)
SEQ ID n°2005	Prot n°PL-2796.1	Contig28	51967	52926	75%	sp Q05600 CBIB_SALTY CBIB PROTEIN gb AA27253.1 (L12006) putative [Salmonella typhimurium] Length = 319	Identities = 210/319 (65%), Positives = 249/319 (77%)
SEQ ID n°2006	Prot n°PL-2797.1	Contig28	52923	54533	65%	sp P29946 CBIA_SALTY COBYRINIC ACID A,C-DIAMIDE SYNTHASE gb AAA27252.1 (L12006) precorrin amidase [Salmonella typhimurium]	Identities = 298/453 (65%), Positives = 352/453 (76%)
SEQ ID n°2007	Prot n°PL-2798.1	Contig28	56065	57609	No Hits found		
SEQ ID n°2008	Prot n°PL-2799.1	Contig28	61050	61685	No Hits found		
SEQ ID n°2009	Prot n°PL-28.1	Contig41	48309	50456	68%	Identities = 342/721 (47%), Positives = 492/721 (67%), Gaps = 6/721 (0%) gb AAD21564.1 (AF104912) putative transmembrane protein Wzc [Escherichia coli] Length = 721	
SEQ ID n°2010	Prot n°PL-280.1	Contig41	467012	467638	No Hits found		
SEQ ID n°2011	Prot n°PL-2800.1	Contig28	62108	62636	37%	Identities = 73/160 (45%), Positives = 90/160 (55%), Gaps = 19/160 (11%) pir S18687 ScSvN protein - Escherichia coli plasmid p158 emb CAA44050.1 (X82121) DNA inversion product [Escherichia coli] Length = 762	
SEQ ID n°2012	Prot n°PL-2801.1	Contig28	62893	63462	52%	Identities = 75/195 (38%), Positives = 114/195 (58%), Gaps = 2/195 (1%) ref NP_037719.1 Gp29 gb AAF31112.1 (AF069529) Gp29 [Bacteriophage HK97] Length = 202	
SEQ ID n°2013	Prot n°PL-2802.1	Contig28	63872	65428	54%	Identities = 181/503 (35%), Positives = 284/503 (55%), Gaps = 13/503 (2%) sp P75785 YBIP_ECOLI HYPOTHETICAL 59.7 KDA PROTEIN IN OMPX-MOEB INTERGENIC REGION pir G64818 probable membrane protein ybip - Escherichia coli gb AAC73902.1 (AE000163) putative enzyme [Escherichia coli] dbj BAA35487.1 (D90718) Hypothetical protein HI1005 [Escherichia coli] dbj BAA35497.1 (D90719) Hypothetical protein HI1005 [Escherichia coli] Length = 527	
SEQ ID n°2014	Prot n°PL-2803.2	Contig28	65518	66618			
SEQ ID n°2015	Prot n°PL-2804.1	Contig28	67182	67985	32%	Identities = 63/131 (48%), Positives = 88/131 (65%), Gaps = 6/131 (4%) dbj BAA76527.2 (AB017338) tail fiber [Pectobacterium carotovorum] Length = 667	
SEQ ID n°2016	Prot n°PL-2805.1	Contig28	69636	70613	51%	Identities = 107/329 (32%), Positives = 172/329 (51%), Gaps = 7/329 (2%) gb AAC68672.1 (AF018746) putative beta 1,3-glucosyltransferase WaaV [Escherichia coli] Length = 327	

TABLEAU I

SEQ ID n°2017	Prot n°PL-2806.1	Contig28	70983	71951	60%	Identities = 168/322 (52%), Positives = 214/322 (65%), Gaps = 2/322 (0%) gb AAAF41490.1 (AE002460) transposase, IS30 family [Neisseria meningitidis MC58] Length = 321
SEQ ID n°2018	Prot n°PL-2807.1	Contig28	72341	73117	39%	Identities = 65/202 (32%), Positives = 103/202 (50%), Gaps = 5/202 (2%) sp P75785 YBIP_ECOLI_HYPOTHETICAL_59.7_KDA_PROTEIN_IN_OMPX-MOEB_INTERGENIC_REGION_pir G64818_probable_membrane_protein_ybIP_Escherichia_coli_gb AAC73902.1 (AE000183) putative enzyme [Escherichia coli] dbj BAA35487.1 (D90718) Hypothetical protein H1005 [Escherichia coli] dbj BAA35497.1 (D90719) Hypothetical protein H1005 [Escherichia coli] Length = 527
SEQ ID n°2019	Prot n°PL-2808.1	Contig37	367472	368146	63%	Identities = 93/229 (40%), Positives = 147/229 (63%), Gaps = 7/229 (3%) sp P42914 YRAL_ECOLI_HYPOTHETICAL_25.7_KD_FIMBRIAL_CHAPERONE_IN_AGAI-MTR_INTERGENIC_REGION_PRECURSOR_pir C65104_hypothetical_25.7_kD_fimbrial_chaperone_in_agai-mtr_intergen-Escherichia_coli_(strain_K-12)_gb AAA57946.1 (U18997) ORF_0231 [Escherichia coli] gb AAC76177.1 (AE000395) putative chaperone Identities = 348/808 (43%), Positives = 527/808 (65%), Gaps = 27/808 (3%) sp P43682 LPFC_SALTY_OUTER_MEMBRANE_USHER_PROTEIN_LPFC_PRECURSOR_pir C56271_outer_membrane usher protein lpfc precursor - Salmonella typhimurium gb AAA73968.1 (U18559) lpfc gene product [Salmonella typhimurium] Length = 842
SEQ ID n°2020	Prot n°PL-2809.1	Contig37	368088	370724	59%	Identities = 129/577 (22%), Positives = 244/577 (41%), Gaps = 59/577 (10%) sp P18177 TOXB_CLODI_TOXIN_B_pir S10317_toxin_B - Clostridium difficile emb CAA37298.1 (X53136) toxin B (AA 1 - 2366) [Clostridium difficile] emb CAA63562.1 (X92982) tcdB [Clostridium difficile] Length = 2368 Identities = 83/325 (25%), Positives = 147/325 (42%), Gaps = 22/325 (6%) sp P21848 MRKD_KLEPN_FIMBRIA_ADHESIN_PROTEIN_PRECURSOR_pir B32801_fimbrial_adhesin_precursor_type_3 - Klebsiella pneumoniae gb AAA26098.1 (M55912) mrkD [Klebsiella pneumoniae] gb AAA25098.1 (M24536) fimbrial adhesin [Klebsiella pneumoniae] Length = 321 Identities = 60/185 (32%), Positives = 91/185 (48%), Gaps = 29/185 (15%) gb AAAF19107.1 (AF143456_2) (AF143456) BdrC1 - [Borrelia parkeri] gb AAAF19107.1 (AF143456_2) (AF143456) BdrC1 - [Borrelia parkeri] Length = 172
SEQ ID n°2021	Prot n°PL-281.1	Contig41	464909	474037	8%	Identities = 38/146 (26%), Positives = 81/146 (55%), Gaps = 8/146 (5%) gb AAAF19774.1 (AF128451_1) (AF128451) repeat motif protein bdrA8 [Borrelia turicatae] Length = 251
SEQ ID n°2022	Prot n°PL-2810.1	Contig37	370708	371736	41%	Identities = 984/1241 (79%), Positives = 1115/1241 (89%), Gaps = 1/1241 (0%) sp P43323 HRPA_ECOLI_ATP-DEPENDENT_HELICASE_HRPA_pir H64892_ATP-dependent_helicase_hrpA - Escherichia coli dbj BAA15029.1 (D90780) ATP-dependent helicase HrpA homolog. [Escherichia coli] gb AAC74495.1 (AE000238) helicase, ATP-dependent [Escherichia coli]
SEQ ID n°2023	Prot n°PL-2811.1	Contig37	373067	373975	30%	
SEQ ID n°2024	Prot n°PL-2812.1	Contig37	373282	374028	32%	
SEQ ID n°2025	Prot n°PL-2813.1	Contig37	374759	378502	89%	

TABLEAU I

SEQ ID n°2026	Prot n°PL-2814.1	Contig37	378793	378395	80%	<p>Identities = 131/200 (65%), Positives = 164/200 (81%)</p> <p>spiP41407 ACPD_ECOLI_ACYL_CARRIER_PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) pir G64892 [acyl-carrier-protein] phosphodiesterase (EC 3.1.4.14) acpD - Escherichia coli dbj BAA15024.1 (D90779) Acyl carrier protein phosphodiesterase (ACP phosphodiesterase) (fragment) [Escherichia coli] dbj BAA15028.1 (D90780) Acyl carrier protein phosphodiesterase (ACP phosphodiesterase) (fragment) [Escherichia coli] gb AAC74494.1 (AE000238) acyl carrier protein phosphodiesterase [Escherichia coli] Length = 201</p>
SEQ ID n°2027	Prot n°PL-2815.2	Contig37	379996	382623		<p>Identities = 156/287 (54%), Positives = 197/287 (68%), Gaps = 1/287 (0%)</p> <p>emb CAB84714.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis] emb CAB84719.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis] Length = 321</p>
SEQ ID n°2028	Prot n°PL-2816.1	Contig34	166004	166978	57%	<p>Identities = 163/313 (52%), Positives = 230/313 (73%), Gaps = 4/313 (1%)</p> <p>gb AAF81206.1 AF247502_1 (AF247502) Y12 [Salmonella dublin] Length = 316</p>
SEQ ID n°2030	Prot n°PL-2818.1	Contig34	162652	163392	80%	<p>Identities = 208/246 (84%), Positives = 227/246 (91%)</p> <p>spiP09374 PFLA_ECOLI_PYRUVATE_FORMATE-LYASE 1 ACTIVATING ENZYME (PFL-ACTIVATING ENZYME) pir S01789 pyruvate formate-lyase activating enzyme (EC 1.97.1.4), lyase 1-specific - Escherichia coli (strain K-12) emb CAA30829.1 (X08035) pyruvate formate-lyase activating enzyme (AA 1-246) [Escherichia coli] gb AAC73988.1 (AE000192) pyruvate formate lyase activating enzyme 1 [Escherichia coli] dbj BAA35637.1 (D90728) Pyruvate formate-lyase 1 activating enzyme (EC 1.97.1.4). [Escherichia coli] Length = 246</p>
SEQ ID n°2031	Prot n°PL-2819.1	Contig34	160296	162578	94%	<p>Identities = 681/760 (89%), Positives = 725/760 (94%)</p> <p>spiP09373 PFLB_ECOLI_FORMATE_ACETYLTRANSFERASE 1 (PYRUVATE FORMATE-LYASE 1) pir S01788 formate C-acetyltransferase (EC 2.3.1.54) 1 - Escherichia coli emb CAA30828.1 (X08035) pyruvate formate-lyase (AA 1-760) [Escherichia coli] dbj BAA35638.1 (D90728) Formate c-acetyltransferase (EC 2.3.1.54). [Escherichia coli] gb AAC73989.1 (AE000192) formate acetyltransferase 1 [Escherichia coli] Length = 760</p>
SEQ ID n°2032	Prot n°PL-282.1	Contig41	474781	476139	25%	<p>Identities = 68/268 (25%), Positives = 117/268 (43%), Gaps = 30/268 (11%)</p> <p>gb AAF96712.1 (AE004409) agmatinase [Vibrio cholerae] Length = 309</p>

TABLEAU I

SEQ ID n°2033	Prot n°PL-2820.1	Contig34	159383	180240	81%	<p>sp P21501 FOCA_ECOLI PROBABLE FORMATE TRANSPORTER 1 (FORMATE CHANNEL 1) pir A32305 probable formate transporter protein - Escherichia coli dbj BAA35639.1 (D90728) Probable formate transporter [Escherichia coli] dbj BAA35648.1 (D90729) Probable formate transporter [Escherichia coli] gb AAC73990.1 (AE000192) probable formate transporter (formate channel 1) [Escherichia coli] Length = 285</p> <p>Identities = 202/285 (70%), Positives = 241/285 (83%)</p>
SEQ ID n°2034	Prot n°PL-2821.1	Contig34	157291	159083	86%	<p>sp P75838 YCAO_ECOLI HYPOTHETICAL 65.7 KD PROTEIN IN FOCA-SERC INTERGENIC REGION Length = 586</p> <p>Identities = 463/584 (79%), Positives = 512/584 (87%)</p>
SEQ ID n°2035	Prot n°PL-2822.1	Contig34	156118	157161	81%	<p>Identities = 243/348 (69%), Positives = 287/348 (81%), Gaps = 1/348 (0%)</p> <p>sp P00805 ASG2_ECOLI L-ASPARAGINASE II PRECURSOR (L-ASPARAGINE AMIDOHYDROLASE II) (L-ASNASE II) (COLASPASE) pir XDEC asparaginase (EC 3.5.1.1) II precursor - Escherichia coli gb AAA23445.1 (M34234) L-asparaginase II (ansB) (EC 3.5.1.1) [Escherichia coli] gb AAA24062.1 (M34277) L-asparaginase II (ansB) precursor [Escherichia coli] gb AAA69124.1 (U28377) L-asparaginase [Escherichia coli] gb AAC75994.1 (AE000378) periplasmic L-asparaginase II [Escherichia coli] Length = 284/362 (78%), Positives = 322/362 (88%), Gaps = 1/362 (0%)</p> <p>sp P19689 SERC_YEREN PHOSPHOSERINE AMINOTRANSFERASE (PSAT) pir XNEBPY phosphoserine transaminase (EC 2.6.1.52) - Yersinia enterocolitica gb AA27665.1 (M32213) 3-phosphoserine aminotransferase (serC) [Yersinia enterocolitica] Length = 361</p>
SEQ ID n°2036	Prot n°PL-2823.1	Contig34	153913	155001	88%	<p>Identities = 348/425 (81%), Positives = 374/425 (87%), Gaps = 1/425 (0%)</p> <p>sp P19688 AROA_YEREN 3-PHOSPHOSHIMKIMATE 1-CARBOXYVINYLTRANSFERASE (5-ENOLPYRUVYL-SHIMKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS) pir XUEBY 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) - Yersinia enterocolitica gb AA27666.1 (M32213) 5-enolpyruvylshikimate 3-phosphate synthase (aroA) [Yersinia enterocolitica] Length = 427</p>
SEQ ID n°2037	Prot n°PL-2824.1	Contig34	152377	153663	84%	<p>Identities = 179/226 (79%), Positives = 200/226 (88%)</p> <p>sp P23863 KCY_ECOLI CYTIDYLATE KINASE (CK) (CYTIDINE MONOPHOSPHATE KINASE) (CMP KINASE) (MSSA PROTEIN) (P25) pir E64830 cytidylate kinase (EC 2.7.4.14) - Escherichia coli pdb 2CMK A Chain A, Cytidine Monophosphate Kinase In Complex With Cytidine-Di-Phosphate dbj BAA35645.1 (D90728) Cytidylate kinase (EC 2.7.4.14) (ck) (cytidine monophosphate kinase) (CMP kinase) (MssA protein) (p25). [Escherichia coli] dbj BAA35654.1 (D90729) Cytidylate kinase (EC 2.7.4.14) (ck) (cytidine monophosphate kinase) (CMP kinase) (MssA protein) (p25). [Escherichia coli] gb AAC73996.1 (AE000183) cytidylate kinase [Escherichia coli] Length = 227</p>

TABLEAU I

SEQ ID n°2038	Prot n°PL-2827.1	Contig34	149534	151222	96%	Identities = 530/557 (95%), Positives = 546/557 (97%) sp P02349 RS1_ECOLI 30S RIBOSOMAL PROTEIN S1 pir R3EC1 ribosomal protein S1 - Escherichia coli dbj BAA35655.1 (D90729) 30S ribosomal protein S1. [Escherichia coli] gb AAC73997.1 (AE000193) 30S ribosomal subunit protein S1 [Escherichia coli] Length = 557
SEQ ID n°2040	Prot n°PL-2828.1	Contig34	147282	148220	No Hits found	Identities = 62/194 (31%), Positives = 103/194 (52%), Gaps = 5/194 (2%) dbj BAB05888.1 (AP001514) unknown conserved protein [Bacillus halodurans] Length = 209
SEQ ID n°2041	Prot n°PL-2829.1	Contig34	145923	146588	46%	Identities = 65/223 (29%), Positives = 97/223 (43%), Gaps = 20/223 (8%) dbj BAA25511.1 (AB011157) KIAA0585 protein [Homo sapiens] Length = 416
SEQ ID n°2042	Prot n°PL-283.1	Contig41	476037	476780	39%	Identities = 65/277 (23%), Positives = 113/277 (40%), Gaps = 27/277 (9%) dbj BAB06652.1 (AP001517) unknown [Bacillus halodurans] Length = 287/760 (37%), Positives = 440/760 (57%), Gaps = 13/760 (1%) sp P37443 YCAL_ECOLI_HYPOTHETICAL 87.3 KDA PROTEIN IN HIMD-MSBA INTERGENIC REGION pir H64830 probable membrane protein ycal - Escherichia coli gb AAC73999.1 (AE000193) orf, hypothetical protein [Escherichia coli] dbj BAA35657.1 (D90729) Hypothetical protein (msbA 5' region) [Escherichia coli] Length = 780
SEQ ID n°2043	Prot n°PL-2830.1	Contig34	145100	145948	39%	Identities = 245/291 (84%), Positives = 267/291 (91%) sp P27299 MSBA_ECOLI_PROBABLE_TRANSPORT_ATP-BINDING_PROTEIN MSBA pir S27998 probable ABC-type transport protein msbA - Escherichia coli emb CAA77839.1 (Z11796) member of ATP-dependent transport family, very similar to ndr proteins and hemolysin B, export protein [Escherichia coli] dbj BAA35658.1 (D90729) MsbA protein. [Escherichia coli] gb AAC74000.1 (AE000193) ATP-binding transport protein; multicopy suppressor of htrB [Escherichia coli] Length = 582 "
SEQ ID n°2044	Prot n°PL-2831.1	Contig34	141900	144233	56%	
SEQ ID n°2045	Prot n°PL-2832.1	Contig34	140983	141861	87%	
SEQ ID n°2046	Prot n°PL-2833.1	Contig34	140117	141016	88%	Identities = 237/289 (82%), Positives = 265/289 (91%) sp P27299 MSBA_ECOLI_PROBABLE_TRANSPORT_ATP-BINDING_PROTEIN MSBA pir S27998 probable ABC-type transport protein msbA - Escherichia coli emb CAA77839.1 (Z11796) member of ATP-dependent transport family, very similar to ndr proteins and hemolysin B, export protein [Escherichia coli] dbj BAA35658.1 (D90729) MsbA protein. [Escherichia coli] gb AAC74000.1 (AE000193) ATP-binding transport protein; multicopy suppressor of htrB [Escherichia coli] Length = 582 "

TABLEAU I

SEQ ID n°2047	Prot n°PL-2834.1	Contig34	139125	140120	68%	<p>Identities = 206/328 (62%), Positives = 243/328 (73%), Gaps = 1/328 (0%) sp P27300 LPXK_ECOLI TETRAACYCLIDISACCHARIDE 4'-KINASE (LIPID A 4'-KINASE) pir B64831 ycaH protein - Escherichia coli gb AAC74001.1 (AE000193) putative EC 1.2 enzyme [Escherichia coli] dbj BAA35661.1 (D90730) Hypothetical protein E (msbA 3' region) [Escherichia coli] Length = 328</p>
SEQ ID n°2048	Prot n°PL-2835.1	Contig34	137017	137766	81%	<p>Identities = 180/242 (74%), Positives = 205/242 (84%) sp P04951 KDSB_ECOLI 3-DEOXY-MANNO-OCTULOSONATE CYTIDYLTRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO 3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS) pir A26322 3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38) - Escherichia coli gb AAA83877.1 (J02614) CMP-KDO synthetase [Escherichia coli] dbj BAA35664.1 (D90730) 3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38) [Escherichia coli] gb AAC74004.1 (AE000193) CTP-CMP-3-deoxy-D-manno-octulosonate transferase Length = 259</p>
SEQ ID n°2049	Prot n°PL-2836.1	Contig34	135949	136788	70%	<p>Identities = 163/264 (61%), Positives = 198/264 (74%), Gaps = 8/264 (3%) sp P36565 YCBC_ECOLI HYPOTHETICAL 28.7 KDA PROTEIN IN KDSB-MUKF INTERGENIC REGION pir G64831 probable membrane protein ycbC - Escherichia coli gb AAC74006.1 (AE000194) orf, hypothetical protein [Escherichia coli] dbj BAA35666.1 (D90730) Hypothetical protein in kdsB-mukF intergenic region. [Escherichia coli] Length = 259</p>
SEQ ID n°2050	Prot n°PL-2837.1	Contig34	134891	135670	73%	<p>Identities = 155/255 (60%), Positives = 198/255 (78%) sp P36566 SMTA_ECOLI SMTA PROTEIN pir H64831 probable S-adenosylmethionine-dependent methyltransferase - Escherichia coli dbj BAA35667.1 (D90730) SmtA protein. [Escherichia coli] gb AAC74007.1 (AE000194) S-adenosylmethionine-dependent methyltransferase Length = 243</p>
SEQ ID n°2051	Prot n°PL-2838.1	Contig34	133558	134880	88%	<p>Identities = 350/440 (79%), Positives = 397/440 (89%) sp P36567 MUKF_ECOLI MUKF PROTEIN (KILLING FACTOR KICB) pir S43911 mukF protein - Escherichia coli dbj BAA05457.1 (D28440) MukF [Escherichia coli] dbj BAA35668.1 (D90730) MukF protein (killing factor KicB). [Escherichia coli] gb AAC74008.1 (AE000194) mukF protein (killing factor KicB) [Escherichia coli] Length = 440</p>
SEQ ID n°2052	Prot n°PL-2839.1	Contig34	132855	133604	88%	<p>Identities = 194/248 (78%), Positives = 222/248 (89%), Gaps = 5/248 (2%) pir S43912 kicA protein - Escherichia coli dbj BAA35669.1 (D90730) MukE protein [Escherichia coli] Length = 243</p>
SEQ ID n°2053	Prot n°PL-284.1	Contig41	476755	478626	42%	<p>Identities = 162/531 (30%), Positives = 263/531 (49%), Gaps = 33/531 (6%) pir S75352 ABC-type transport protein sir2019 - Synechocystis sp. (strain PCC 6803) dbj BAA17266.1 (D90804) ABC transporter [Synechocystis sp.] Length = 593</p>

TABLEAU I

SEQ ID n°2054	Prot n°PL-2840.1	Contig34	128410	132858	88%	Identities = 1155/1474 (78%), Positives = 1307/1474 (88%) sp P22523 MUKB_ECOLI_CELL_DIVISION_PROTEIN_MUKB_pir C64832 cell division protein mukB - Escherichia coli (strain K-12, substrain MG1655) dbj BA335670.1 (D90730) MukB protein [Escherichia coli] gb AAC74010.1 (AE000194) kinesin-like cell division protein involved in chromosome partitioning [Escherichia coli] Length = 1486
SEQ ID n°2055	Prot n°PL-2841.1	Contig34	127419	128144	No Hits found	
SEQ ID n°2056	Prot n°PL-2842.1	Contig34	126733	127380	No Hits found	
SEQ ID n°2057	Prot n°PL-2843.1	Contig34	125168	128130	76%	Identities = 190/321 (59%), Positives = 252/321 (78%), Gaps = 9/321 (2%) sp P37415 YTL2_SALTY_HYPOTHETICAL_35.3_KD_PROTEIN_NEAR_TLPA_OPERON_pir S41385 hypothetical yadD homolog - Salmonella typhimurium emb CAA82634.1 (Z29513) 30 kDa protein similar to E. coli yadD and yrgA [Salmonella typhimurium] Length = 313
SEQ ID n°2058	Prot n°PL-2844.1	Contig34	123806	124774	21%	Identities = 39/108 (36%), Positives = 69/108 (63%), Gaps = 2/108 (1%) gb AAG06749.1 AE004758_8 (AE004758) hypothetical protein [Pseudomonas aeruginosa] Length = 115
SEQ ID n°2059	Prot n°PL-2845.1	Contig34	122982	123866	59%	Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U83985) putative protease [Porphyromonas gingivalis] Length = 300
SEQ ID n°2060	Prot n°PL-2846.1	Contig34	121839	122672	No Hits found	
SEQ ID n°2061	Prot n°PL-2847.1	Contig34	120400	121356	47%	Identities = 108/251 (43%), Positives = 153/251 (60%), Gaps = 3/251 (1%) gb AAG05302.1 AE004617_6 (AE004617) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 408
SEQ ID n°2062	Prot n°PL-2848.1	Contig34	119913	120623	55%	Identities = 85/245 (34%), Positives = 132/245 (53%), Gaps = 19/245 (7%) gb AAA96022.1 (U38815) halovibrin [Vibrio fischeri] Length = 300
SEQ ID n°2063	Prot n°PL-2849.1	Contig34	118438	119445	17%	Identities = 40/118 (33%), Positives = 69/118 (49%), Gaps = 6/118 (5%) sp Q47279 HRPN_ERWCA_HARPIN (HARPIN-ECC) gb AAB49733.1 (L78834) putative [Pectobacterium carotovorum] Length = 356
SEQ ID n°2064	Prot n°PL-285.1	Contig41	479577	483278	No Hits found	
SEQ ID n°2065	Prot n°PL-2850.1	Contig34	117347	118354	No Hits found	
SEQ ID n°2066	Prot n°PL-2851.1	Contig34	115320	117428	24%	Identities = 122/302 (40%), Positives = 174/302 (57%), Gaps = 12/302 (3%) emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)] Length = 690
SEQ ID n°2067	Prot n°PL-2853.1	Contig41	770240	771169	85%	Identities = 233/309 (75%), Positives = 271/309 (87%) pir XYECM homoserine O-succinyltransferase (EC 2.3.1.46) - Escherichia coli gb AAC43107.1 (U00006) homoserine transsuccinylase [Escherichia coli] gb AAC76983.1 (AE000474) homoserine transsuccinylase [Escherichia coli] Length =

TABLEAU I

SEQ ID n°2068	Prot n°PL-2854.1	Contig41	768342	769940	87%	Identities = 415/532 (78%), Positives = 488/532 (87%), Gaps = 1/532 (0%) sp P08997 MASY_ECOLI_MALATE SYNTHASE A (MSA) pir SYECMA_malate synthase (EC 4.1.3.2) A - Escherichia coli emb CAA30973.1 (X12431) malate synthase [Escherichia coli] gb AAC43108.1 (U00006) malate synthase A [Escherichia coli] gb AAC76984.1 (AE000474) malate synthase A [Escherichia coli] Length = 533
SEQ ID n°2069	Prot n°PL-2855.1	Contig41	766938	768245	90%	Identities = 372/432 (86%), Positives = 399/432 (92%) sp P05313 ACEA_ECOLI_ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) pir WZECIC isocitrate lyase (EC 4.1.3.1) - Escherichia coli emb CAA30974.1 (X12431) isocitrate lyase [Escherichia coli] gb AAC43109.1 (U00006) isocitrate lyase [Escherichia coli] gb AAC76985.1 (AE000474) isocitrate lyase [Escherichia coli] Length = 434
SEQ ID n°2070	Prot n°PL-2856.1	Contig41	765129	766886	81%	Identities = 420/569 (73%), Positives = 481/569 (83%) gb AAC43891.1 (U43356) isocitrate dehydrogenase kinase/phosphatase [Salmonella enterica] gb AAC43893.1 (U43357) isocitrate dehydrogenase kinase/phosphatase [Salmonella enterica] Length = 594
SEQ ID n°2071	Prot n°PL-2857.1	Contig41	764141	764746	No Hits found	Identities = 192/276 (69%), Positives = 237/276 (85%), Gaps = 2/276 (0%) pir RPPECIR acetate operon repressor - Escherichia coli gb AAA60561.1 (M63914) repressor of the aceBAK operon [Escherichia coli] gb AAC43112.1 (U00006) CG Site No. 614 [Escherichia coli] gb AAC76988.1 (AE000475) repressor of aceBA operon [Escherichia coli] Length = 287
SEQ ID n°2073	Prot n°PL-2859.1	Contig41	760755	762290	34%	Identities = 106/382 (27%), Positives = 177/382 (45%), Gaps = 39/382 (10%) gb AAF57570.1 (AE003796) CG10073 gene product [Drosophila melanogaster] Length = 765
SEQ ID n°2074	Prot n°PL-288.1	Contig41	483716	484783	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°2075	Prot n°PL-2860.1	Contig41	759117	759977	34%	Identities = 59/242 (24%), Positives = 98/242 (40%), Gaps = 25/242 (10%) gb AAG04628.1 (AE004553) hypothetical protein [Pseudomonas aeruginosa] Length = 294
SEQ ID n°2076	Prot n°PL-2861.1	Contig41	757797	758708	No Hits found	Identities = 74/281 (25%), Positives = 114/291 (38%), Gaps = 11/291 (3%) gb AAC44790.1 (U76608) isobutylamine N-hydroxylase [Streptomyces viridifaciens] Length = 378
SEQ ID n°2077	Prot n°PL-2862.1	Contig41	756702	757798	31%	Identities = 117/318 (36%), Positives = 163/318 (50%), Gaps = 25/318 (7%) sp D86442 ARGD_AQUAE_ACETYLORNITHINE AMINOTRANSFERASE (ACOAT) pir G70301 N-acetylornithine aminotransferase - Aquifex aeolicus gb AAC06390.1 (AE000669) N-acetylornithine aminotransferase [Aquifex aeolicus] Length = 376
SEQ ID n°2078	Prot n°PL-2863.1	Contig41	754042	756842	18%	

TABLEAU I

SEQ ID n°2078	Prot n°PL-2864.1	Contig41	753021	754178	45%	Identities = 114/328 (34%), Positives = 174/328 (52%), Gaps = 15/328 (4%) embjCAB99167.1 (AL390188) hypothetical protein 2SCG18.34c [Streptomyces coelicolor A3(2)] Length = 320	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°2080	Prot n°PL-2865.1	Contig41	751332	752813	53%	Identities = 163/487 (33%), Positives = 264/487 (53%), Gaps = 35/487 (7%) gb AAD01942.1 (AF032440) D-alanine-D-alanyl carrier protein ligase; DltA [Staphylococcus xylosum] Length = 487	
SEQ ID n°2081	Prot n°PL-2866.1	Contig41	750208	751353	48%	Identities = 113/387 (29%), Positives = 185/387 (47%), Gaps = 41/387 (10%) sp P39580 DLTB_BACSU DLTB PROTEIN pir S39659 dltB protein - Bacillus subtilis embjCAA51560.1 (X73124) ipa-4r [Bacillus subtilis]	
SEQ ID n°2082	Prot n°PL-2867.1	Contig41	748853	750085	43%	embjCAB15877.1 (Z99123) alternate gene name: ipa-4r [Bacillus subtilis] Identities = 94/415 (22%), Positives = 180/415 (42%), Gaps = 34/415 (8%) embjCAB51822.1 (AJ012255) extramembranal protein [Listeria monocytogenes] Length = 424	
SEQ ID n°2083	Prot n°PL-2868.1	Contig41	746290	747684	80%	Identities = 320/445 (71%), Positives = 373/445 (82%), sp P08660 AK3_ECOLI LYSINE-SENSITIVE ASPARTOKINASE III (ASPARTATE KINASE III) pir KIECD3 aspartate kinase (EC 2.7.2.4) III, lysine-sensitive - Escherichia coli gb AAC43118.1 (U00006) aspartokinase III [Escherichia coli] gb AAC76994.1 (AE000475) aspartokinase III, lysine sensitive [Escherichia coli] embjCAC09236.1 (AX028723) unnamed protein product [Escherichia coli] Length = 449	
SEQ ID n°2084	Prot n°PL-2869.1	Contig41	744360	746006	87%	Identities = 456/548 (83%), Positives = 508/548 (92%) sp P11243 G6PL_CLAUN GLUCOSE-6-PHOSPHATE ISOMERASE, CHLOROPLAST (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) Length = 548	
SEQ ID n°2085	Prot n°PL-287.1	Contig41	485344	487023	No Hits found	Identities = 215/286 (75%), Positives = 248/286 (86%) sp O52366 UBIA_PROST 4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (4-HB POLYPRENYLTRANSFERASE) gb AAB88868.1 (AF036909) 4-hydroxybenzoate octaprenyltransferase Identities = 613/813 (75%), Positives = 703/813 (86%), Gaps = 2/813 (0%) pir XUECAG glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) - Escherichia coli gb AAC77011.1 (AE000477) glycerol-3-phosphate acyltransferase [Escherichia coli] Length = 827	
SEQ ID n°2086	Prot n°PL-2870.1	Contig41	742651	743517	84%	Identities = 180/204 (88%), Positives = 190/204 (92%), Gaps = 4/204 (1%) sp Q07267 LEXA_PRORE LEXA REPRESSOR pir S33693 lexA protein - Providencia rettgeri embjCAA50300.1 (X70965) LexA repressor [Providencia rettgeri] Length = 205	
SEQ ID n°2087	Prot n°PL-2871.1	Contig41	740151	742607	84%		
SEQ ID n°2088	Prot n°PL-2872.1	Contig41	738925	739530	90%		

TABLEAU I

SEQ ID n°2085	Prot n°PL-2873.1	Contig41	736891	738063	39%	Identities = 91/349 (26%), Positives = 156/349 (44%), Gaps = 31/349 (8%) pir B64936 hypothetical protein b1762 - Escherichia coli (strain K-12) gb AAC74832.1 (AE000271) orf, hypothetical protein [Escherichia coli] Length = 387
SEQ ID n°2086	Prot n°PL-2874.1	Contig41	735475	736563	55%	Identities = 160/354 (45%), Positives = 225/354 (63%), Gaps = 3/354 (0%) pir J39549 Lactate oxidase - Aerococcus viridans db BAA09172.1 (D50611) lactate oxidase [Aerococcus viridans] Length = 374
SEQ ID n°2087	Prot n°PL-2875.1	Contig41	734037	734882	12%	Identities = 27/61 (44%), Positives = 36/61 (58%), Gaps = 2/61 (3%) db BAA98885.1 (AB045036) tail fiber [Pectobacterium carotovorum subsp. carotovorum] Length = 632
SEQ ID n°2088	Prot n°PL-2876.1	Contig41	732864	733475	No Hits found	
SEQ ID n°2089	Prot n°PL-2877.1	Contig41	730186	731223	81%	Identities = 259/344 (75%), Positives = 301/344 (87%) pir H65212 hypothetical 38.4 kD protein in dnf-qor intergenic region - Escherichia coli (strain K-12) gb AAC77019.1 (AE000478) orf, hypothetical protein [Escherichia coli] Length = 345
SEQ ID n°2090	Prot n°PL-2878.1	Contig41	728084	729151	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db BAA06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°2091	Prot n°PL-2879.1	Contig41	727445	728083	No Hits found	
SEQ ID n°2092	Prot n°PL-288.1	Contig41	488773	489375	60%	Identities = 100/200 (50%), Positives = 127/200 (63%), Gaps = 3/200 (1%) pir T36373 hypothetical protein SCE94.13 - Streptomyces coelicolor emb CAB40862.1 (AL049628) hypothetical protein [Streptomyces coelicolor A3(2)] Length = 211
SEQ ID n°2093	Prot n°PL-2880.1	Contig41	725698	726879	83%	Identities = 248/327 (75%), Positives = 274/327 (82%) spiP28304(QOR_ECOLI QUINONE OXIDOREDUCTASE (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN HOMOLOG PROTEIN) pir S45529 quinone oxidoreductase (EC 1.6.5.5) - Escherichia coli pdb 1QOR1A Chain A, Quinone Oxidoreductase Complexed With NADPH pdb 1QOR1B Chain B, Quinone Oxidoreductase Complexed With NADPH gb AAA23691.1 (L02312) quinone oxidoreductase [Escherichia coli] gb AAC43145.1 (U00006) quinone oxidoreductase [Escherichia coli] gb AAC77021.1 (AE000478) quinone oxidoreductase [Escherichia coli] Identities = 408/471 (86%), Positives = 445/471 (93%), Gaps = 2/471 (0%)
SEQ ID n°2094	Prot n°PL-2881.1	Contig41	724316	725725	89%	spiP10338(DNAB_SALTY REPLICATIVE DNA HELICASE Length = 471) Identities = 252/359 (70%), Positives = 283/359 (81%), Gaps = 1/359 (0%)
SEQ ID n°2095	Prot n°PL-2882.1	Contig41	723197	724276	78%	spiP29743(ALR1_ECOLI ALANINE RACEMASE, BIOSYNTHETIC pir PC1296 alanine racemase (EC 5.1.1.1), biosynthetic - Escherichia coli (strain K-12) gb AAC77023.1 (AE000478) alanine racemase 1 [Escherichia coli] Length = 359

TABLEAU I

SEQ ID n°2100	Prot n°PL-2883.1	Contig41	721948	723150	81%	<p>Identities = 277/396 (69%), Positives = 327/396 (81%)</p> <p>sp P04693 TYRB_ECOLI AROMATIC-AMINO-ACID AMINOTRANSFERASE (AROAT) (ARAT) pir XNECY tyrosine transaminase (EC 2.6.1.5) - Escherichia coli pdb 3TATJ Chain A, Tyrosine Aminotransferase From E. Coli pdb 3TATJ Chain B, Tyrosine Aminotransferase From E. Coli pdb 3TATJ Chain C, Tyrosine Aminotransferase From E. Coli pdb 3TATJ Chain D, Tyrosine Aminotransferase From E. Coli pdb 3TATJ Chain E, Tyrosine Aminotransferase From E. Coli pdb 3TATJ Chain F, Tyrosine Aminotransferase From E. Coli pdb 3TATJ Chain F, Tyrosine Aminotransferase From E. Coli pdb 3TATJ Chain F, Tyrosine aminotransferase [Escherichia coli] gb AA24703.1 (M12047) tyrosine aminotransferase [Escherichia coli] gb AAC43148.1 (U00006) tyrosine aminotransferase [Escherichia coli] emb CAA27278.1 (X03628) aromatic aminotransferase (tyrB) [Escherichia coli] gb AAC77024.1 (AE000478) tyrosine aminotransferase, tyrosine repressible [Escherichia coli]</p> <p>Identities = 198/329 (60%), Positives = 245/329 (74%) dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] Length = 345</p>
SEQ ID n°2101	Prot n°PL-2884.1	Contig41	720542	721555	72%	<p>Identities = 185/307 (60%), Positives = 229/307 (74%)</p> <p>sp P30235 YEIC_ECOLI HYPOTHETICAL SUGAR KINASE IN NFO-FRUA INTERGENIC REGION pir E64985 hypothetical 33.8K protein (nfo-fruA intergenic region) - Escherichia coli gb AAA60507.1 (U00007) yeIC [Escherichia coli] gb AAC75227.1 (AE000306) putative kinase [Escherichia coli] prf 2014253BM yeIC gene [Escherichia coli] Length = 313</p> <p>Identities = 228/304 (75%), Positives = 260/304 (85%)</p>
SEQ ID n°2102	Prot n°PL-2885.1	Contig41	717758	718843	59%	<p>sp P33025 YEIN_ECOLI HYPOTHETICAL 32.9 KD PROTEIN IN NFO-FRUA INTERGENIC REGION pir D64985 hypothetical 32.9 kD protein in nfo-fruA intergenic region - Escherichia coli (strain K-12) gb AAA60517.1 (U00007) yeIN [Escherichia coli] gb AAC75226.1 (AE000306) orf, hypothetical protein [Escherichia coli] prf 2014253BL yeIN gene [Escherichia coli]</p> <p>Identities = 841/941 (89%), Positives = 898/941 (95%)</p>
SEQ ID n°2103	Prot n°PL-2886.1	Contig41	716817	717755	79%	<p>sp P37434 UVRA_SALTY EXCINUCLEASE ABC SUBUNIT A gb AA27250.1 (M93014) DNA repair enzyme [Salmonella typhimurium] Identities = 147/179 (82%), Positives = 155/179 (86%), Gaps = 4/179 (2%)</p>
SEQ ID n°2104	Prot n°PL-2887.1	Contig41	713922	716756	94%	<p>sp P25762 SSB_SERMA SINGLE-STRAND BINDING PROTEIN (SSB) (HELIX DESTABILIZING PROTEIN) pir JN0632 single-stranded DNA-binding protein Serratia marcescens emb CAA46208.1 (X55080) single-stranded DNA-binding protein [Serratia marcescens] Length = 176</p> <p>Identities = 94/350 (26%), Positives = 154/350 (43%), Gaps = 67/350 (19%) emb CAB46587.1 (AJ132845) hypothetical protein [Yersinia enterocolitica]</p> <p>Identities = 90/312 (28%), Positives = 135/312 (42%), Gaps = 95/312 (30%) gb AAG12476.1 (AC037197) Putative histidine decarboxylase [Onyza sativa] Length = 424</p>
SEQ ID n°2105	Prot n°PL-2888.1	Contig41	713027	713563	74%	
SEQ ID n°2106	Prot n°PL-2889.1	Contig41	711031	712125	42%	
SEQ ID n°2107	Prot n°PL-289.1	Contig41	490774	491877	36%	

TABLEAU I

SEQ ID n°2108	Prot n°PL-2890.1	Contig41	710064	711044	No Hits found	
SEQ ID n°2109	Prot n°PL-2891.2	Contig26	68688	68728		
SEQ ID n°2110	Prot n°PL-2892.1	Contig26	67801	68397	69%	Identities = 104/201 (51%), Positives = 143/201 (70%), Gaps = 4/201 (1%) gb AAF84422.1 (AE004205) GTP cyclolhydrolyase II [Vibrio cholerae] Length = 216
SEQ ID n°2111	Prot n°PL-2893.1	Contig26	66103	67800	42%	Identities = 145/557 (26%), Positives = 241/557 (43%), Gaps = 55/557 (9%) emb CAB92258.1 (AL356595) putative repetitive protein [Streptomyces coelicolor A3(2)] Length = 626
SEQ ID n°2112	Prot n°PL-2894.1	Contig26	65082	66113	39%	Identities = 102/246 (41%), Positives = 137/246 (55%), Gaps = 18/246 (7%) emb CAB92261.1 (AL356595) hypothetical protein [Streptomyces coelicolor A3(2)] Length = 266
SEQ ID n°2113	Prot n°PL-2895.1	Contig26	63896	64537	70%	Identities = 122/214 (57%), Positives = 151/214 (70%), Gaps = 3/214 (1%) sp P21364 OMPW_ECOLI OUTER MEMBRANE PROTEIN W PRECURSOR pir S07787 ycd protein precursor - Escherichia coli emb CAA31922.1 (X13583) ORF4 protein (AA 1-212) [Escherichia coli] dbj BAA14788.1 (D80763) Outer membrane protein precursor. [Escherichia coli] gb AAC74338.1 (AE000224) putative outer membrane protein [Escherichia coli] Length = 212
SEQ ID n°2114	Prot n°PL-2896.1	Contig26	62695	63465	64%	Identities = 116/248 (46%), Positives = 176/248 (70%), Gaps = 3/248 (1%) pir B64873 probable membrane protein yciC - Escherichia coli dbj BAA14787.1 (D90763) ORF_ID:0252#13; similar to [SwissProt Accession Number P21365] [Escherichia coli] gb AAC74337.1 (AE000223) orf, hypothetical protein [Escherichia coli] Length = 247 "
SEQ ID n°2115	Prot n°PL-2897.1	Contig26	58915	60672	67%	Identities = 295/565 (52%), Positives = 400/565 (70%), Gaps = 7/565 (1%) gb AAF96017.1 (AE004353) sulfate permease family protein [Vibrio cholerae] Length = 592
SEQ ID n°2116	Prot n°PL-2898.1	Contig26	56913	57593	63%	Identities = 114/253 (45%), Positives = 149/253 (58%), Gaps = 28/253 (11%) sp Q05740 TONB_YEREN TONB PROTEIN pir S30290 tonB protein - Yersinia enterocolitica emb CAA47747.1 (X67332) tonB [Yersinia enterocolitica] prf 1912295A tonB gene [Yersinia enterocolitica] Length = 253
SEQ ID n°2117	Prot n°PL-2899.1	Contig26	54797	56266	84%	Identities = 341/486 (70%), Positives = 413/486 (84%), Gaps = 1/486 (0%) (U24197) cardiolipin synthase [Escherichia coli] Length = 486
SEQ ID n°2118	Prot n°PL-29.1	Contig41	50946	52094	75%	Identities = 254/363 (69%), Positives = 307/363 (83%), Gaps = 2/363 (0%) sp Q48450 YCO4_KLEPN PUTATIVE CAPSULE POLYSACCHARIDE EXPORT PROTEIN PRECURSOR (ORF4) pir B56146 probable polysaccharide export protein precursor - Klebsiella pneumoniae dbj BAA04775.1 (D21242) ORF4 [Klebsiella pneumoniae] Length = 378
SEQ ID n°2119	Prot n°PL-290.1	Contig41	493047	494126	No Hits found	

TABLEAU I

SEQ ID n°2120	Prot n°PL-2900.1	Contig26	53226	54227	91%	<p>Identities = 290/329 (88%), Positives = 311/529 (94%)</p> <p>sp P77737 OPPF_ECOLI OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPPF pir B64872 oligopeptide transport ATP-binding protein oppF-Escherichia coli dbj BAA14779.1 (D90763) Oligopeptide transport ATP-binding protein OppF. [Escherichia coli] gb AAC74329.1 (AE000223) homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system [Escherichia coli] Length = 334</p>
SEQ ID n°2121	Prot n°PL-2901.1	Contig26	52231	53229	87%	<p>Identities = 269/326 (82%), Positives = 293/326 (89%), Gaps = 1/326 (0%)</p> <p>sp P76027 OPPD_ECOLI OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPPD pir A64872 oligopeptide transport ATP-binding protein oppD-Escherichia coli. gb AAC74328.1 (AE000223) homolog of Salmonella ATP-binding protein of oligopeptide ABC transport system [Escherichia coli] Length = 337</p>
SEQ ID n°2122	Prot n°PL-2902.1	Contig26	51313	52221	89%	<p>Identities = 272/302 (90%), Positives = 288/302 (95%)</p> <p>sp P77664 OPPC_ECOLI OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC pir H64871 oligopeptide transport system permease protein oppC-Escherichia coli dbj BAA14777.1 (D90763) Oligopeptide transport system permease protein OppC. [Escherichia coli] gb AAC74327.1 (AE000223) homolog of Salmonella oligopeptide transport permease protein [Escherichia coli] dbj BAA16040.1 (D90852) Oligopeptide transport system permease protein OppC.</p>
SEQ ID n°2123	Prot n°PL-2903.1	Contig26	50378	51298	93%	<p>Identities = 273/306 (89%), Positives = 290/306 (94%)</p> <p>sp P08005 OPPB_SALTY OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPB pir QREBOB oligopeptide transport system permease protein oppB-Salmonella typhimurium emb CAA29040.1 (X05491) Opp B (AA1-306) [Salmonella typhimurium] Length = 306</p>
SEQ ID n°2124	Prot n°PL-2904.1	Contig26	48653	50293	83%	<p>Identities = 403/546 (73%), Positives = 459/546 (83%), Gaps = 4/546 (0%)</p> <p>sp P06202 OPPA_SALTY PERIPLASMIC OLIGOPEPTIDE-BINDING PROTEIN PRECURSOR pir QREBOA oligopeptide-binding protein precursor-Salmonella typhimurium emb CAA29039.1 (X05491) Opp A (AA1-542) [Salmonella typhimurium] emb CAA27785.1 (X04194) precursor polypeptide [Salmonella typhimurium] Length = 542</p>
SEQ ID n°2125	Prot n°PL-2905.1	Contig26	46877	48514	74%	<p>Identities = 324/529 (61%), Positives = 409/529 (77%)</p> <p>sp P06202 OPPA_SALTY PERIPLASMIC OLIGOPEPTIDE-BINDING PROTEIN PRECURSOR pir QREBOA oligopeptide-binding protein precursor-Salmonella typhimurium emb CAA29039.1 (X05491) Opp A (AA1-542) [Salmonella typhimurium] emb CAA27785.1 (X04194) precursor polypeptide [Salmonella typhimurium] Length = 542</p>

TABLEAU I

SEQ ID n°2126	Prot n°PL-2906.1	Contig26	45678	46322	80%	<p>Identities = 159/208 (76%), Positives = 176/208 (84%)</p> <p>sp P25743 YCHE_ECOLI_HYPOTHETICAL_23.5_KD_PROTEIN_IN_ADHE-OPPA_INTERGENIC_REGION pir E64871 probable membrane protein yche - Escherichia coli gb AAC74324.1 (AE000222) putative channel protein [Escherichia coli] emb CAA42090.1 (X59501) hypothetical 23.5 kDa protein in adhE-opaA intergenic region [Escherichia coli] Length = 215</p>
SEQ ID n°2127	Prot n°PL-2907.1	Contig26	42633	45266	92%	<p>Identities = 767/877 (87%), Positives = 823/877 (93%)</p> <p>sp P17547 ADHE_ECOLI_ALDEHYDE-ALCOHOL_DEHYDROGENASE [INCLUDES: ALCOHOL DEHYDROGENASE (ADH); ACETALDEHYDE DEHYDROGENASE [ACETYLATING] (ACDH); PYRUVATE-FORMATE-LYASE DEACTIVASE (PFL DEACTIVASE)] pir DEEC acetaldehyde dehydrogenase (acetylating) (EC 1.2.1.10) / alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli emb CAA41855.1 (X59263) alcohol dehydrogenase [Escherichia coli] gb AAA23420.1 (M33504) alcohol dehydrogenase (adhE) [Escherichia coli] db BAA36121.1 (D90759) Alcohol dehydrogenase (EC 1.1.1.1) [Escherichia coli] gb AAC74323.1 (AE000222) CoA-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase; pyruvate-formate-lyase deactivase [Escherichia coli] db BAA16034.1 (D90852) alcohol dehydrogenase (EC 1.1.1.1) [Escherichia coli] db BAA77747.1 (AB008676) alcohol dehydrogenase [Escherichia coli] db BAA77748.1 (AB008676) thymidine kinase [Escherichia coli] Length = 205</p>
SEQ ID n°2128	Prot n°PL-2908.1	Contig26	41782	42390	77%	<p>Identities = 136/190 (71%), Positives = 159/190 (83%) db BAA77748.1 (AB008676) thymidine kinase [Escherichia coli] Length = 205</p>
SEQ ID n°2129	Prot n°PL-2909.1	Contig26	39411	40436	79%	<p>Identities = 239/333 (71%), Positives = 275/333 (81%), Gaps = 1/333 (0%) gb AAD50494.1 (AF172324)_12 (AF172324) WbNF [Escherichia coli] Length = 334</p>
SEQ ID n°2130	Prot n°PL-291.1	Contig41	404157	495272	58%	<p>Identities = 127/336 (37%), Positives = 219/336 (64%), Gaps = 3/336 (0%)</p> <p>sp P37635 YAAN_BACSU_HYPOTHETICAL_43.8_KD_PROTEIN_IN_XPAC-ABRB_INTERGENIC_REGION pir S66056 yaan protein - Bacillus subtilis db BAA05262.1 (D26165) unknown [Bacillus subtilis] emb CAB11802.1 (Z99104) similar to toxic cation resistance [Bacillus subtilis] Length = 127/336 (37%)</p>
SEQ ID n°2131	Prot n°PL-2910.1	Contig26	38071	39414	76%	<p>Identities = 288/442 (65%), Positives = 350/442 (79%)</p> <p>gb AAC06947.1 (AE004776)_10 (AE004776) probable nucleotide sugar dehydrogenase [Pseudomonas aeruginosa] Length = 464</p>

TABLEAU I

SEQ ID n°2132	Prot n°PL-2911.1	Contig26	36989	38047	72%	<p>Identities = 229/289 (79%), Positives = 258/289 (89%), Gaps = 2/289 (0%) sp P25520 GALU_ECOLI_UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHATE URIDYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE) pir JC2285 UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) galu - Escherichia coli emb CAA42564.1 (X58940) ORF 1 [Escherichia coli] gb AA20118.1 (M88830) glucosylphosphate uridylyltransferase [Escherichia coli] gb AAD15244.1 (L32811) UDP-glucose pyrophosphorylase [Shigella flexneri] dbj BAA36104.1 (D90758) UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) [Escherichia coli] dbj BAA36116.1 (D90759) UTP-glucose-1- phosphate uridylyltransferase (EC 2.7.7.9) [Escherichia coli] gb AAC74318.1 (AE000222) glucose-1-phosphate uridylyltransferase [Escherichia coli] dbj BAA16030.1 (D90852) UTP-glucose-1- phosphate uridylyltransferase (EC 2.7.7.9) [Escherichia coli]</p>
SEQ ID n°2133	Prot n°PL-2912.1	Contig26	35637	36662	69%	<p>Identities = 168/337 (49%), Positives = 239/337 (70%), Gaps = 1/337 (0%) sp P37055 HNR_ECOLI_HNR_PROTEIN pir JA36871 37K regulator response protein homolog - Escherichia coli emb CAA48802.1 (X66003) hnr [Escherichia coli] dbj BAA36103.1 (D90758) 37k regulator response protein homolog [Escherichia coli] dbj BAA36115.1 (D90759) 37k regulator response protein homolog [Escherichia coli] gb AAC74317.1 (AE000222) Hnr protein [Escherichia coli] dbj BAA16029.1 (D90852) 37K regulator response protein homolog [Escherichia coli] Length = 337</p>
SEQ ID n°2134	Prot n°PL-2913.1	Contig26	34105	34953	86%	<p>Identities = 235/277 (84%), Positives = 255/277 (91%) sp P37051 IPURU_ECOLI_FORMYL-TETRAHYDROFOLATE DEFORMYLASE (FORMYL-FH(4) HYDROLASE) pir JC36871 formyltetrahydrofolate deformylase (EC 3.5.1.10) - Escherichia coli gb AAC36846.1 (L20251) formyltetrahydrofolate hydrolase [Escherichia coli] dbj BAA36100.1 (D90758) Formyltetrahydrofolate deformylase (EC 3.5.1.10) (formyl-fh(4) hydrolase), [Escherichia coli] dbj BAA36112.1 (D90759) Formyltetrahydrofolate deformylase (EC 3.5.1.10) (formyl-fh(4) hydrolase), [Escherichia coli] gb AAC74314.1 (AE000221) formyltetrahydrofolate deformylase; for purT-dependent FGAR synthesis [Escherichia coli] dbj BAA16026.1 (D90852) FORMYL-TETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)</p>
SEQ ID n°2135	Prot n°PL-2914.1	Contig26	31269	32174	72%	<p>Identities = 169/294 (57%), Positives = 224/294 (75%), Gaps = 1/294 (0%) sp Q46888 YGBJ_ECOLI_HYPOTHETICAL_30.8_KD_PROTEIN_IN_PPHB- RPOS_INTERGENIC_REGION pir JD65054 hypothetical protein b2736 - Escherichia coli (strain K-12) gb AAA69246.1 (U29579) ORF_o302 [Escherichia coli] gb AAC75778.1 (AE000357) putative dehydrogenase [Escherichia coli] Length = 302</p>

TABLEAU I

SEQ ID n°2136	Prot n°PL-2915.1	Contig26	29992	31269	65%	<p>Identities = 211/419 (50%), Positives = 255/419 (67%), Gaps = 8/419 (1%) sp P44083 YGBK_HAEIN HYPOTHETICAL PROTEIN HI1011 pir C64018 hypothetical protein HI1011 - Haemophilus influenzae (strain Rd KW20) gb AAC22872.1 (U32782) conserved hypothetical protein [Haemophilus influenzae Rd] Length = 413</p>
SEQ ID n°2137	Prot n°PL-2916.1	Contig26	29358	30017	61%	<p>Identities = 112/205 (54%), Positives = 143/205 (69%) sp Q46890 YGBL_ECOLI HYPOTHETICAL 23.2 KDA PROTEIN IN PPHB- RPOS INTERGENIC REGION pir F65054 L-fucose-phosphate aldolase (EC 4.1.2.17) - Escherichia coli (strain K-12) gb AA69248.1 (U29579) ORF_0212 [Escherichia coli] gb AAC75780.1 (AE000357) putative epimerase/aldolase [Escherichia coli] gb AAG14969.1 AF242208_2 (AF242208) putative enzyme [Escherichia coli] gb AAG14982.1 AF242210_1 (AF242210) putative enzyme [Escherichia coli] Length = 212</p>
SEQ ID n°2138	Prot n°PL-2917.1	Contig26	28560	29339	66%	<p>Identities = 133/253 (52%), Positives = 176/253 (68%) gb AAG14970.1 AF242208_3 (AF242208) unknown [Escherichia coli] Length = 258</p>
SEQ ID n°2139	Prot n°PL-2918.1	Contig26	27780	28547	66%	<p>Identities = 123/253 (48%), Positives = 174/253 (68%), Gaps = 1/253 (0%) sp P44978 YGBL_HAEIN HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI1009 gb AAC22670.1 (U32781) glycerol-3-phosphate regulon repressor (gpR) [Haemophilus influenzae Rd] Length = 256</p>
SEQ ID n°2140	Prot n°PL-2919.1	Contig26	26642	27607	71%	<p>Identities = 185/312 (59%), Positives = 235/312 (75%), Gaps = 1/312 (0%) sp P44094 YA14_HAEIN HYPOTHETICAL PROTEIN HI1014 pir D64018 hypothetical protein HI1014 - Haemophilus influenzae (strain Rd KW20) gb AAC22675.1 (U32782) conserved hypothetical protein [Haemophilus influenzae Rd] Length = 315</p>
SEQ ID n°2141	Prot n°PL-292.1	Contig41	486292	497797	53%	<p>Identities = 201/511 (39%), Positives = 273/511 (53%), Gaps = 38/511 (7%) db BAA84886.1 (AB024946) orf51 [Escherichia coli] Length = 523</p>
SEQ ID n°2142	Prot n°PL-2920.1	Contig26	25254	26639	80%	<p>Identities = 321/456 (70%), Positives = 380/456 (82%), Gaps = 4/456 (0%) sp P71384 YA15_HAEIN HYPOTHETICAL PERMEASE HI1015 pir D64108 gluconate transport protein homolog - Haemophilus influenzae (strain Rd KW20) gb AAC22676.1 (U32782) gluconate permease (gntP) [Haemophilus influenzae Rd] Length = 488</p>
SEQ ID n°2143	Prot n°PL-2921.1	Contig26	23936	25099	No Hits found	
SEQ ID n°2144	Prot n°PL-2922.1	Contig26	22571	23515	No Hits found	
SEQ ID n°2145	Prot n°PL-2923.1	Contig26	21525	22445	25%	<p>Identities = 45/180 (25%), Positives = 77/180 (42%), Gaps = 35/180 (19%) emb CAB77354.1 (AL160331) hypothetical protein SCD8A.33c (fragment) [Streptomyces coelicolor A3(2)] Length = 224</p>
SEQ ID n°2146	Prot n°PL-2924.1	Contig26	19431	21524	23%	<p>Identities = 116/275 (42%), Positives = 166/275 (60%), Gaps = 3/275 (1%) emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)] Length = 690</p>
SEQ ID n°2147	Prot n°PL-2925.1	Contig26	17439	19430	No Hits found	

TABLEAU I

SEQ ID n°2148	Prot n°PL-2926.1	Contig26	16232	17512	20%	Identities = 46/196 (23%), Positives = 86/196 (43%), Gaps = 28/196 (14%) pir JQ1866 hypothetical 87.1K protein - bovine adenovirus 3 Length =
SEQ ID n°2149	Prot n°PL-2927.1	Contig26	13210	16128	No Hits found	
SEQ ID n°2150	Prot n°PL-2928.1	Contig26	10473	13232	No Hits found	
SEQ ID n°2151	Prot n°PL-2929.1	Contig26	7937	9577	13%	Identities = 40/169 (23%), Positives = 74/169 (43%), Gaps = 18/169 (10%) gb AAE95932.1 (AE004345) ygrG protein [Vibrio cholerae] Length = Identities = 976/1043 (93%), Positives = 1016/1043 (96%) gb AAC38630.1 (AF047028) insecticidal toxin complex protein TccC [Photobacterium luminescens] Length = 1043
SEQ ID n°2152	Prot n°PL-293.1	Contig41	498816	501947	96%	Identities = 81/276 (29%), Positives = 136/276 (48%), Gaps = 12/276 (4%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°2153	Prot n°PL-2931.1	Contig26	5417	6661	32%	Identities = 74/183 (40%), Positives = 109/183 (59%), Gaps = 1/183 (0%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°2154	Prot n°PL-2932.1	Contig26	4010	5416	21%	Identities = 86/237 (36%), Positives = 126/237 (52%), Gaps = 13/237 (5%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°2155	Prot n°PL-2933.1	Contig26	2865	3998	33%	Identities = 86/237 (36%), Positives = 126/237 (52%), Gaps = 13/237 (5%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534
SEQ ID n°2156	Prot n°PL-2934.1	Contig26	1075	1677	No Hits found	
SEQ ID n°2157	Prot n°PL-2935.1	Contig35	83790	85148	81%	Identities = 322/457 (70%), Positives = 371/457 (80%) dbj BAA16470.1 (D90886) CDP-DIACYLGLYCEROL--SERINE O- PHOSPHATIDYLTRANSFERASE (EC 2.7.8.8) (PHOSPHATIDYL SERINE SYNTHASE), [Escherichia coli] dbj BAA16473.1 (D90887) CDP-DIACYLGLYCEROL--SERINE O- PHOSPHATIDYLTRANSFERASE (EC 2.7.8.8) (PHOSPHATIDYL SERINE SYNTHASE), [Escherichia coli] Length =
SEQ ID n°2158	Prot n°PL-2936.1	Contig35	80984	83629	82%	Identities = 632/880 (71%), Positives = 744/880 (83%) sp P76594 YFIQ_EC01 HYPOTHETICAL 98.0 KD PROTEIN IN UNG-PSSA INTERGENIC REGION pir G65036 hypothetical protein b2584 - Escherichia coli (strain K-12) gb AAC75637.1 (AE000344) orf, hypothetical protein [Escherichia coli] Length = 886
SEQ ID n°2159	Prot n°PL-2937.1	Contig35	79648	80684	73%	Identities = 219/346 (63%), Positives = 262/346 (75%), Gaps = 9/346 (2%) sp P33635 YFIF_EC01 HYPOTHETICAL TRNA/RNA METHYLTRANSFERASE YFIF pir D65036 hypothetical 37.8 kD protein in ung 3' region - Escherichia coli (strain K-12) gb AAC75634.1 (AE000344) orf, hypothetical protein [Escherichia coli] Length = 345

Unknown, similar to
insecticidal toxins

TABLEAU I

SEQ ID n°2160	Prot n°PL-2938.1	Contig35	78057	79598	87%	<p>Identities = 382/506 (75%), Positives = 457/506 (89%)</p> <p>sp P27304 EMRB_ECOLI MULTIDRUG RESISTANCE PROTEIN B pir G85048 multidrug resistance protein B - Escherichia coli gb AAC75733.1 (AE000353) multidrug resistance; probably membrane translocase [Escherichia coli] db JBA16548.1 (D90891) multidrug resistant protein emrB [Escherichia coli] db JBA16553.1 (D90892) multidrug resistant protein emrB [Escherichia coli] Length = 512</p>	
SEQ ID n°2161	Prot n°PL-2939.1	Contig35	76858	78042	75%	<p>Identities = 244/386 (63%), Positives = 305/386 (78%), Gaps = 1/386 (0%)</p> <p>sp P27303 EMRA_ECOLI MULTIDRUG RESISTANCE PROTEIN A pir F85048 multidrug resistance protein A - Escherichia coli gb AAC75732.1 (AE000353) multidrug resistance secretion protein [Escherichia coli] db JBA16547.1 (D90891) multidrug resistant protein emrA [Escherichia coli] db JBA16552.1 (D90892) multidrug resistant protein emrA [Escherichia coli] Identities = 1485/1565 (94%), Positives = 1513/1565 (95%), Gaps = 3/1565 (0%) gb AAC38629.1 (AF047028) insecticidal toxin complex protein TccB [Photobacterium luminescens] Length = 1565</p>	Unknown, similar to insecticidal toxins
SEQ ID n°2162	Prot n°PL-294.1	Contig41	502081	508775	98%	<p>Identities = 157/223 (70%), Positives = 189/223 (84%)</p> <p>sp P76630 YGZ_ECOLI HYPOTHETICAL 26.1 KD PROTEIN IN PROX- MPRA INTERGENIC REGION pir JG85048 hypothetical protein b2882 - Escherichia coli (strain K-12) gb AAC75728.1 (AE000353) orf, hypothetical protein [Escherichia coli] Length = 245</p>	
SEQ ID n°2163	Prot n°PL-2940.1	Contig35	74850	75632	72%	<p>Identities = 193/297 (64%), Positives = 239/297 (79%) pir JG85048 hypothetical protein b2681 - Escherichia coli (strain K-12) gb AAC75728.1 (AE000352) putative transport protein [Escherichia coli] Length = 305</p>	
SEQ ID n°2164	Prot n°PL-2941.1	Contig35	73558	74748	57%	<p>Identities = 235/328 (71%), Positives = 277/328 (83%)</p> <p>sp P14177 PROX_ECOLI GLYCINE BETAIN-BINDING PERIPLASMIC PROTEIN PRECURSOR pir JBLECGP glycine betaine/proline transport system binding protein proX precursor - Escherichia coli gb AAA24429.1 (M24856) proX peptide precursor [Escherichia coli] gb AAC75726.1 (AE000352) high-affinity transport system for glycine betaine and proline [Escherichia coli] db JBA16544.1 (D90891) GLYCINE BETAIN-BINDING PERIPLASMIC PROTEIN PRECURSOR.</p>	
SEQ ID n°2165	Prot n°PL-2942.1	Contig35	72184	73182	77%	<p>Identities = 259/359 (72%), Positives = 303/359 (84%), Gaps = 9/359 (2%)</p> <p>sp P14178 PROW_ECOLI GLYCINE BETAIN-BINDING PROLINE TRANSPORT SYSTEM PERMEASE PROTEIN PROW pir JMMECPW glycine betaine/L- proline transport system permease protein P - Escherichia coli gb AAA24428.1 (M24856) proW peptide [Escherichia coli] gb AAC75725.1 (AE000352) high-affinity transport system for glycine betaine and proline [Escherichia coli] db JBA16543.1 (D90891) glycine betaine/proline transport system protein proW [Escherichia coli] Length = 354</p>	
SEQ ID n°2166	Prot n°PL-2943.1	Contig35	71029	72114	82%		

TABLEAU I

SEQ ID n°2167	Prot n°PL-2944.1	Contig35	69837	71036	84%	<p>sp P14175 PROV_ECOLI GLYCINE BETAINEL-PROLINE TRANSPORT ATP-BINDING PROTEIN PROV pir BVECPV glycine betaine/L-proline transport ATP-binding protein prov - Escherichia coli gb AAA24427.1 (M24856) proV peptide [Escherichia coli] gb AAC75724.1 (AE00352) ATP-binding component of transport system for glycine, betaine and proline [Escherichia coli] db BAA16542.1 (D90891) GLYCINE BETAINEL-PROLINE TRANSPORT ATP-BINDING PROTEIN PROV. [Escherichia coli]</p> <p>Identities = 291/398 (73%), Positives = 344/398 (86%)</p>
SEQ ID n°2168	Prot n°PL-2945.1	Contig35	68280	69239	84%	<p>sp P17424 IR4_SALTY RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 2 BETA CHAIN (RIBONUCLEOTIDE REDUCTASE 2) (R2F PROTEIN) pir S34272 ribonucleoside-diphosphate reductase (EC 1.17.4.1) - Salmonella typhimurium pdb 2R2FJA Chain A, Ribonucleotide Reductase R2f Protein From Salmonella Typhimurium (Oxidized) pdb 2R2FIB Chain B, Ribonucleotide Reductase R2f Protein From Salmonella Typhimurium (Oxidized) pdb 1R2FJA Chain A, Ribonucleotide Reductase R2f Protein From Salmonella Typhimurium (Oxidized) R2f Protein From Salmonella Typhimurium em CAA51895.1 (X73226) ribonucleoside-diphosphate reductase [Salmonella typhimurium] Length = 319</p> <p>Identities = 542/702 (77%), Positives = 616/702 (87%) gb AA64444.1 (L34407) ribonucleotide reductase R1 subunit [Mycobacterium tuberculosis] Length = 723</p>
SEQ ID n°2169	Prot n°PL-2946.1	Contig35	66130	68259	85%	<p>Identities = 298/321 (92%), Positives = 309/321 (96%) sp P25845 LIPA_ECOLI LIPIC ACID SYNTHETASE (LIP-SYN) (LIPOATE SYNTHASE) pir B64797 lipic acid synthase (EC 2.8.1.-) - Escherichia coli db BAA35271.1 (D90703) Lipic acid synthetase (lip-syn) [Escherichia coli] gb AAB40828.1 (U82598) lipic acid synthetase [Escherichia coli] gb AAC73729.1 (AE000167) lipote synthesis, sulfur insertion? [Escherichia coli] Length = 321</p> <p>Identities = 133/206 (64%), Positives = 168/206 (80%), Gaps = 1/206 (0%) gb AAF94106.1 (AE004177) lipote-protein ligase B [Vibrio cholerae] Length = 219</p>
SEQ ID n°2170	Prot n°PL-2947.1	Contig35	62690	63655	87%	
SEQ ID n°2171	Prot n°PL-2948.1	Contig35	61938	62579	72%	
SEQ ID n°2172	Prot n°PL-2949.2	Contig35	60233	61402		
SEQ ID n°2173	Prot n°PL-295.1	Contig41	506870	509770	93%	<p>Identities = 900/966 (93%), Positives = 923/966 (95%), Gaps = 1/966 (0%) gb AAC38628.1 (AF047028) insecticidal toxin complex protein TccA [Photobacterium luminescens] Length = 965</p>
SEQ ID n°2174	Prot n°PL-2950.2	Contig35	59030	60028		Unknown, similar to insecticidal toxins

TABLEAU I

SEQ ID n°2175	Prot n°PL-2951.1	Contig35	57904	59016	90%	<p>Identities = 301/370 (81%), Positives = 338/370 (91%)</p> <p>spiP15035[RODA_EC01 ROD SHAPE-DETERMINING PROTEIN RODA pir JBVECRD rod shape-determining protein mrdB - Escherichia coli gb AAA24571.1 (M22857) rod-shape-determining protein [Escherichia coli] dbj BAA35277.1 (D90703) Rod shape-determining protein MrdB. [Escherichia coli] gb AAB40834.1 (U82598) rod-shape-determining protein [Escherichia coli] gb AAC73735.1 (AE000168) rod shape-determining membrane protein; sensitivity to radiation and drugs [Escherichia coli] dbj BAA35281.1 (D90704) Rod shape-determining protein MrdB. [Escherichia coli]</p>	
SEQ ID n°2176	Prot n°PL-2952.1	Contig35	56000	57895	84%	<p>Identities = 479/625 (76%), Positives = 542/625 (86%), Gaps = 3/625 (0%)</p> <p>spiP08150 PBP2_EC01 PENICILLIN-BINDING PROTEIN 2 (PBP-2) pir ZPECP2 penicillin-binding protein 2 - Escherichia coli emb CAA28201.1 (X04516) penicillin-binding protein 2 (PBP2) [Escherichia coli] dbj BAA35282.1 (D90704) Penicillin-binding protein 2 (pbp-2) [Escherichia coli] gb AAB40835.1 (U82598) penicillin-binding protein 2 [Escherichia coli] gb AAC73736.1 (AE000168) cell elongation, e phase; peptidoglycan synthetase; penicillin-binding protein 2 [Escherichia coli] Length =</p>	
SEQ ID n°2177	Prot n°PL-2953.1	Contig35	54333	55061	63%	<p>Identities = 120/210 (57%), Positives = 155/210 (73%)</p> <p>spiP52085 YBEN_EC01 PROTEIN YBEN pir E64798 hypothetical protein b0639 - Escherichia coli gb AAA64852.1 (U23163) OrfUU [Escherichia coli] gb AAB40840.1 (U82598) orfUU; hypothetical protein [Escherichia coli] gb AAC73740.1 (AE000168) orf, hypothetical protein [Escherichia coli] dbj BAA35286.1 (D90704) Hypothetical 24.5 kd protein in phbB-holA intergenic region (orfUU). [Escherichia coli] Length = 213 "</p>	
SEQ ID n°2178	Prot n°PL-2954.1	Contig35	53360	54400	72%	<p>Identities = 222/342 (64%), Positives = 275/342 (79%)</p> <p>spiP28630 HOLA_EC01 DNA POLYMERASE III, DELTA SUBUNIT pir A46251 DNA-directed DNA polymerase (EC 2.7.7.7) III delta chain - Escherichia coli gb AA23675.1 (L04576) DNA polymerase III delta subunit [Escherichia coli] gb AAB59047.1 (M94267) DNA polymerase III delta subunit [Escherichia coli] dbj BAA35287.1 (D90704) DNA-directed DNA polymerase (EC 2.7.7.7) III delta chain [Escherichia coli] gb AAB40841.1 (U82598) DNA-directed DNA polymerase III delta chain [Escherichia coli] gb AAC73741.1 (AE000168) DNA polymerase III, delta subunit Identities = 683/863 (79%), Positives = 769/863 (88%) gb AAB40843.1 (U82598) leucine tRNA synthetase [Escherichia coli] Length = 907</p>	
SEQ ID n°2179	Prot n°PL-2955.1	Contig35	50219	52801	88%		

TABLEAU I

SEQ ID n°2180	Prot n°PL-2956.1	Contig35	49328	50056	90%	<p>sp P41076 GLTL_ECOLI GLUTAMATE/ASPARTATE TRANSPORT ATP-BINDING-PROTEIN GLT.L. pir B64800 glutamate/aspartate transport protein gltL - Escherichia coli gb AA60982.1 (U10981) GlT [Escherichia coli] dbj BAA35304.1 (D90705) Glutamate/aspartate transport atp-binding protein gltL - Escherichia coli gb AAB40853.1 (U82598) glutamate/aspartate transport ATP-binding protein [Escherichia coli] gb AAC73753.1 (AE000169) ATP-binding protein of glutamate/aspartate transport system [Escherichia coli] Length = 241</p>
SEQ ID n°2181	Prot n°PL-2957.1	Contig35	48657	49331	91%	<p>sp P41075 GLTK_ECOLI GLUTAMATE/ASPARTATE TRANSPORT SYSTEM PERMEASE PROTEIN GLT.K. pir C64800 glutamate/aspartate transport protein gltK - Escherichia coli gb AAA60981.1 (U10981) GlTK [Escherichia coli] dbj BAA35305.1 (D90705) Glutamate/aspartate transport system permease protein gltK [Escherichia coli] gb AAB40854.1 (U82598) glutamate/aspartate transport system permease protein [Escherichia coli] gb AAC73754.1 (AE000169) glutamate/aspartate transport system permease [Escherichia coli] Length = 224</p>
SEQ ID n°2182	Prot n°PL-2958.1	Contig35	47916	48656	79%	<p>sp P41074 GLTJ_ECOLI GLUTAMATE/ASPARTATE TRANSPORT SYSTEM PERMEASE PROTEIN GLT.J. pir D64800 glutamate/aspartate transport protein gltJ - Escherichia coli gb AAA60980.1 (U10981) GlTJ [Escherichia coli] dbj BAA35306.1 (D90705) Glutamate/aspartate transport system permease protein gltJ [Escherichia coli] gb AAB40855.1 (U82598) glutamate/aspartate transport system permease protein [Escherichia coli] gb AAC73755.1 (AE000169) glutamate/aspartate transport system permease [Escherichia coli] Length = 246</p>
SEQ ID n°2183	Prot n°PL-2959.1	Contig35	46890	47783	75%	<p>Identities = 228/323 (70%), Positives = 269/323 (82%), Gaps = 14/323 (4%) dbj BAA35307.1 (D90705) Hypothetical protein in gltJ 5'region. [Escherichia coli] Length = 327</p>
SEQ ID n°2184	Prot n°PL-296.1	Contig41	514086	515747	27%	<p>Identities = 104/287 (36%), Positives = 152/287 (52%), Gaps = 22/287 (7%) pir A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77986) Killer protein of pyocin S3 [Pseudomonas aeruginosa] Length = 766</p>
SEQ ID n°2185	Prot n°PL-2960.1	Contig35	44798	46327	77%	<p>Identities = 332/506 (65%), Positives = 395/506 (77%), Gaps = 1/506 (0%) gb AAD08824.1 (AF116773) apolipoprotein N-acyltransferase [Salmonella typhimurium] Length = 512</p>

TABLEAU I

SEQ ID n°2186	Prot n°PL-2961.1	Contig35	43909	44790	91%	<p>Identities = 250/292 (85%), Positives = 272/292 (92%)</p> <p>sp P77392 YBEX_ECOLI HYPOTHETICAL 33.3 KDA PROTEIN IN CUTE-ASNB INTERGENIC REGION pir H64800 ybeX protein - Escherichia coli gb AAB40860.1 (U82598) similar to H. influenzae [Escherichia coli] gb AAC73759.1 (AE000170) putative transport protein [Escherichia coli] identities = 285/342 (83%), Positives = 319/342 (92%) emb CAB62264.1 (AJ249116) YbeZ protein [Salmonella typhimurium] length = 361 identities = 408/472 (86%), Positives = 441/472 (92%) emb CAB62263.1 (AJ249116) MiaB protein [Salmonella typhimurium] length = 474 </p>
SEQ ID n°2187	Prot n°PL-2962.1	Contig35	42320	43372	90%	
SEQ ID n°2188	Prot n°PL-2963.1	Contig35	40865	42307	91%	
SEQ ID n°2189	Prot n°PL-2964.1	Contig35	39497	40678	63%	<p>Identities = 244/390 (62%), Positives = 285/390 (72%)</p> <p>sp P75728 YLEB_ECOLI HYPOTHETICAL 43.0 KDA PROTEIN IN CUTE-GLNX INTERGENIC REGION pir D64801 probable monooxygenase (EC 1.14.13.-) yleB - Escherichia coli (strain K-12) gb AAC73763.1 (AE000170) orf, hypothetical protein [Escherichia coli] db BAA35316.1 (D90706) VisC protein [Escherichia coli] length = 391 identities = 299/400 (74%), Positives = 348/400 (86%)</p>
SEQ ID n°2190	Prot n°PL-2965.1	Contig35	37274	38500	85%	<p>sp P15301 NAGC_ECOLI N-ACETYLGLUCOSAMINE REPRESSOR pir C64802 N-acetylglucosamine repressor - Escherichia coli db BAA35319.1 (D90706) N-acetylglucosamine repressor. [Escherichia coli] db BAA35324.1 (D90707) N-acetylglucosamine repressor. [Escherichia coli] gb AAC73770.1 (AE000171) transcriptional repressor of nag (N-acetylglucosamine) operon [Escherichia coli] gb AAC09326.1 (AF052007) N-acetylglucosamine repressor [Escherichia coli] length =</p>
SEQ ID n°2191	Prot n°PL-2966.2	Contig35	36101	37261		
SEQ ID n°2192	Prot n°PL-2967.2	Contig35	35204	36016		
SEQ ID n°2193	Prot n°PL-2968.1	Contig35	33412	34926	67%	<p>Identities = 275/510 (53%), Positives = 355/510 (68%), Gaps = 19/510 (3%)</p> <p>gb AAF94156.1 (AE004181) PTS system, N-acetylglucosamine-specific IIABC component [Vibrio cholerae] length = 523 </p>
SEQ ID n°2194	Prot n°PL-2969.1	Contig35	30694	32361	87%	<p>Identities = 468/554 (84%), Positives = 514/554 (92%) sp P00962 SYQ_ECOLI GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE-TRNA LIGASE) (GLNRS) pir SYECQT glutamine-tRNA ligase (EC 6.1.1.18) - Escherichia coli emb CAA24894.1 (V01575) glutamyl-tRNA synthetase precursor [Escherichia coli] gb AAC73774.1 (AE000171) glutamine tRNA synthetase [Escherichia coli] db BAA35328.1 (D90707) Glutamyl-tRNA synthetase (EC 6.1.1.18) [glutamine-tRNA ligase] [GlnRS]. [Escherichia coli] </p>
SEQ ID n°2195	Prot n°PL-297.1	Contig41	518080	516719	No Hits found	
SEQ ID n°2196	Prot n°PL-2970.1	Contig35	29631	30524	68%	<p>Identities = 156/289 (53%), Positives = 208/289 (70%)</p> <p>gb AAG06704.1 AE004657_11 (AE004657) probable transcriptional regulator [Pseudomonas aeruginosa] length = 297 </p>
SEQ ID n°2197	Prot n°PL-2971.2	Contig35	28417	29181		
SEQ ID n°2198	Prot n°PL-2972.1	Contig36	459332	459934	No Hits found	

TABLEAU I

SEQ ID n°2198	Prot n°PL-2973.1	Contig36	457126	457911	No Hits found		
SEQ ID n°2200	Prot n°PL-2974.1	Contig36	454868	455518	No Hits found		
SEQ ID n°2201	Prot n°PL-2975.1	Contig36	451749	452615	32%	Identities = 53/225 (23%), Positives = 95/225 (41%), Gaps = 28/225 (12%) emb CAA10420.1 (AJ131559) rlsA protein [Erwinia amylovora] Length = 266	
SEQ ID n°2202	Prot n°PL-2976.1	Contig36	450443	451249	88%	Identities = 209/268 (78%), Positives = 239/268 (89%) sp P09030 EX3_ECOLI EXODEOXYRIBONUCLEASE III (EXONUCLEASE III) (EXO III) (AP ENDONUCLEASE VI) pir NCECX3 exodeoxyribonuclease III (EC 3.1.11.2) - Escherichia coli pdb 1AKO Exonuclease III From Escherichia Coli emb CAA31424.1 (X13002) exonuclease III [Escherichia coli] dbj BAA15540.1 (D90818) Exodeoxyribonuclease III (EC 3.1.11.2) [Escherichia coli] dbj BAA15544.1 (D90819) Exodeoxyribonuclease III (EC 3.1.11.2) [Escherichia coli] gb AAC74819.1 (AE000270) exonuclease III [Escherichia coli] Length = 268	
SEQ ID n°2203	Prot n°PL-2977.1	Contig36	448457	450385	87%	Identities = 508/641 (79%), Positives = 568/641 (88%), Gaps = 3/641 (0%) sp P14294 TOP3_ECOLI DNA TOPOISOMERASE III pir JW0049 DNA topoisomerase (EC 5.99.1.2) II - Escherichia coli gb AAA83923.1 (J05076) topoisomerase III [Escherichia coli] dbj BAA15551.1 (D90819) DNA topoisomerase III (EC 5.99.1.-) [Escherichia coli] dbj BAA15554.1 (D90820) DNA topoisomerase III (EC 5.99.1.-) [Escherichia coli] gb AAC74833.1 (AE000271) DNA topoisomerase III [Escherichia coli] Length = 653	
SEQ ID n°2204	Prot n°PL-2978.1	Contig36	447408	448451	83%	Identities = 261/341 (76%), Positives = 293/341 (85%) sp P16458 SELD_ECOLI SELENIDE WATER DIKINASE (SELENOPHOSPHATE SYNTHETASE) (SELENIUM DONOR PROTEIN) pir JW0033 selenophosphate synthase - Escherichia coli gb AAA74748.1 (M30184) selenium metabolism protein [Escherichia coli] dbj BAA15555.1 (D90820) Selenide,water dikinase (EC 2.7.9.3) (Selenophosphate synthetase) (Selenium donor protein). [Escherichia coli] gb AAC74834.1 (AE000271) selenophosphate synthase, H(2)Se added Identities = 377/621 (60%), Positives = 478/621 (76%), Gaps = 3/621 (0%) pir PRECT4 proteinase IV (EC 3.4.-.-) - Escherichia coli dbj BAA15557.1 (D90820) Proteinase IV (EC 3.4.-.-) [Escherichia coli] gb AAC74836.1 (AE000271) protease IV, a signal peptide peptidase [Escherichia coli] Length = 618	
SEQ ID n°2206	Prot n°PL-298.1	Contig41	516148	517083	19%	Identities = 47/144 (32%), Positives = 61/144 (41%), Gaps = 14/144 (9%) gb AAC44553.1 (U34346) unknown [Paracoccus denitrificans] Length = 173	

TABLEAU I

SEQ ID n°2207	Prot n°PL-2980.1	Contig36	443539	444558	82%	<p>Identities = 256/335 (76%), Positives = 284/335 (84%)</p> <p>sp P18840 ASG1_ECOLI L-ASPARAGINASE I (L-ASPARAGINE AMIDOHYDROLASE I) (L-ASNASE I) pir JXDEC1 asparaginase (EC 3.5.1.1) Escherichia coli dbj BAA15558.1 (D90820) L-asparaginase I (EC 3.5.1.1) (L-asparagine amidohydrolase I) [Escherichia coli] gb AAC74837.1 (AE000271) cytoplasmic L-asparaginase I [Escherichia coli] Length = 335</p> <p>Identities = 118/208 (56%), Positives = 142/208 (68%) pir JQECAS5</p> <p>hypothetical 23.4K protein (ansa 3' region) - Escherichia coli gb AAC74838.1 (AE000271) orf, hypothetical protein [Escherichia coli] Length = 219</p>
SEQ ID n°2208	Prot n°PL-2981.1	Contig36	442888	443526	65%	<p>Identities = 301/331 (90%), Positives = 314/331 (93%)</p> <p>sp P06977 G3P1_ECOLI GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A (GAPDH-A) pir DDECG3 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) A - Escherichia coli emb CAA26498.1 (X02662) put. GAPDH (aa 1-332) [Escherichia coli] dbj BAA15576.1 (D90821) Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) A [Escherichia coli] gb AAC74849.1 (AE000273) glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli] Length = 331</p>
SEQ ID n°2209	Prot n°PL-2982.1	Contig36	440597	441592	81%	<p>Identities = 117/250 (46%), Positives = 158/250 (62%), Gaps = 3/250 (1%)</p> <p>sp P77489 YEAF_ECOLI HYPOTHETICAL 27.8 KD PROTEIN IN GAPA-RND INTERGENIC REGION pir F64938 hypothetical protein b1782 - Escherichia coli (strain K-12) dbj BAA15583.1 (D90822) Outer membrane protein precursor [Escherichia coli] dbj BAA15579.1 (D90821) Outer membrane protein precursor [Escherichia coli] gb AAC74852.1 (AE000273) orf, hypothetical protein [Escherichia coli] Length = 248</p> <p>Identities = 205/356 (57%), Positives = 278/356 (76%), Gaps = 3/356 (0%)</p> <p>gb AAC61705.1 (AF081283) alanine racemase [Escherichia coli] Length = 356</p>
SEQ ID n°2210	Prot n°PL-2983.1	Contig36	439744	440496	62%	
SEQ ID n°2211	Prot n°PL-2984.1	Contig36	438311	439399	75%	<p>Identities = 310/432 (71%), Positives = 352/432 (80%)</p> <p>sp P29011 DADA_ECOLI D-AMINO ACID DEHYDROGENASE SMALL SUBUNIT pir B53383 D-amino-acid dehydrogenase (EC 1.4.99.1) small chain - Escherichia coli gb AAC36880.1 (L02948) D-amino acid dehydrogenase [Escherichia coli] dbj BAA36044.1 (D90753) D-amino acid dehydrogenase small subunit (EC 1.4.99.1) [Escherichia coli] gb AAC74273.1 (AE000217) D-amino acid dehydrogenase subunit</p> <p>Identities = 181/235 (77%), Positives = 205/235 (87%)</p> <p>sp P09371 FADR_ECOLI FATTY ACID METABOLISM REGULATOR PROTEIN pir H64864 DNA-binding protein, fatty acid/fatty acyl-responsive - Escherichia coli emb CAA30881.1 (X08087) fadR [Escherichia coli] dbj BAA36042.1 (D90753) Fatty acid metabolism regulator protein. [Escherichia coli] gb AAC74271.1 (AE000217) negative regulator for fad regulon, and positive activator of fabA [Escherichia coli]</p>
SEQ ID n°2212	Prot n°PL-2985.1	Contig36	438991	438304	78%	
SEQ ID n°2213	Prot n°PL-2986.1	Contig36	435751	436470	82%	

TABLEAU I

SEQ ID n°2214	Prot n°PL-2987.1	Contig36	433981	435528	81%	Identities = 368/513 (71%), Positives = 432/513 (83%), Gaps = 2/513 (0%) sp P27377 NHAB_ECOLI_NA(+)/H(+)-ANTIPORTER 2_pir JC64864_Na+/H+- exchanging protein nhaB - Escherichia coli db BAA38033.1 (D90752) Na+/H+- antiporter protein nhaB [Escherichia coli] db BAA38041.1 (D90753) Na+/H+- antiporter protein nhaB [Escherichia coli] gb AAC74270.1 (AE000217) Na+/H+- antiporter, pH independent [Escherichia coli]
SEQ ID n°2215	Prot n°PL-2988.1	Contig36	429597	430652	No Hits found	Identities = 259/305 (84%), Positives = 283/305 (91%), Gaps = 2/305 (0%) sp P76055 YDAO_ECOLI_HYPOTHETICAL 35.6 KD PROTEIN IN DBPA-INTR INTERGENIC REGION_pir JC64884_ydaO protein - Escherichia coli gb AAC74426.1 (AE000232) orf, hypothetical protein [Escherichia coli] Length = 311
SEQ ID n°2217	Prot n°PL-299.1	Contig41	517068	518342	43%	Identities = 107/438 (24%), Positives = 185/438 (41%), Gaps = 41/438 (9%) db BAA76335.1 (AB011837) ORF12 [Bacillus halodurans] Length =
SEQ ID n°2218	Prot n°PL-2990.1	Contig36	423769	424752	72%	Identities = 185/327 (56%), Positives = 244/327 (74%) pir A64884 probable transport protein b1342 - Escherichia coli gb AAC74424.1 (AE000232) orf, hypothetical protein [Escherichia coli] Length = 327
SEQ ID n°2219	Prot n°PL-2991.1	Contig36	422130	423752	73%	Identities = 379/541 (70%), Positives = 437/541 (80%), Gaps = 3/541 (0%) pir D64882_periplasmic oligopeptide-binding protein precursor - Escherichia coli db BAA14922.1 (D90771) Periplasmic oligopeptide-binding protein precursor. [Escherichia coli] db BAA14932.1 (D90772) Periplasmic oligopeptide-binding protein precursor. [Escherichia coli] gb AAC74411.1 (AE000231) putative transport periplasmic protein [Escherichia coli] Length = 544
SEQ ID n°2220	Prot n°PL-2992.1	Contig36	421453	421956	71%	Identities = 122/167 (73%), Positives = 145/167 (86%) sp P37901 TPX_ECOLI THIOL PEROXIDASE (SCAVENGASE P20) pir JC5504 thioredoxin peroxidase (EC 1.11.1.-) - Escherichia coli gb AAC74408.1 (AE000230) thiol peroxidase [Escherichia coli] gb AAC45284.1 (U93212) scavengase p20 [Escherichia coli] gb AAF28734.1 (AF153317_31 (AF153317) thiol peroxidase [Shigella dysenteriae] Length = 168
SEQ ID n°2221	Prot n°PL-2993.1	Contig36	419832	421415	77%	Identities = 344/521 (66%), Positives = 415/521 (79%), Gaps = 1/521 (0%) sp Q9ZIB7 TYRR_ERWHE_TRANSCRIPTIONAL REGULATORY PROTEIN TYRR gb AAD02000.1 (AF035010) regulatory protein TyrR [Erwinia herbicola] Length = 521

TABLEAU I

SEQ ID n°2222	Prot n°PL-2994.1	Contig36	418511	419575	78%	Identities = 242/345 (70%), Positives = 280/345 (81%), Gaps = 1/345 (0%) sp P45526 YCF_ECOLI_HYPOTHETICAL_39.4_KDA_PROTEIN_IN_PSPE-TYRR_INTERGENIC_REGION_pir E64881_membrane_protein_ycf_Escherichia_coli_dbj BAA14903.1 (D90770) ORF_ID:α260#4; similar to [SwissProt Accession Number P43931] [Escherichia coli] dbj BAA14914.1 (D90771) ORF_ID:α260#4-similar to [SwissProt Accession Number P43931] [Escherichia coli] gb AAC74404.1 (AE000230) orf, hypothetical protein [Escherichia coli] Length = 353 "
SEQ ID n°2223	Prot n°PL-2995.1	Contig36	417117	418514	83%	Identities = 362/465 (77%), Positives = 407/465 (86%) gb AAF28131.1 AF153317_28 (AF153317) YgX [Shigella dysenteriae] Length = 465
SEQ ID n°2224	Prot n°PL-2996.1	Contig36	415768	416442	84%	Identities = 165/222 (74%), Positives = 191/222 (85%) pir C64879 phage shock protein A - Escherichia coli_dbj BAA14873.1 (D90768) Phage shock protein A [Escherichia coli] dbj BAA14881.1 (D90769) Phage shock protein A [Escherichia coli] gb AAC74386.1 (AE000228) phage shock protein, inner membrane protein [Escherichia coli] Length = 222
SEQ ID n°2225	Prot n°PL-2997.1	Contig38	414582	415604	80%	Identities = 236/330 (71%), Positives = 278/330 (83%), Gaps = 6/330 (1%) pir B64879 transcription activator pspF - Escherichia coli_gb AAC74385.1 (AE000228) psp operon transcriptional activator [Escherichia coli] Length = 330
SEQ ID n°2226	Prot n°PL-2998.1	Contig36	412660	414333	81%	Identities = 375/536 (69%), Positives = 453/536 (83%), Gaps = 2/536 (0%) sp Q47622 SAPA_ECOLI_PEPTIDE_TRANSPORT_PERIPLASMIC_PROTEIN_SAPA_PRECURSOR_pir A64878_peptide_transport_periplasmic_protein_sapa_precursor - Escherichia coli_emb CAA65937.1 (X97282) SapA protein [Escherichia coli] gb AAC74376.1 (AE000227) homolog of Salmonella peptide transport periplasmic protein [Escherichia coli] Length =
SEQ ID n°2227	Prot n°PL-2999.1	Contig36	411698	412663	91%	Identities = 245/321 (76%), Positives = 295/321 (91%) sp P36668 SAPB_SALTY_PEPTIDE_TRANSPORT_SYSTEM_PERMEASE_PROTEIN_SAPB_pir S39586_peptide_transport_system_permease_protein_sapB - Salmonella typhimurium_emb CAA52285.1 (X74212) sapB [Salmonella typhimurium] Length = 321
SEQ ID n°2228	Prot n°PL-3.1	Contig41	2252	5632	15%	Identities = 117/387 (28%), Positives = 172/387 (43%), Gaps = 53/387 (13%) dbj BAB05094.1 (AP001511) DNA primase [Bacillus halodurans] = 599
SEQ ID n°2229	Prot n°PL-30.1	Contig41	54817	55806	39%	Identities = 78/244 (31%), Positives = 131/244 (52%), Gaps = 1/244 (0%) sp P11290 YIBD_ECOLI_HYPOTHETICAL_40.5_KDA_PROTEIN_IN_SECB-TDH_INTERGENIC_REGION_pir S47836_hypothetical_protein_f344 - Escherichia coli_pir Q3ECTH_hypothetical_40.5K_protein(secb-tdh 5' region) - Escherichia coli_gb AAB18592.1 (U00039) alternate gene name yibD [Escherichia coli] gb AAC76639.1 (AE000439) putative regulator [Escherichia coli] Length = 344

TABLEAU I

SEQ ID n°2230	Prot n°PL-300.1	Contig41	518369	520786	17%	<p>Identities = 90/354 (25%), Positives = 143/354 (39%), Gaps = 22/354 (6%) pir A42951 fatty-acyl-CoA reductase luxC (EC 1.2.1.-) - Xenorhabdus luminescens gb AAD05355.1 (M90092) fatty acid reductase [Xenorhabdus luminescens] Length = 480</p>
SEQ ID n°2231	Prot n°PL-3000.1	Contig36	410821	411711	82%	<p>Identities = 215/296 (72%), Positives = 250/296 (83%) sp Q47624 SAPC_ECOLI PEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN SAPC pir G64877 peptide transport system permease protein sapC - Escherichia coli emb CAA65939.1 (X97282) SapC protein [Escherichia coli] dbj BAA14845.1 (D90766) Peptide transport system permease protein SapC. [Escherichia coli] dbj BAA14853.1 (D90767) Peptide transport system permease protein SapC. [Escherichia coli] dbj BAA14862.1 (D90768) Peptide transport system permease protein SapC. [Escherichia coli] gb AAC74374.1 (AE000227) homolog of Salmonella peptide transport permease protein [Escherichia coli] Length = Identities = 288/329 (80%), Positives = 294/329 (88%) emb CAA10912.1 (AJ222849) sapD [Erwinia chrysanthemi] Length = 330</p>
SEQ ID n°2232	Prot n°PL-3001.1	Contig36	409829	410821	87%	<p>Identities = 215/267 (80%), Positives = 246/267 (91%) sp P36638 SAPF_SALTY PEPTIDE TRANSPORT SYSTEM ATP-BINDING PROTEIN SAPF pir S39589 peptide transport system ATP-binding protein sapF - Salmonella typhimurium emb CAA52288.1 (X74212) sapF [Salmonella typhimurium] Length = 268</p>
SEQ ID n°2234	Prot n°PL-3003.1	Contig36	408056	408844	88%	<p>Identities = 221/262 (84%), Positives = 244/262 (92%) sp P16657 FABI_SALTY ENOYL-ACYL-CARRIER-PROTEIN] REDUCTASE [NADH] (NADH-DEPENDENT ENOYL-ACP REDUCTASE) pir B43729 enoyl-acyl-carrier-protein] reductase (NADH) (EC 1.3.1.9) - typhimurium gb AAA27059.1 (M31806) envM protein [Salmonella typhimurium] Length = 268</p>
SEQ ID n°2235	Prot n°PL-3004.1	Contig36	408863	407696	32%	<p>Identities = 47/197 (23%), Positives = 99/197 (44%), Gaps = 10/197 (5%) gb AAF98067.1 (AF196348) reticulocyte-binding protein 2 homolog B [Plasmodium falciparum] Length = 1098</p>
SEQ ID n°2236	Prot n°PL-3005.1	Contig36	405764	406369	72%	<p>Identities = 132/202 (65%), Positives = 160/202 (78%) sp P15214 GT_PROMI GLUTATHIONE S-TRANSFERASE GST-6.0 (GST B1-1) pir S29772 glutathione transferase (EC 2.5.1.18) - Proteus mirabilis pir S71882 glutathione transferase (EC 2.5.1.18) B1-1 - Proteus mirabilis pdb 1PMT Glutathione Transferase From Proteus Mirabilis pdb 2PMT A Chain A, Glutathione Transferase From Proteus Mirabilis pdb 2PMT B Chain B, Glutathione Transferase From Proteus Mirabilis pdb 2PMT C Chain C, Glutathione Transferase From Proteus Mirabilis pdb 2PMT D Chain D, Glutathione Transferase From Proteus Mirabilis gb AAC44362.1 (U38482) glutathione transferase [Proteus mirabilis] Length = 203</p>

TABLEAU I

SEQ ID n°2237	Prot n°PL-3006.1	Contig36	404804	405667	84%	Identities = 223/289 (77%), Positives = 246/289 (84%), Gaps = 2/289 (0%) sp Q51892 PDXY_PROMI PYRIDOXAMINE KINASE (PM KINASE) Length = 289
SEQ ID n°2238	Prot n°PL-3007.1	Contig36	403216	404490	89%	Identities = 356/424 (83%), Positives = 393/424 (91%) sp P00951 SYE_ECOLI TYROSYL-TRNA SYNTHETASE (TYROSINE-TRNA LIGASE) (TYRRS) pir S VECTY tyrosine-tRNA ligase (EC 6.1.1.1) - Escherichia coli gb AAA24707.1 (J01719) tyrosyl-tRNA synthetase (tyrS) [Escherichia coli] gb AAC74709.1 (AE000259) tyrosine tRNA synthetase [Escherichia coli] Length = 424
SEQ ID n°2239	Prot n°PL-3008.1	Contig36	402442	403095	82%	Identities = 152/218 (69%), Positives = 186/218 (84%), Gaps = 1/218 (0%) sp P28225 PDXH_ECOLI PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE) pir B43261 pyridoxamine-phosphate oxidase (EC 1.4.3.5) pdxH - Escherichia coli gb AAA24709.1 (M92351) pyridoxamine phosphate oxidase [Escherichia coli] gb AAC74710.1 (AE000259) pyridoxinephosphate oxidase [Escherichia coli] Length = 218
SEQ ID n°2240	Prot n°PL-3009.1	Contig36	401274	402392	80%	Identities = 258/368 (70%), Positives = 300/368 (81%) sp P77570 YDHH_ECOLI HYPOTHETICAL 39.5 KD PROTEIN IN PDXH-SLYB INTERGENIC REGION pir B64921 conserved hypothetical protein b1640 - Escherichia coli db BAA15401.1 (D90807) ORF ID: o316#19, similar to [SwissProt Accession Number P31485] [Escherichia coli] gb AAC74712.1 (AE000259) orf, hypothetical protein [Escherichia coli]
SEQ ID n°2241	Prot n°PL-301.1	Contig41	520776	521948	38%	Identities = 88/353 (24%), Positives = 150/353 (41%), Gaps = 14/353 (3%) pir S26478 rfbN protein - Vibrio cholerae emb CAA42144.1 (X59554) rfbN. [Vibrio cholerae] pir J203284D rfbN gene [Vibrio cholerae] Length =
SEQ ID n°2242	Prot n°PL-3010.2	Contig34	41202	43208	No Hits found	
SEQ ID n°2243	Prot n°PL-3011.1	Contig34	38396	41114	No Hits found	
SEQ ID n°2244	Prot n°PL-3012.1	Contig34	38091	38395	21%	Identities = 57/222 (25%), Positives = 95/222 (42%), Gaps = 33/222 (14%) ref NP_050283.1 fiber protein gb AAC71676.1 (AF021254) fibre homolog [fowl adenovirus 8] gb AAD50350.1 (AF083975) fiber protein [fowl adenovirus 8] Length = 571
SEQ ID n°2245	Prot n°PL-3013.1	Contig34	34952	37903	No Hits found	
SEQ ID n°2246	Prot n°PL-3014.1	Contig34	32269	35004	No Hits found	
SEQ ID n°2247	Prot n°PL-3015.1	Contig34	31102	31830	24%	Identities = 32/105 (30%), Positives = 60/105 (56%), Gaps = 1/105 (0%) emb CAB77339.1 (AL160331) hypothetical protein SCD8A.18c [Streptomyces coelicolor A3(2)] Length = 150
SEQ ID n°2248	Prot n°PL-3016.1	Contig34	29458	31098	31%	Identities = 103/464 (22%), Positives = 174/464 (37%), Gaps = 75/464 (16%) emb CAB77340.1 (AL160331) hypothetical protein SCD8A.19c [Streptomyces coelicolor A3(2)] Length = 643
SEQ ID n°2249	Prot n°PL-3018.1	Contig34	26959	28182	35%	Identities = 82/282 (29%), Positives = 143/282 (50%), Gaps = 15/282 (5%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534

TABLEAU I

SEQ ID n°2250	Prot n°PL-3019.1	Contig34	25558	26949	22%	Identities = 75/189 (39%), Positives = 113/189 (59%), Gaps = 1/189 (0%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534	Unknown, similar to insecticidal toxins
SEQ ID n°2251	Prot n°PL-302.1	Contig41	523619	526516	59%	Identities = 493/693 (71%), Positives = 583/693 (83%), Gaps = 10/693 (1%) gb AAC38630.1 (AF047028) insecticidal toxin complex protein TccC [Photobacterium luminescens] Length = 1043	
SEQ ID n°2252	Prot n°PL-3020.1	Contig34	24410	26546	31%	Identities = 81/207 (39%), Positives = 120/207 (57%), Gaps = 6/207 (2%) emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)] Length = 534	
SEQ ID n°2253	Prot n°PL-3021.1	Contig34	21545	23386	10%	Identities = 41/157 (26%), Positives = 65/157 (41%), Gaps = 9/157 (5%) sp P38078 VATA_CANTR VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A [CONTAINS: VMA1-DERIVED ENDONUCLEASE (VDE) (PI-CTR) ENDONUCLEASE] pir JA46080 H+-transporting ATPase (EC 3.6.1.35) chain A precursor, vacuolar - yeast (Candida tropicalis) gb AAB03895.1 (M64984) ORF [Candida tropicalis] Length = 1088	
SEQ ID n°2254	Prot n°PL-3022.1	Contig34	20295	20909	41%	Identities = 47/184 (25%), Positives = 85/184 (45%), Gaps = 25/184 (13%) dbj BAA31138.1 (AB007463) type IV prepilin [Plasmid Collib-P9] dbj BAA75180.1 (AB021078) typeIV prepilin [Plasmid Collib-P9] gnl PID1038914 typeIV prepilin Length = 204	
SEQ ID n°2255	Prot n°PL-3023.1	Contig34	19343	20137	59%	Identities = 125/255 (49%), Positives = 162/255 (63%), Gaps = 16/255 (6%) sp P31712 LEP4_ERWCA TYPE 4 PREPILIN-LIKE PROTEINS LEADER PEPTIDE PROCESSING ENZYME (PECTIC ENZYMES SECRETION PROTEIN OUTO) [INCLUDES: LEADER PEPTIDASE (PREPILIN PEPTIDASE); N-METHYLTRANSFERASE] pir S32869 secretion protein outo - Erwinia carotovora subsp. carotovora emb CAA49655.1 (X70049) outO [Erwinia carotovora] Length = 279	
SEQ ID n°2256	Prot n°PL-3024.1	Contig34	18128	19315	35%	Identities = 85/387 (21%), Positives = 141/387 (35%), Gaps = 76/387 (19%) gb AAAF81218.1 (AF247502_13 (AF247502) PIV2 [Salmonella dublin] Length = 434	
SEQ ID n°2257	Prot n°PL-3025.1	Contig34	15433	17136	54%	Identities = 192/545 (35%), Positives = 309/545 (56%), Gaps = 33/545 (6%) dbj BAA75185.1 (AB021078) lipoprotein [Plasmid Collib-P9] dbj BAA77974.1 (AB027308) lipoprotein [Plasmid R64] gnl PID1038919 lipoprotein Length = 560	
SEQ ID n°2258	Prot n°PL-3026.1	Contig34	14137	15432	40%	Identities = 102/435 (23%), Positives = 173/435 (39%), Gaps = 59/435 (13%) gb AAAF14815.2 (AF000001) PILO [Salmonella typhi] gb AAAF81211.1 (AF247502_6 (AF247502) PILO [Salmonella dublin] Length = 428	
SEQ ID n°2259	Prot n°PL-3027.1	Contig34	12024	13607	45%	Identities = 156/423 (36%), Positives = 242/423 (56%), Gaps = 21/423 (4%) dbj BAA75182.1 (AB021078) ATP-binding protein [Plasmid Collib-P9] dbj BAA77977.1 (AB027308) nucleotide-binding protein [Plasmid R64] gnl PID1038916 ATP-binding protein Length = 517	

TABLEAU I

SEQ ID n°2260	Prot n°PL-3028.1	Contig34	10920	12017	51%	Identities = 113/348 (32%), Positives = 191/348 (54%), Gaps = 3/348 (0%) pir S70972 bfpE protein - Escherichia coli emb CAA92332.1 (Z88186) BfpE [Escherichia coli] gb AAC44044.1 (U27184) BfpE [Escherichia coli] dbj BAA84844.1 (AB024946) BfpE [Escherichia coli] Length = 352
SEQ ID n°2261	Prot n°PL-3029.1	Contig34	8892	10247	38%	Identities = 111/393 (28%), Positives = 174/393 (44%), Gaps = 45/393 (11%) sp Q01911 TETX_BACFR TETRACYCLINE RESISTANCE PROTEIN (TRANSPONSON TN4351/TN4400) pir A39191 probable oxidoreductase (EC 1.-.-.-) - Bacteroides fragilis gb AA27471.1 (M37699) tetracycline resistance protein [Transposon Tn4351] Length = 388
SEQ ID n°2262	Prot n°PL-303.1	Contig41	526833	527978	20%	Identities = 47/167 (28%), Positives = 78/167 (46%), Gaps = 6/167 (3%) sp P53554 BIOL_BAGSU BIOTIN BIOSYNTHESIS; CYTOCHROME P450-LIKE ENZYME pir G99594 cytochrome P450 biol - Bacillus subtilis gb AAB17462.1 (U51868) cytochrome P450-like enzyme [Bacillus subtilis] gb AAC00266.1 (AF008220) cytochrome P450 enzyme [Bacillus subtilis] emb CAB14997.1 (Z99119) cytochrome P450-like enzyme [Bacillus subtilis]
SEQ ID n°2263	Prot n°PL-3030.1	Contig34	8097	8789	38%	Identities = 53/187 (28%), Positives = 90/187 (47%), Gaps = 1/187 (0%) gb AAG07066.1 (AE004787_6 (AE004787) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 212
SEQ ID n°2264	Prot n°PL-3031.1	Contig34	5677	7323	29%	Identities = 87/394 (22%), Positives = 184/394 (41%), Gaps = 60/394 (16%) gb AAG00942.1 (AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae] Length = 552
SEQ ID n°2265	Prot n°PL-3032.1	Contig34	4275	5660	74%	Identities = 267/495 (53%), Positives = 343/495 (68%), Gaps = 42/495 (8%) sp P22525 YCB_ECOLI HYPOTHETICAL 67.8 KDA PROTEIN IN MUKB-ASPC INTERGENIC REGION pir D84832 ycbB protein precursor - Escherichia coli gb AAC74011.1 (AE000194) putative amidase [Escherichia coli] dbj BAA35671.1 (D90730) Hypothetical protein 63 (MukB 3' region) [Escherichia coli] Length = 615
SEQ ID n°2266	Prot n°PL-3033.1	Contig34	3634	4182	73%	Identities = 126/182 (69%), Positives = 148/182 (81%) sp P75848 YCBK_ECOLI HYPOTHETICAL 20.4 KDA PROTEIN IN MUKB-ASPC INTERGENIC REGION pir E84832 ycbK protein precursor - Escherichia coli gb AAC74012.1 (AE000195) orf, hypothetical protein [Escherichia coli] dbj BAA35672.1 (D90730) Hypothetical protein HI1666 [Escherichia coli] dbj BAA35678.1 (D90731) Hypothetical protein HI1666 [Escherichia coli] Length = 149/215 (69%), Positives = 177/215 (82%)
SEQ ID n°2267	Prot n°PL-3034.1	Contig34	2941	3588	77%	Identities = 149/215 (69%), Positives = 177/215 (82%) sp P75849 YCB_ECOLI HYPOTHETICAL 23.8 KDA PROTEIN IN MUKB-ASPC INTERGENIC REGION pir F84832 probable hydrolase (EC 3.-.-.-) ycbL - Escherichia coli gb AAC74013.1 (AE000195) orf, hypothetical protein [Escherichia coli] dbj BAA35673.1 (D90730) Hypothetical 23.2 kd protein in sodA-comGA intergenic region. [Escherichia coli] dbj BAA35679.1 (D90731) Hypothetical 23.2 kd protein in sodA-comGA intergenic region. [Escherichia coli] Length = 215

TABLEAU I

SEQ ID n°2268	Prot n°PL-3035.1	Contig34	1334	2524	84%	Identities = 316/396 (79%), Positives = 354/396 (88%) pdb1ART] Aspartate Aminotransferase (E.C.2.6.1.1) Complexed With Pyridoxal-5'-Phosphate And 2-Methylaspartate Length = 398
SEQ ID n°2269	Prot n°PL-3036.1	Contig34	1	684	78%	Identities = 155/216 (71%), Positives = 180/216 (82%), Gaps = 1/216 (0%) sp Q56828 OMP_F_XENNE OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF) (OUTER MEMBRANE PROTEIN OMPF) pi J570847 outer membrane porin ompF precursor - Xenorhabdus nematophilus gb AAB41114.1 (L40919) ompF gene product [Xenorhabdus nematophilus] pr J2204378A OmpF-like porin [Xenorhabdus nematophilus] Length = 684
SEQ ID n°2270	Prot n°PL-3037.1	Contig35	6849	7652	45%	Identities = 75/282 (26%), Positives = 123/282 (43%), Gaps = 50/282 (17%) pi J47283 calphostin - fruit fly (Drosophila melanogaster) gb AAA28420.1 (L05080) calphostin [Drosophila melanogaster] Length = 873
SEQ ID n°2271	Prot n°PL-3038.2	Contig35	281	8842		Identities = 188/318 (59%), Positives = 226/318 (70%), Gaps = 18/318 (5%) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558
SEQ ID n°2272	Prot n°PL-3039.1	Contig35	8852	9901	64%	Identities = 52/134 (38%), Positives = 70/134 (51%), Gaps = 12/134 (8%) pi J575566 probable repressor protein - Deinococcus radiodurans (strain R1) gb AAF08645.1 (AE001868_7 (AE001868) repressor protein, putative [Deinococcus radiodurans] Length = 316
SEQ ID n°2273	Prot n°PL-304.1	Contig41	529953	530726	27%	Identities = 493/693 (71%), Positives = 589/693 (84%), Gaps = 1/693 (0%) gb AAF94605.1 (AE004223) RTX toxin transporter [Vibrio cholerae] Length = 720
SEQ ID n°2274	Prot n°PL-3040.1	Contig35	11115	13220	83%	Identities = 303/438 (69%), Positives = 363/438 (82%) gb AAD21060.1 (AF119150) RtxD protein [Vibrio cholerae] gb AAF94604.1 (AE004223) RTX toxin transporter [Vibrio cholerae] Length = 467
SEQ ID n°2275	Prot n°PL-3041.1	Contig35	13195	14568	79%	Identities = 513/698 (73%), Positives = 604/698 (86%), Gaps = 2/698 (0%) gb AAF94603.1 (AE004223) toxin secretion transporter, putative [Vibrio cholerae] Length = 721
SEQ ID n°2276	Prot n°PL-3042.1	Contig35	14550	16721	83%	Identities = 78/286 (27%), Positives = 145/286 (50%), Gaps = 3/286 (1%) gb AAG07824.1 (AE004858_2 (AE004858) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 299
SEQ ID n°2277	Prot n°PL-3043.1	Contig35	16888	17877	43%	Identities = 588/889 (66%), Positives = 709/889 (79%), Gaps = 4/889 (0%) sp Q54468 CHB_SERMA CHITINASE PRECURSOR (N-ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) pi J4732 beta-N-acetylhexosaminidase (EC 3.2.1.52) - Serratia marcescens gb AAB03808.1 (L43594) N-acetyl-beta-D-glucosaminidase [Serratia marcescens] Length = 885
SEQ ID n°2278	Prot n°PL-3044.1	Contig35	20771	23446	78%	Identities = 198/552 (35%), Positives = 300/552 (53%), Gaps = 11/552 (1%) emb CAA51370.1 (X72850) 2,4-dihydroxybenzoate monooxygenase [Sphingomonas sp.] Length = 630

TABLEAU I

SEQ ID n°2280	Prot n°PL-3046.1	Contig25	20063	21520	No Hits found	
SEQ ID n°2281	Prot n°PL-3047.1	Contig25	18964	20139	38%	Identities = 88/288 (30%), Positives = 151/288 (51%), Gaps = 10/288 (3%) gb AAAG07125.1 AE004793_2 (AE004793) integrase/recombinase XerD [Pseudomonas aeruginosa] Length = 298
SEQ ID n°2282	Prot n°PL-3048.1	Contig25	16626	17210	69%	Identities = 103/165 (62%), Positives = 141/165 (85%) sp P39902 SPRT_ECOLI SPRT PROTEIN pir G65079 hypothetical 19.3 kD protein in galP-endA intergenic region - Escherichia coli (strain K-12) gb AAA69111.1 (U28377) ORF_0165; alternate name yggI [Escherichia coli] dbj BAA12021.1 (D83644) SprT [Escherichia coli] gb AAC75981.1 (AE000377) orf, hypothetical protein [Escherichia coli] Length = 165 "
SEQ ID n°2283	Prot n°PL-3049.1	Contig25	15305	16477	92%	Identities = 349/384 (90%), Positives = 365/384 (94%) sp P04384 METK_ECOLI S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) pir SYEC5M methionine adenosyltransferase (EC 2.5.1.6) - Escherichia coli gb AAA69109.1 (U28377) CG Site No. 507 [Escherichia coli] gb AAC75979.1 (AE000377) methionine adenosyltransferase 1 (AdoMet synthetase); methyl and propylamine donor, corepressor of met genes [Escherichia coli] emb CAC07714.1 (AX018960) unnamed protein product [Escherichia coli] emb CAC07718.1 (AX018968) unnamed protein product [Escherichia coli] emb CAC07720.1 (AX018972) unnamed protein product [Escherichia coli] Length = 384 "
SEQ ID n°2284	Prot n°PL-305.1	Contig41	531607	532794	23%	Identities = 56/223 (25%), Positives = 92/223 (41%), Gaps = 16/223 (7%) pir T30216 hypothetical protein Z - Streptomyces hygroscopicus emb CAA60450.1 (X86780) orfZ [Streptomyces hygroscopicus] Length = 389
SEQ ID n°2285	Prot n°PL-3050.1	Contig25	12769	14673	88%	Identities = 516/640 (80%), Positives = 573/640 (88%), Gaps = 2/640 (0%) pir A65079 arginine decarboxylase (EC 4.1.1.19) - Escherichia coli gb AAA69105.1 (U28377) CG Site No. 161 [Escherichia coli] gb AAC75975.1 (AE000377) biosynthetic arginine decarboxylase [Escherichia coli] Length = 658
SEQ ID n°2286	Prot n°PL-3051.1	Contig25	11676	12599	88%	Identities = 251/306 (82%), Positives = 282/306 (92%) sp P16936 SPEB_ECOLI AGMATINASE (AGMATINE UREOHYDROLASE) (AUH) pir C42604 agmatinase (EC 3.5.3.11) - Escherichia coli gb AAA83909.1 (M32363) agmatine ureohydrolase [Escherichia coli] gb AAA69104.1 (U28377) agmatine ureohydrolase [Escherichia coli] gb AAC75974.1 (AE000377) agmatinase [Escherichia coli] Length =

TABLEAU I

SEQ ID n°2287	Prot n°PL-3052.1	Contig25	10700	11413	87%	<p>Identifies = 186/234 (79%), Positives = 209/234 (89%), Gaps = 1/234 (0%)</p> <p>sp Q46931 YGDQ_ECOLI_HYPOTHETICAL 26.2 KD PROTEIN IN MUTH-TAS INTERGENIC REGION pir JA65086 hypothetical protein b2832 - Escherichia coli (strain K-12) gb AAB40479.1 (U29581) ORF_o237 [Escherichia coli] gb AAC75871.1 (AE000367) putative transport protein [Escherichia coli]</p> <p>Length = 237</p>
SEQ ID n°2288	Prot n°PL-3053.1	Contig25	8921	10607	79%	<p>Identifies = 164/221 (74%), Positives = 188/221 (84%) pdb 2AZO B Chain B, Dna Mismatch Repair Protein Muth From E. Coli pdb 2AZO A Chain A, Dna Mismatch Repair Protein Muth From E. Coli</p> <p>Length = 232</p>
SEQ ID n°2289	Prot n°PL-3054.1	Contig25	7674	9335	72%	<p>Identifies = 314/550 (57%), Positives = 407/550 (73%), Gaps = 2/550 (0%)</p> <p>sp P33596 YABN_ECOLI_HYPOTHETICAL 63.9 KD PROTEIN IN TBPA-LEUD INTERGENIC REGION (ORF103)</p> <p>Length = 551</p>
SEQ ID n°2290	Prot n°PL-3055.1	Contig25	6624	7229	79%	<p>Identifies = 160/200 (80%), Positives = 175/200 (87%)</p> <p>sp P30126 LEUD_ECOLI 3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI) pir S40585 3-isopropylmalate dehydratase (EC 4.2.1.33) small chain - Escherichia coli db BAA01340.1 (D10483) leuD protein homolog (PIR:S07306) [Escherichia coli] gb AAC73182.1 (AE000117) isopropylmalate isomerase subunit [Escherichia coli]</p> <p>Length = 201</p>
SEQ ID n°2291	Prot n°PL-3056.1	Contig25	5208	6615	89%	<p>Identifies = 394/464 (84%), Positives = 426/464 (90%) pir H64728 3-isopropylmalate dehydratase (EC 4.2.1.33) alpha chain - Escherichia coli gb AAC73183.1 (AE000117) 3-isopropylmalate isomerase (dehydratase) subunit [Escherichia coli]</p> <p>Length = 466</p>
SEQ ID n°2292	Prot n°PL-3057.1	Contig25	4113	5204	85%	<p>Identifies = 305/363 (84%), Positives = 326/363 (89%)</p> <p>sp P37412 LEU3_SALTY 3-ISOPROPYLMALATE DEHYDROGENASE (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) pdb 1CNZ A Chain A, 3-Isopropylmalate Dehydrogenase (ipmdh) From Salmonella Typhimurium pdb 1CNZ B Chain B, 3-Isopropylmalate Dehydrogenase (ipmdh) From Salmonella Typhimurium gb AAB60185.1 (U20795) 3-isopropylmalate dehydrogenase [Salmonella typhimurium]</p> <p>Length = 363</p>
SEQ ID n°2293	Prot n°PL-3058.1	Contig25	2548	4110	84%	<p>Identifies = 402/523 (76%), Positives = 456/523 (86%), Gaps = 3/523 (0%)</p> <p>sp P09151 LEU1_ECOLI 2-ISOPROPYLMALATE SYNTHASE (ALPHA-ISOPROPYLMALATE SYNTHASE) (ALPHA-IPM SYNTHETASE) pir B84729 2-isopropylmalate synthase (EC 4.1.3.12) - Escherichia coli gb AAC73185.1 (AE000117) 2-isopropylmalate synthase [Escherichia coli]</p> <p>Length = 523</p>
SEQ ID n°2294	Prot n°PL-3059.1	Contig25	646	1590	70%	<p>Identifies = 187/302 (61%), Positives = 223/302 (72%)</p> <p>gb AAD26893.1 AF117227_5 (AF117227) LeuO [Salmonella typhimurium]</p> <p>Length = 341</p>

TABLEAU I

SEQ ID n°2285	Prot n°PL-306.1	Contig41	532781	534250	27%	<p>Identities = 86/319 (26%), Positives = 135/319 (41%), Gaps = 15/319 (4%) gb AAAF00205.1 AF184960_1 (AF184960) cyclase [Streptomyces fradiae] Length = 311</p>	Unknown, similar to proteins involved in antibiotic biosynthesis
						<p>Identities = 201/339 (59%), Positives = 262/339 (76%) sp P37417 IMURB_SALTY_UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (UDP-N-ACETYLMURAMATE DEHYDROGENASE) gb AAA27163.1 (L14816) UDP-N-acetylenolpyruvoylglucosamine reductase [Salmonella typhimurium] gb AAF33492.1 (AF170176) Salmonella typhimurium UDP-N-acetylenolpyruvoylglucosamine reductase (MURB) (SW:P37417) [Salmonella typhimurium LT2] Length = 342</p>	
SEQ ID n°2296	Prot n°PL-3060.1	Contig41	1137186	1138211	76%		
SEQ ID n°2297	Prot n°PL-3081.1	Contig41	1136230	1137189	81%		
SEQ ID n°2298	Prot n°PL-3082.1	Contig41	1135236	1136186	80%	<p>Identities = 252/316 (79%), Positives = 288/316 (89%) gb AAF33512.1 (AF170176) 96% identity over 316 amino acids with E. coli pantothenate kinase (SW:P15044) [Salmonella typhimurium LT2] Length = 320</p>	
SEQ ID n°2299	Prot n°PL-3063.1	Contig41	1133076	1134260	96%	<p>Identities = 372/393 (94%), Positives = 384/393 (97%) sp P21694 EFTU_SALTY_ELONGATION FACTOR TU (EF-TU) pir S13561 translation elongation factor EF-Tu.B - Salmonella typhimurium emb CAA38913.1 (X55117) elongation factor Tu [Salmonella typhimurium] emb CAA38912.1 (X55116) elongation factor Tu [Salmonella typhimurium] gb AAF33513.1 (AF170176) Salmonella typhimurium translation elongation factors TU (EF-TU) (SW:P21694); contains similarity to PFam domain PF00009 (GTP_EFTU, Score=541.8 E=4.9e-159, N=1) [Salmonella typhimurium] Length = 209</p>	
SEQ ID n°2300	Prot n°PL-3064.1	Contig41	1130298	1130927	94%	<p>Identities = 191/209 (91%), Positives = 202/209 (96%) sp P02386 RL3_ECOLI_50S RIBOSOMAL PROTEIN L3 pir R5EC3 ribosomal protein L3 - Escherichia coli emb CAA26460.1 (X02613) ribosomal protein L3 (rplC) (aa 1-209) [Escherichia coli] gb AAA58117.1 (U19997) 50S ribosomal subunit protein L3 [Escherichia coli] gb AAC76345.1 (AE000408) 50S ribosomal subunit protein L3 [Escherichia coli] prf J0509226A protein L3 [Escherichia coli] Length = 209</p>	
SEQ ID n°2301	Prot n°PL-3065.1	Contig41	1129676	1130281	92%	<p>Identities = 191/201 (95%), Positives = 198/201 (98%) sp P11253 RL4_YERP5_50S RIBOSOMAL PROTEIN L4 pir R5EB4Y ribosomal protein L4 - Yersinia pseudotuberculosis emb CAA32543.1 (X14363) ribosomal protein L4 (AA 1 - 201) [Yersinia pseudotuberculosis] Length = 209</p>	
SEQ ID n°2302	Prot n°PL-3066.1	Contig41	1128633	1129367	97%	<p>Identities = 265/274 (96%), Positives = 271/274 (98%) sp P49239 RL2_YEREN_50S RIBOSOMAL PROTEIN L2 gb AAC43513.1 (U11251) ribosomal protein L2 [Yersinia enterocolitica] Length = 274</p>	

TABLEAU I

SEQ ID n°2303	Prot n°PL-3067.1	Contig41	1127174	1127875	80%	Identities = 222/233 (95%), Positives = 228/233 (97%) sp P02352 RS3_ECOLI 30S RIBOSOMAL PROTEIN S3 pir IRSEC3 ribosomal protein S3 - Escherichia coli emb CAA26466.1 (X02613) ribosomal protein S3 (rpsC) (aa 1-233) [Escherichia coli] gb AAA58111.1 (U18997) 30S ribosomal subunit protein S3 [Escherichia coli] gb AAC76339.1 (AE000408) 30S ribosomal subunit protein S3 [Escherichia coli] Length = 233	
SEQ ID n°2304	Prot n°PL-3068.1	Contig41	1123584	1124117	84%	Identities = 154/177 (87%), Positives = 169/177 (95%) sp P02390 RL6_ECOLI 50S RIBOSOMAL PROTEIN L6 pir R5EC8 ribosomal protein L6 - Escherichia coli gb AAA58102.1 (U18997) 50S ribosomal subunit protein L6 [Escherichia coli] gb AAC76330.1 (AE000408) 50S ribosomal subunit protein L6 [Escherichia coli] Length = 177	
SEQ ID n°2305	Prot n°PL-3069.1	Contig41	1120744	1122075	98%	Identities = 434/443 (97%), Positives = 439/443 (98%) sp P03844 SECY_ECOLI PREPROTEIN TRANSLOCASE SECY SUBUNIT pir IQECSY preprotein translocase secY - Escherichia coli emb CAA25725.1 (X01563) SecY (Pha) polypeptide (aa 1-443) [Escherichia coli] gb AAA58097.1 (U18997) secY [Escherichia coli] gb AAC76325.1 (AE000408) putative ATPase subunit of translocase [Escherichia coli]	
SEQ ID n°2306	Prot n°PL-307.1	Contig41	534223	535782	44%	Identities = 124/528 (23%), Positives = 230/528 (43%), Gaps = 44/528 (8%) dbj BAB05725.1 (AP001514) long-chain acyl-CoA synthetase (ligase) [Bacillus halodurans] Length = 513	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°2307	Prot n°PL-3070.1	Contig41	1119026	1119646	85%	Identities = 194/206 (94%), Positives = 202/206 (97%) sp P02354 RS4_ECOLI 30S RIBOSOMAL PROTEIN S4 pir IR3EC4 ribosomal protein S4 - Escherichia coli emb CAA26394.1 (X02543) ribosomal protein S4 (aa 1-206) [Escherichia coli] gb AAA58094.1 (U18997) 30S ribosomal subunit protein S4 [Escherichia coli] gb AAC76321.1 (AE000407) 30S ribosomal subunit protein S4 [Escherichia coli] Length = 206	
SEQ ID n°2308	Prot n°PL-3071.1	Contig41	1118011	1119000	97%	Identities = 328/328 (99%), Positives = 328/328 (99%) sp P00574 RPOA_ECOLI DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN (TRANSCRIPTASE ALPHA CHAIN) (RNA POLYMERASE ALPHA SUBUNIT) pir IRNECA DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - Escherichia coli pir A41658 DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - Salmonella typhimurium emb CAA25337.1 (X00766) RNA polymerase alpha subunit [Escherichia coli] gb AAA24577.1 (J01685) RNA polymerase alpha subunit [Escherichia coli] gb AAA27214.1 (M77750) RNA polymerase alpha-subunit [Salmonella typhimurium] gb AAA58092.1 (U18997) CG Site No. 234 [Escherichia coli] gb AAC76320.1 (AE000407) RNA polymerase, alpha subunit [Escherichia coli]	

TABLEAU I

SEQ ID n°2309	Prot n°PL-3072.1	Contig41	1115034	1116410	90%	<p>Identities = 377/458 (82%), Positives = 425/458 (92%)</p> <p>sp P23868 TRKA_ECOLI TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKA pir S36252 constitutive potassium transport system protein trkA - Escherichia coli emb CAA36359.1 (X52114) TrkA protein of the constitutive K⁺-transport system Trk [Escherichia coli] emb CAA54371.1 (X77091) trkA [Escherichia coli] gb AAA58087.1 (U18997) TrkA protein of the constitutive K⁺-transport system Trk [Escherichia coli] gb AAC76315.1 (AE000407) transport of potassium [Escherichia coli] Identities = 280/429 (65%), Positives = 339/429 (78%) sp P36929 SUN_ECOLI SUN PROTEIN (FMU PROTEIN) pir D65121 fmu protein - Escherichia coli emb CAA71359.1 (Y10307) sun [Escherichia coli] gb AAC76314.1 (AE000407) orf, hypothetical protein [Escherichia coli] Length = 429</p>
SEQ ID n°2310	Prot n°PL-3073.1	Contig41	1113670	1114977	77%	<p>Identities = 226/314 (71%), Positives = 266/314 (83%) sp P23882 FMT_ECOLI METHIONYL-TRNA FORMYLTRANSFERASE pir S23108 methionyl-TRNA formyltransferase (EC 2.1.2.9) - Escherichia coli emb CAA45207.1 (X63666) methionyl-TRNA formyltransferase [Escherichia coli] emb CAA54368.1 (X77091) methionyl-TRNA formyltransferase [Escherichia coli] gb AAC76313.1 (AE000407) 10-formyltetrahydrofolate:L-methionyl-TRNA (fMet) N-formyltransferase [Escherichia coli] Length = 315</p>
SEQ ID n°2311	Prot n°PL-3074.1	Contig41	1112670	1113617	82%	<p>Identities = 179/357 (50%), Positives = 225/357 (62%), Gaps = 1/357 (0%)</p> <p>sp P30852 SMF_ECOLI SMF PROTEIN emb CAA46763.1 (X65946) smf [Escherichia coli] emb CAA54366.1 (X77091) smf [Escherichia coli] Length = 374</p>
SEQ ID n°2312	Prot n°PL-3075.1	Contig41	1110914	1111989	59%	<p>Identities = 107/150 (71%), Positives = 125/150 (83%)</p> <p>sp P45771 YRDD_ECOLI HYPOTHETICAL 18.6 KDA PROTEIN IN AROE-SMG INTERGENIC REGION (F169) pir F65120 hypothetical 18.6 kD protein in aroE-smg intergenic region - Escherichia coli (strain K-12) gb AAA58080.1 (U18997) ORF_f169 [Escherichia coli] gb AAC76308.1 (AE000406) putative DNA topoisomerase [Escherichia coli] Length = 161/270 (59%), Positives = 199/270 (73%)</p>
SEQ ID n°2314	Prot n°PL-3077.1	Contig41	1108896	1109714	71%	<p>sp P15770 AROE_ECOLI SHIKIMATE 5-DEHYDROGENASE pir S00252 shikimate 5-dehydrogenase (EC 1.1.1.25) - Escherichia coli emb CAA68700.1 (Y00710) shikimate dehydrogenase [Escherichia coli] gb AAA58078.1 (U18997) shikimate dehydrogenase [Escherichia coli] gb AAC76306.1 (AE000406) dehydroshikimate reductase [Escherichia coli]</p>
SEQ ID n°2315	Prot n°PL-3078.2	Contig38	437516	438415	No Hits found	
SEQ ID n°2316	Prot n°PL-3079.1	Contig38	436433	437446	No Hits found	
SEQ ID n°2317	Prot n°PL-308.1	Contig41	536077	537195	34%	<p>Identities = 81/260 (31%), Positives = 130/260 (49%), Gaps = 13/260 (5%)</p> <p>gb AAF83483.1 AE003911_5 (AE003911) 3-oxoacyl-[ACP] synthase II [Xylella fastidiosa] Length = 411</p> <p>Unknown, similar to proteins involved in antibiotic biosynthesis</p>

TABLEAU I

SEQ ID n°2318	Prot n°PL-3080.1	Contig38	433331	434431	73%	gb AAD56248.1 AF186235_1 (AF186235) L-arginine:lysine amidinotransferase [Pseudomonas syringae pv. phaseolicola] Length = 362
SEQ ID n°2319	Prot n°PL-3081.1	Contig38	432311	433324	No Hits found	
SEQ ID n°2320	Prot n°PL-3082.1	Contig38	431356	432552	28%	Identities = 58/273 (21%), Positives = 114/273 (41%), Gaps = 25/273 (9%) dbj BAB06652.1 (AP001517) unknown [Bacillus halodurans] Length = 284
SEQ ID n°2321	Prot n°PL-3083.1	Contig38	430315	431196	64%	Identities = 154/284 (54%), Positives = 197/284 (69%), Gaps = 4/284 (1%) gb AAG06100.1 AE004899_5 (AE004899) hypothetical protein [Pseudomonas aeruginosa] Length = 287
SEQ ID n°2322	Prot n°PL-3084.1	Contig38	428350	429957	29%	Identities = 92/314 (29%), Positives = 157/314 (49%), Gaps = 19/314 (6%) emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis] Length = 456
SEQ ID n°2323	Prot n°PL-3085.1	Contig38	425599	427203	31%	Identities = 94/339 (27%), Positives = 166/339 (48%), Gaps = 19/339 (5%) emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis] Length = 456
SEQ ID n°2324	Prot n°PL-3086.1	Contig38	423571	425109	29%	Identities = 89/291 (30%), Positives = 149/291 (50%), Gaps = 20/291 (6%) emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis] Length = 456
SEQ ID n°2325	Prot n°PL-3087.1	Contig38	421667	423406	24%	Identities = 92/294 (31%), Positives = 142/294 (48%), Gaps = 26/294 (8%) emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis] Length = 456
SEQ ID n°2326	Prot n°PL-3088.1	Contig38	419985	421586	26%	Identities = 94/293 (32%), Positives = 144/293 (49%), Gaps = 19/293 (6%) emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis] Length = 456
SEQ ID n°2327	Prot n°PL-3089.1	Contig38	418126	419475	51%	Identities = 161/414 (38%), Positives = 230/414 (54%), Gaps = 32/414 (7%) gb AAF83351.1 (AE004108) deoxycytidylate deaminase-related protein [Vibrio cholerae] Length = 532
SEQ ID n°2328	Prot n°PL-309.1	Contig41	537185	538471	59%	Identities = 168/417 (40%), Positives = 261/417 (62%), Gaps = 11/417 (2%) sp Q02578 KAS1_STRGN PUTATIVE POLYKETIDE BETA-KETOACYL SYNTHASE 1 pir JUC1210 polyketide beta-ketoacyl synthase (EC 2.3.1.-) chain 1 - Streptomyces cyaneus gb AA426726.1 (M33704) curA protein [Streptomyces cyaneus] emb CAA44380.1 (X62518) beta-ketoacyl synthase [Streptomyces cyaneus] prf 18071298 curA gene [Streptomyces cyaneus] Length = 422
SEQ ID n°2329	Prot n°PL-3090.1	Contig38	416172	417359	83%	Identities = 291/392 (74%), Positives = 332/392 (84%) sp P44488 UXUA_HAEIN MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE) pir JEG4045 mannonate dehydratase (EC 4.2.1.8) - Haemophilus influenzae (strain Rd KW20) gb AAC21733.1 (U32680) mannonate dehydratase (uxuA) [Haemophilus influenzae Rd] Length = 392

Unknown, similar to
proteins involved in
antibiotic
biosynthesis

TABLEAU I

SEQ ID n°2330	Prot n°PL-3091.1	Contig38	415391	416134	71%	<p>Identities = 160/251 (63%), Positives = 193/251 (76%), Gaps = 6/251 (2%) sp P39161 UXUR_ECOLI_UXU OPERON TRANSCRIPTIONAL REGULATOR pir S56549 regulatory protein uxuR - Escherichia coli gb AA97220.1 (U14003) CG Site No. 12 [Escherichia coli] dbj BAA02592.1 (D13329) uxu regulon repressor [Escherichia coli] gb AAC77280.1 (AE000503) regulator for uxu operon [Escherichia coli] Length = 257</p>
SEQ ID n°2331	Prot n°PL-3092.1	Contig38	414292	415272	54%	<p>Identities = 117/285 (41%), Positives = 190/285 (66%), Gaps = 1/285 (0%) dbj BAB04420.1 (AP001509) C4-dicarboxylate transport system (C4- dicarboxylate-binding protein) [Bacillus halodurans] Length = 341</p>
SEQ ID n°2332	Prot n°PL-3093.1	Contig38	412147	413460	79%	<p>Identities = 275/424 (64%), Positives = 351/424 (81%), Gaps = 1/424 (0%) sp P40800 YGIK_SALTY_HYPOTHETICAL_46.1 KD PROTEIN IN PLSC 3'REGION gb AA56680.1 (U09309) YgiK [Salmonella typhimurium] Length = 435</p>
SEQ ID n°2333	Prot n°PL-3094.1	Contig38	410638	412119	74%	<p>Identities = 323/480 (67%), Positives = 377/480 (78%), Gaps = 6/480 (1%) sp P39160 UXUB_ECOLI_D-MANNONATE OXIDOREDUCTASE (FRUCTURONATE REDUCTASE) pir S56548 fructuronate reductase (EC 1.1.1.57) uxuB - Escherichia coli gb AA97219.1 (U14003) D-mannionate oxidoreductase [Escherichia coli] gb AAC77278.1 (AE000503) D-mannionate oxidoreductase [Escherichia coli] dbj BAA02591.1 (D13329) Mannonate oxidoreductase [Escherichia coli] Length = 486</p>
SEQ ID n°2334	Prot n°PL-3095.1	Contig38	409217	410641	76%	<p>Identities = 303/469 (64%), Positives = 368/469 (77%), Gaps = 2/469 (0%) sp P42607 UXAC_ECOLI_URONATE ISOMERASE (GLUCURONATE ISOMERASE) (URONIC ISOMERASE) pir A65098 glucuronate isomerase (EC 5.3.1.12) - Escherichia coli dbj BAA02587.1 (D13328) Uronate isomerase [Escherichia coli] gb AAC76127.1 (AE000391) uronate isomerase [Escherichia coli] Length = 470</p>
SEQ ID n°2335	Prot n°PL-3096.1	Contig38	408276	409220	67%	<p>Identities = 171/314 (54%), Positives = 222/314 (70%), Gaps = 2/314 (0%) sp P44482 KDGK_HAEIN_2-DEHYDRO-3-DEOXYGLUCONOKINASE (2'- KETO-3-DEOXYGLUCONOKINASE) (3-DEOXY-2-OXO-D- GLUCONATE KINASE) (KDG KINASE) pir C64045 2-dehydro-3- deoxyglucuronokinas homolog - Haemophilus influenzae KW20) gb AAC21727.1 (U32690) 2-dehydro-3-deoxyglucuronokinas (kdgK) [Haemophilus influenzae Rd] Length = 314</p>

TABLEAU I

SEQ ID n°2336	Prot n°PL-3097.1	Contig38	407629	408261	75%	<p>Identities = 139/206 (67%), Positives = 167/206 (80%) sp P44480 ALKH_HAEIN PUTATIVE KHGKDPG ALDOLASE [INCLUDES: 4-HYDROXY-2-OXOGLUTARATE ALDOLASE (2-KETO-4-HYDROXYGLUTARATE ALDOLASE) (KHG-ALDOLASE); 2-DEHYDRO-3-DEOXYPHOSPHOGLUCONATE ALDOLASE (PHOSPHO-2-DEHYDRO-3-DEOXYGLUCONATE ALDOLASE) (PHOSPHO-2-KETO-3-DEOXYGLUCONATE ALDOLASE) pir A64045 2-dehydro-3-deoxyphosphogluconate aldolase homolog H10047 - Haemophilus influenzae (strain Rd KW20) gb AAC21725.1 (U32690) 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxyphosphogluconate aldolase (eda) [Haemophilus influenzae Rd] Length = 212 "</p>
SEQ ID n°2337	Prot n°PL-3098.1	Contig38	404154	405859	70%	<p>Identities = 255/503 (50%), Positives = 366/503 (72%), Gaps = 2/503 (0%) gb AAD38229.1 (U17224) CarA [Pectobacterium carotovorum] Length = 503</p>
SEQ ID n°2338	Prot n°PL-3099.1	Contig38	403402	404151	78%	<p>Identities = 150/250 (60%), Positives = 202/250 (80%), Gaps = 1/250 (0%) gb AAD38230.1 (U17224) CarB [Pectobacterium carotovorum] Length = 250</p>
SEQ ID n°2339	Prot n°PL-31.1	Contig41	58120	59004	63%	<p>Identities = 144/289 (49%), Positives = 185/289 (66%), Gaps = 3/289 (1%) gb AAC46213.1 (AF035922) PepD [Pseudomonas aeruginosa] = 295</p>
SEQ ID n°2340	Prot n°PL-310.1	Contig41	539123	539938	57%	<p>Identities = 107/272 (39%), Positives = 159/272 (58%), Gaps = 19/272 (6%) gb AAFO1818.1 (AF187532_14 (AF187632) putative polyketide cyclase [Streptomyces nogalater] Length = 324</p>
SEQ ID n°2341	Prot n°PL-3100.1	Contig38	402567	403388	89%	<p>Identities = 220/273 (80%), Positives = 244/273 (88%) gb AAD38231.1 (U17224) CarC [Pectobacterium carotovorum] Length = 273</p>
SEQ ID n°2342	Prot n°PL-3101.1	Contig38	401306	402502	62%	<p>Identities = 168/372 (44%), Positives = 251/372 (66%), Gaps = 4/372 (1%) sp Q9XB58 CARD_ERWCA CARBAPENEM ANTIBIOTICS BIOSYNTHESIS PROTEIN CARD gb AAD38232.1 (U17224) CarD [Pectobacterium carotovorum] Length = 376</p>
SEQ ID n°2343	Prot n°PL-3102.2	Contig37	491118	491924	No Hits found	
SEQ ID n°2344	Prot n°PL-3103.2	Contig37	492020	493045		
SEQ ID n°2345	Prot n°PL-3104.1	Contig37	493763	494941		
SEQ ID n°2346	Prot n°PL-3105.1	Contig37	495076	496500	78%	<p>Identities = 310/471 (65%), Positives = 377/471 (79%) emb CAA21342.1 (AL031866) ORF19, len: 473 aa, similar to tyrosine aminotransferase, highly similar to E. coli D90784_2, Fasta scores opt:1842, E): 0 [Yersinia pestis] Length = 473</p>

Unknown, similar to proteins involved in antibiotic biosynthesis

Unknown, similar to proteins involved in antibiotic biosynthesis

TABLEAU I

SEQ ID n°2347	Prot n°PL-3106.1	Contig37	496629	497966	85%	Identities = 342/439 (77%), Positives = 365/439 (86%), Gaps = 2/439 (0%) emb CAA71556.1 (Y10528) cyanide insensitive terminal oxidase [Pseudomonas aeruginosa] gb AAG07317.1 AE004810_9 (AE004810) cyanide insensitive terminal oxidase [Pseudomonas aeruginosa] Length = 488
SEQ ID n°2348	Prot n°PL-3107.1	Contig37	497956	498963	79%	Identities = 227/335 (67%), Positives = 267/335 (78%) emb CAA71556.1 (Y10528) cyanide insensitive terminal oxidase [Pseudomonas aeruginosa] gb AAG07316.1 AE004810_8 (AE004810) cyanide insensitive terminal oxidase [Pseudomonas aeruginosa] Length = 335
SEQ ID n°2348	Prot n°PL-3108.1	Contig37	499128	500399	45%	Identities = 129/348 (37%), Positives = 192/348 (55%), Gaps = 22/348 (6%) emb CAA21343.1 (AL031866) ORF20, len: 593 aa, probable nitrate/nitrite sensor protein, highly similar to many, e.g. E. coli P10956, 47.9% identity in 595 aa overlap FastA scores: opt: 1801, E0:0, and PSNARXL_2 Pseudomonas aeruginosa narX, 33.1% identity in 596 aa ove> Length = 593
SEQ ID n°2350	Prot n°PL-3109.1	Contig37	500508	501371	50%	Identities = 89/263 (33%), Positives = 144/263 (53%), Gaps = 5/263 (1%) sp Q56646 VIUB_VIBCH VIBRIOBACTIN UTILIZATION PROTEIN VIUB gb AAB86829.1 (AF030977) ViuB protein [Vibrio cholerae] gb AAF5354.1 (AE004293) vibriobactin utilization protein ViuB [Vibrio cholerae] Length = 271
SEQ ID n°2351	Prot n°PL-311.1	Contig41	539931	540653	33%	Identities = 51/188 (27%), Positives = 61/188 (42%), Gaps = 17/188 (9%) gb AAD10395.1 (U46488) NrpG [Proteus mirabilis] Length = 249
SEQ ID n°2352	Prot n°PL-3110.1	Contig37	501806	502594	88%	Identities = 201/262 (76%), Positives = 232/262 (87%), Gaps = 1/262 (0%) sp P31544 PHOH_ECOLI PHOH PROTEIN (PHOSPHATE STARVATION- INDUCIBLE PROTEIN PSIH) pir B47065 phosphate starvation-inducible protein psih - Escherichia coli db BAA01230.1 (D10391) PhoH protein [Escherichia coli] db BAA35801.1 (D90739) PhoH protein (phosphate starvation-inducible protein Psih). [Escherichia coli] gb AAC74105.1 (AE000204) PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation [Escherichia coli] Length = 354 *
SEQ ID n°2353	Prot n°PL-3111.2	Contig37	503246	504244		Identities = 20/34 (58%), Positives = 26/34 (75%) db BAA06865.1 (AB045036) tail fiber [Pectobacterium carotovorum subsp. carotovorum] Length = 632
SEQ ID n°2354	Prot n°PL-3112.1	Contig37	504478	505809	5%	Identities = 84/197 (42%), Positives = 120/197 (60%), Gaps = 2/197 (1%) sp Q47427 TFAB_ECOLI TAIL FIBER ASSEMBLY PROTEIN HOMOLOG pir S18684 gene T protein - Escherichia coli plasmid p158 emb CAA44047.1 (X62121) T [Escherichia coli] Length = 203
SEQ ID n°2355	Prot n°PL-3113.1	Contig37	506002	506649	55%	

Unknown, similar to
proteins involved in
antibiotic
biosynthesis

TABLEAU I

SEQ ID n°2356	Prot n°PL-3114.1	Contig37	506650	507384	39%	Identities = 75/153 (49%), Positives = 87/153 (63%), Gaps = 13/153 (8%) pir S18689 ScSvP protein - Escherichia coli plasmid p158 emb CAA44052.1 (X62121) DNA inversion product [Escherichia coli] Length = 753 Identities = 176/230 (76%), Positives = 202/230 (87%)
SEQ ID n°2357	Prot n°PL-3115.1	Contig37	507752	508447	85%	spiP48838 AQPZ, ECOLI AQUAPORIN Z (BACTERIAL NODULIN-LIKE INTRINSIC PROTEIN) pir C64826 aquaporin Z - Escherichia coli gb AAC73962.1 (AE000189) transmembrane water channel; aquaporin Z [Escherichia coli] dbj BAA35589.1 (D90724) Aquaporin Z, [Escherichia coli] dbj BAA35593.1 (D90725) Aquaporin Z, [Escherichia coli] Length Identities = 167/218 (76%), Positives = 201/218 (91%) emb CAA64809.1 (X95564) expA [Erwinia carotovora] Length = 218
SEQ ID n°2358	Prot n°PL-3116.1	Contig37	511601	512266	85%	Identities = 48/7610 (79%), Positives = 555/610 (90%) dbj BAA15733.1 (D90832) Exonuclease ABC subunit C, [Escherichia coli] Length = 610 Identities = 108/214 (49%), Positives = 133/214 (61%), Gaps = 16/214 (7%)
SEQ ID n°2360	Prot n°PL-3118.1	Contig37	516114	516887	51%	pir S18690 ScSvQ protein - Escherichia coli plasmid p15B emb CAA44053.1 (X62121) DNA inversion product [Escherichia coli] Length = 748 Identities = 84/185 (45%), Positives = 110/185 (59%), Gaps = 1/185 (0%)
SEQ ID n°2361	Prot n°PL-3119.1	Contig37	516918	518429	21%	ref NP_040605.1 orf-194 sp P03740 TFA_LAMBD TAIL FIBER ASSEMBLY PROTEIN pir QXBP3L hypothetical protein A-194 - phage lambda gb AAA96558.1 (J02459) orf-194 [bacteriophage lambda] Length = 194
SEQ ID n°2362	Prot n°PL-312.2	Contig41	540647	541423		Identities = 88/156 (56%), Positives = 108/156 (67%), Gaps = 9/156 (5%) pir S18690 ScSvQ protein - Escherichia coli plasmid p15B emb CAA44053.1 (X62121) DNA inversion product [Escherichia coli] Length = 748
SEQ ID n°2363	Prot n°PL-3120.1	Contig37	519193	520110	31%	Identities = 89/299 (29%), Positives = 159/299 (52%), Gaps = 19/299 (6%) gb AAD37764.1 (AF146532) putative glycosyltransferase [Klebsiella pneumoniae] Length = 302
SEQ ID n°2364	Prot n°PL-3121.1	Contig37	521343	522257	52%	Identities = 57/223 (25%), Positives = 95/223 (42%), Gaps = 29/223 (13%) gb AAG04736.1 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°2365	Prot n°PL-3122.1	Contig37	523298	523981	41%	Identities = 60/165 (30%), Positives = 88/165 (44%), Gaps = 26/165 (13%) gb AAF6971.1 (AE004433) transcriptional regulator, LuxR family [Vibrio cholerae] Length = 319
SEQ ID n°2366	Prot n°PL-3123.2	Contig37	524730	525356		Identities = 52/211 (24%), Positives = 97/211 (45%), Gaps = 9/211 (4%) gb AAG04736.1 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°2367	Prot n°PL-3124.1	Contig37	528742	527413	39%	Identities = 111/387 (28%), Positives = 172/387 (43%), Gaps = 53/387 (13%) dbj BAB05094.1 (AP001511) DNA primase [Bacillus halodurans] = 599
SEQ ID n°2368	Prot n°PL-3125.1	Contig37	527503	528213	40%	
SEQ ID n°2369	Prot n°PL-3126.1	Contig24	5324	7681	21%	
SEQ ID n°2370	Prot n°PL-3127.1	Contig24	3239	4189	No Hits found	

TABLEAU I

SEQ ID n°2371	Prot n°PL-3128.1	Contig24	2774	3577	No Hits found	Identities = 77/223 (34%), Positives = 132/223 (59%), Gaps = 3/223 (1%) gb AAF89876.1 (AF173869) putative site-specific recombinase XerD [Staphylococcus aureus] Length = 295
SEQ ID n°2372	Prot n°PL-3129.1	Contig24	1083	2417	29%	
SEQ ID n°2373	Prot n°PL-313.1	Contig41	544419	545822	18%	Identities = 56/195 (28%), Positives = 85/195 (42%), Gaps = 2/195 (1%) gb AAG05045.1 (AE004593_7) (AE004593) hypothetical protein [Pseudomonas aeruginosa] Length = 518
SEQ ID n°2374	Prot n°PL-3130.1	Contig24	2	1300	No Hits found	
SEQ ID n°2375	Prot n°PL-3131.2	Contig32	28437	29543		
SEQ ID n°2376	Prot n°PL-3132.1	Contig32	25895	27625	63%	Identities = 278/580 (47%), Positives = 387/580 (65%), Gaps = 5/580 (0%) sp P75867 LONH_ECOLI PUTATIVE PROTEASE LA HOMOLOG pir B64836 probable ATP-dependent proteinase b0955 - Escherichia coli gb AAC74041.1 (AE000197) putative ATP-dependent protease [Escherichia coli] Length = 586
SEQ ID n°2377	Prot n°PL-3133.1	Contig32	21324	22973	79%	Identities = 363/543 (66%), Positives = 443/543 (80%) sp P43671 PQIB_ECOLI PARAQUAT-INDUCIBLE PROTEIN B pir F64835 paraquat-inducible protein pqiB - Escherichia coli db BAA35709.1 (D90733) Paraquat-inducible protein B. [Escherichia coli] gb AAC74037.1 (AE000197) paraquat-inducible protein B [Escherichia coli] Length = 546
SEQ ID n°2378	Prot n°PL-3134.1	Contig32	20056	21303	74%	Identities = 275/408 (67%), Positives = 341/408 (83%) sp P43670 PQIA_ECOLI PARAQUAT-INDUCIBLE PROTEIN A pir E64835 paraquat-inducible protein pqiA - Escherichia coli db BAA35708.1 (D90733) Paraquat-inducible protein A. [Escherichia coli] gb AAC74036.1 (AE000197) paraquat-inducible protein A [Escherichia coli] Length = 417
SEQ ID n°2379	Prot n°PL-3135.1	Contig32	18056	19966	86%	Identities = 475/635 (74%), Positives = 557/635 (86%), Gaps = 2/635 (0%) sp P43672 UUP_ECOLI ABC TRANSPORTER ATP-BINDING PROTEIN UUP pir B64835 ABC-type transport protein uup - Escherichia coli gb AAC74035.1 (AE000197) putative ATP-binding component of a transport system [Escherichia coli] db BAA35707.1 (D90733) Hypothetical protein H1300 [Escherichia coli] Length = 635
SEQ ID n°2380	Prot n°PL-3136.1	Contig32	15918	18050	84%	Identities = 523/702 (74%), Positives = 608/702 (86%), Gaps = 1/702 (0%) sp P75864 YCBY_ECOLI HYPOTHETICAL 78.9 KDA PROTEIN IN PYRD- PQIA INTERGENIC REGION pir C64835 hypothetical protein b0948 - Escherichia coli gb AAC74034.1 (AE000197) putative oxidoreductase [Escherichia coli] db BAA35703.1 (D90732) Hypothetical protein H10115 [Escherichia coli] db BAA35706.1 (D90733) Hypothetical protein H10115 [Escherichia coli] Length = 702
SEQ ID n°2381	Prot n°PL-3137.1	Contig32	14715	15830	76%	Identities = 217/367 (59%), Positives = 284/367 (77%), Gaps = 1/367 (0%) pir B64835 probable iron-sulfur-binding protein b0947 - Escherichia coli gb AAC74033.1 (AE000196) orf, hypothetical protein [Escherichia coli] Length = 369

TABLEAU I

SEQ ID n°2382	Prot n°PL-3138.1	Contig32	13427	14440	49%	Identities = 103/338 (30%), Positives = 167/338 (48%), Gaps = 11/338 (3%) dbj BAA83130.1 (AB023953) N-glycosylation [Saccharothrix aerocolonigenes] Length = 414
SEQ ID n°2383	Prot n°PL-3139.1	Contig32	12037	12921	59%	Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300
SEQ ID n°2384	Prot n°PL-314.1	Contig41	54805	547923	36%	Identities = 81/308 (26%), Positives = 138/308 (44%), Gaps = 10/308 (3%) gb AAF96025.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 338
SEQ ID n°2385	Prot n°PL-3140.1	Contig32	10620	11915	50%	Identities = 137/425 (32%), Positives = 221/425 (51%), Gaps = 22/425 (5%) dbj BAA83130.1 (AB023953) N-glycosylation [Saccharothrix aerocolonigenes] Length = 414
SEQ ID n°2386	Prot n°PL-3141.1	Contig32	8362	9372	85%	Identities = 268/336 (79%), Positives = 289/336 (88%) sp P05021 PYRD_ECOLI_DIHYDROOROTATE_DEHYDROGENASE (DIHYDROOROTATE OXIDASE) (DHODASE) (DHOD) pir DEECDO dihydroorotate oxidase (EC 1.3.3.1) - Escherichia coli emb CAA26594.1 (X02826) dihydroorotate dehydrogenase (aa 1-336) [Escherichia coli] dbj BAA35700.1 (D90732) Dihydroorotate oxidase (EC 1.3.3.1) [Escherichia coli] gb AAC74031.1 (AE000198) dihydro-orotate dehydrogenase [Escherichia coli] Length = 338
SEQ ID n°2387	Prot n°PL-3142.1	Contig32	5063	7675	85%	Identities = 664/869 (76%), Positives = 749/869 (85%), Gaps = 1/869 (0%) sp P04825 AMPN_ECOLI_AMINOPEPTIDASE_N (ALPHA- AMINOACYLPEPTIDE HYDROLASE) pir DPECN membrane alanyl aminopeptidase (EC 3.4.11.2) - Escherichia coli gb AA24317.1 (M15273) peptidase N [Escherichia coli] gb AAA24318.1 (M15676) aminopeptidase N [Escherichia coli] gb AAC74018.1 (AE000196) aminopeptidase N [Escherichia coli] dbj BAA35684.1 (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli] Length = Identities = 272/403 (67%), Positives = 321/403 (79%), Gaps = 4/403 (0%)
SEQ ID n°2388	Prot n°PL-3143.1	Contig32	3503	4717	78%	sp P18133 PNCB_ECOLI_NICOTINATE_PHOSPHORIBOSYLTRANSFERASE (NAPRTASE) pir JQ0756 nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Escherichia coli gb AAA24400.1 (J05568) nicotinic acid phosphoribosyl transferase (pncB) (EC 2.4.2.11) [Escherichia coli] dbj BAA35683.1 (D90731) Nicotinate phosphoribosyltransferase (EC 2.4.2.11) [Escherichia coli] gb AAC74017.1 (AE000195) nicotinate phosphoribosyltransferase [Escherichia coli] Length = 400

TABLEAU I

SEQ ID n°2388	Prot n°PL-3144.1	Contig32	1898	3298	83%	Identities = 395/466 (84%), Positives = 440/466 (93%) sp P17242 SYN_ECOLI ASPARAGINYL-TRNA SYNTHETASE (ASPARAGINE-TRNA LIGASE) (ASPRS) pir J15VECNT asparagine--trna ligase (EC 6.1.1.22) - Escherichia coli emb CAA48274.1 (X68192) Asparaginyl-tRNA synthetase [Escherichia coli] gb AAA24666.1 (M33145) asparaginyl-tRNA synthetase (asnS) [Escherichia coli] dbj BAA35682.1 (D90731) Asparaginyl-tRNA synthetase (EC 6.1.1.22) (asparagine-tRNA ligase) (asnRS) [Escherichia coli] gb AAC74016.1 (AE000195) asparagine tRNA synthetase [Escherichia coli]
SEQ ID n°2390	Prot n°PL-3145.2	Contig32	416	1561		Identities = 414/483 (85%), Positives = 447/483 (91%) sp P21166 TRKH_ECOLI TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH pir J58151 trkH protein (corrected) - Escherichia coli Length = 1561
SEQ ID n°2391	Prot n°PL-3146.1	Contig41	778391	778942	92%	Identities = 126/200 (63%), Positives = 157/200 (78%) sp P27862 YIGZ_ECOLI HYPOTHETICAL 21.9 KD PROTEIN IN PEPQ-TRKH INTERGENIC REGION (O205) pir J30739 hypothetical protein (pepQ 5' region) - Escherichia coli gb AAA67645.1 (M87049) similar to product of an uncharacterized ORF of B. subtilis [Escherichia coli] gb AAC76851.1 (AE000460) orf, hypothetical protein [Escherichia coli] Length = 205
SEQ ID n°2392	Prot n°PL-3147.1	Contig41	778880	780491	72%	Identities = 318/443 (71%), Positives = 374/443 (83%), Gaps = 1/443 (0%) sp P21166 PEPO_ECOLI XAA-PRO DIPEPTIDASE (X-PRO DIPEPTIDASE) (PROLINE DIPEPTIDASE) (PROLIDASE) (IMIDODIPEPTIDASE) pir J465189 X-Pro dipeptidase (EC 3.4.13.9) - Escherichia coli (strain K-12) gb AAC76850.1 (AE000460) proline dipeptidase [Escherichia coli] Length = 443
SEQ ID n°2393	Prot n°PL-3148.1	Contig41	780491	781825	83%	
SEQ ID n°2394	Prot n°PL-3149.2	Contig41	782099	784285		Identities = 180/579 (31%), Positives = 289/579 (51%), Gaps = 31/579 (5%) gb AAF96024.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 589
SEQ ID n°2395	Prot n°PL-315.1	Contig41	547845	549611	48%	
SEQ ID n°2396	Prot n°PL-3150.1	Contig32	177457	178977	14%	Identities = 52/158 (32%), Positives = 74/158 (45%), Gaps = 25/158 (15%) sp P26007 ITAG_CHICK INTEGRIN ALPHA-6 PRECURSOR (VLA-6) pir J38457 integrin alpha-6 chain precursor - chicken emb CAA39909.1 (X56559) integrin alpha 6 subunit [Gallus gallus] Length = 1072
SEQ ID n°2397	Prot n°PL-3151.1	Contig32	175902	177404	No Hits found	
SEQ ID n°2398	Prot n°PL-3152.1	Contig32	173840	175441	No Hits found	
SEQ ID n°2399	Prot n°PL-3153.1	Contig32	171456	172469	72%	Identities = 198/329 (60%), Positives = 245/329 (74%) dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] Length = 345
SEQ ID n°2400	Prot n°PL-3154.1	Contig32	168202	170283	88%	Identities = 578/690 (83%), Positives = 636/690 (91%) sp Q56887 FLHA_YEREN FLAGELLAR BIOSYNTHESIS PROTEIN FLHA pir J54214 flagellar biosynthesis protein flhA - Yersinia enterocolitica emb CAA88186.1 (Z48169) flhA [Yersinia enterocolitica] Length = 692
SEQ ID n°2401	Prot n°PL-3155.1	Contig32	167991	168782	No Hits found	

TABLEAU I

SEQ ID n°2402	Prot n°PL-3156.1	Contig32	167058	168209	81%	sp Q56886 FLHB_YEREN FLAGELLAR BIOSYNTHETIC PROTEIN FLHB pir S54213 flagellar biosynthetic protein flhB - Yersinia enterocolitica emb CAA88185.1 [Z48169] flhB [Yersinia enterocolitica] Length = 383
SEQ ID n°2403	Prot n°PL-3157.2	Contig32	165064	166752		
SEQ ID n°2404	Prot n°PL-3158.1	Contig22	3506	4747	31%	Identities = 77/223 (34%), Positives = 132/223 (59%), Gaps = 3/223 (1%) gb AAF89876.1 (AF173869) putative site-specific recombinase XerD [Staphylococcus aureus] Length = 295
SEQ ID n°2405	Prot n°PL-3159.1	Contig22	283	3630	17%	Identities = 108/406 (26%), Positives = 190/406 (46%), Gaps = 50/406 (12%) sp P47762 PRIM_LISMO DNA PRIMASE gb AAC43305.1 (U13165) DNA primase [Listeria monocytogenes] pir J2104269B DNA primase [Listeria monocytogenes] Length = 626
SEQ ID n°2406	Prot n°PL-316.1	Contig41	550259	550918	No Hits found	
SEQ ID n°2407	Prot n°PL-3160.1	Contig23	2209	5187	11%	Identities = 77/264 (29%), Positives = 115/264 (43%), Gaps = 38/264 (14%) sp O67465 PRIM_AQUAE DNA PRIMASE pir G70429 DNA primase - Aquifex aeolicus gb AAC07430.1 (AE000743) DNA primase [Aquifex aeolicus] Length = 498
SEQ ID n°2408	Prot n°PL-3161.1	Contig23	826	2208	57%	Identities = 208/489 (42%), Positives = 269/489 (54%), Gaps = 47/489 (9%) pdb 1F31 A Chain A, Crystal Structure Of Tn5 Transposase Complexed With Transposon End Dna Length = 481
SEQ ID n°2409	Prot n°PL-3162.1	Contig28	18955	20379	22%	Identities = 75/200 (37%), Positives = 108/200 (52%), Gaps = 45/200 (22%) db BAA76527.2 (AB017338) tail fiber [Pectobacterium carotovorum] Length = 667
SEQ ID n°2410	Prot n°PL-3163.1	Contig28	17747	18520	17%	Identities = 39/94 (41%), Positives = 44/94 (46%), Gaps = 7/94 (7%) ref NP_037718.1 tail fiber gb AAF31111.1 (AF089528) tail fiber [Bacteriophage HK97] Length = 321
SEQ ID n°2411	Prot n°PL-3164.1	Contig28	16626	17228	27%	Identities = 37/103 (35%), Positives = 55/103 (52%), Gaps = 9/103 (8%) db BAB03228.1 (AB046380) tail fiber protein [Pseudomonas aeruginosa] Length = 701
SEQ ID n°2412	Prot n°PL-3165.1	Contig28	14592	15512	15%	Identities = 33/98 (33%), Positives = 48/98 (48%), Gaps = 5/98 (5%) db BAA36247.1 (AB008550) orf20; similar to H gene of P2 [Pseudomonas aeruginosa phage phi CTX] Length = 762 "
SEQ ID n°2413	Prot n°PL-3166.1	Contig28	12549	13616	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°2414	Prot n°PL-3167.1	Contig28	11019	11846	28%	Identities = 59/112 (52%), Positives = 78/112 (68%), Gaps = 8/112 (7%) ref NP_046925.1 gp30 pir T13116 protein gp30 - phage N15 gb AAC19072.1 (AF064539) gp30 [Bacteriophage N15] Length = 264
SEQ ID n°2415	Prot n°PL-3168.1	Contig28	8614	9807	44%	Identities = 110/403 (27%), Positives = 177/403 (43%), Gaps = 48/403 (11%) db BAA75916.1 (AB024602) similar to integrase [Pseudomonas putida] Length = 389

TABLEAU I

SEQ ID n°2416	Prot n°PL-3169.1	Contig28	6661	7306	49%	Identities = 75/189 (39%), Positives = 110/189 (57%), Gaps = 22/189 (11%) gb AAF72345.1 AF192329.6 (AF192329) Muni-like protein [Enterococcus faecalis] Length = 180
SEQ ID n°2417	Prot n°PL-317.1	Contig41	549690	551321	38%	Identities = 124/472 (26%), Positives = 210/472 (44%), Gaps = 28/472 (5%) gb AAG05045.1 AE004593.7 (AE004593) hypothetical protein [Pseudomonas aeruginosa] Length = 518
SEQ ID n°2418	Prot n°PL-3170.1	Contig28	5326	5997	No Hits found	Identities = 158/223 (70%), Positives = 188/223 (83%) pdb 1AVQ A Chain A, Toroidal Structure Of Lambda Exonuclease Determined At 2.4
SEQ ID n°2419	Prot n°PL-3171.1	Contig28	3609	4292	82%	Angstroms pdb 1AVQ B Chain B, Toroidal Structure Of Lambda Exonuclease Determined At 2.4 Angstroms pdb 1AVQ C Chain C, Toroidal Structure Of Lambda Exonuclease Determined At 2.4 Angstroms Length = 67/228 (29%), Positives = 106/228 (46%), Gaps = 23/228 (10%)
SEQ ID n°2420	Prot n°PL-3172.1	Contig28	2655	3608	33%	Identities = 67/228 (29%), Positives = 106/228 (46%), Gaps = 23/228 (10%) ref NP_049474.1 Bet protein gb AAD25419.1 AF125520.14 (AF125520) Bet protein [Bacteriophage 933W] Length = 261
SEQ ID n°2421	Prot n°PL-3173.1	Contig28	1141	2043	58%	Identities = 131/355 (36%), Positives = 177/355 (48%), Gaps = 56/355 (15%) ref NP_061549.1 Orf53 gb AAF80812.1 (AF165214) Orf53 [Pseudomonas phage D3] Length = 354
SEQ ID n°2422	Prot n°PL-3174.1	Contig33	14457	15293	58%	Identities = 127/278 (45%), Positives = 180/278 (64%), Gaps = 1/278 (0%) pir H65028 probable thiosulfate sulfurtransferase (EC 2.8.1.1) - Escherichia coli (strain K-12) gb AAC75574.1 (AE000338) putative thiosulfate sulfurtransferase [Escherichia coli] Length = 334
SEQ ID n°2423	Prot n°PL-3175.1	Contig33	11914	14061	76%	Identities = 462/698 (66%), Positives = 552/698 (78%), Gaps = 1/698 (0%) spiP27296 DING_ECOLI PROBABLE ATP-DEPENDENT HELICASE DING (DNA-DAMAGE-INDUCIBLE PROTEIN G) pir G64816 probable ATP-dependent helicase dinG - Escherichia coli gb AAA53655.1 (L02123) DNA helicase [Escherichia coli] dbj BAA36465.1 (D90717) Probable ATP-dependent helicase ding (DNA-damage-inducible protein G). [Escherichia coli] gb AAC73886.1 (AE000182) probably ATP-dependent helicase [Escherichia coli] Length = 716
SEQ ID n°2424	Prot n°PL-3176.1	Contig33	11006	11914	82%	Identities = 239/293 (81%), Positives = 267/293 (90%) spiP30864 YAF_C ECOLI HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN ASPU-MLTD INTERGENIC REGION (ORF304) pir JS0716 probable transcription regulator yafC - Escherichia coli dbj BAA02171.1 (D12650) ORF304 [Escherichia coli] gb AAB08630.1 (U70214) hypothetical [Escherichia coli] gb AAC73313.1 (AE000129) putative transcriptional regulator LYSR-type [Escherichia coli] dbj BAA77879.1 (D83536) Hypothetical transcriptional regulator in aspU-dnrR intergenic region (orf304). [Escherichia coli] Length = 304

TABLEAU I

SEQ ID n°2425	Prot n°PL-3177.1	Contig33	9760	10872	81%	Identities = 256/367 (69%), Positives = 304/367 (82%) gb AAG04723.1 AE004562_10 (AE004562) probable oxidoreductase [Pseudomonas aeruginosa] Length = 370
SEQ ID n°2426	Prot n°PL-3178.1	Contig33	8691	9497	85%	Identities = 210/267 (78%), Positives = 236/267 (87%) pir A64745 probable aldehyde reductase (EC 1.1.1.-) yafB - Escherichia coli (strain K-12) gb AA08629.1 U70214) hypothetical [Escherichia coli] gb AAC73312.1 (AE000129) putative aldose reductase (EC 1.1.1.21) [Escherichia coli] Length = 267
SEQ ID n°2427	Prot n°PL-3179.1	Contig33	6680	7573	55%	Identities = 126/286 (44%), Positives = 174/286 (60%), Gaps = 1/286 (0%) gb AAF13753.1 AF117351_10 (AF117351) dihydrodipicolinate synthetase [Zymomonas mobilis] Length = 288
SEQ ID n°2428	Prot n°PL-318.1	Contig41	551454	552224	No Hits found	Identities = 70/270 (25%), Positives = 122/270 (44%), Gaps = 16/270 (5%) pir D69790 probable halide peroxidase (EC 1.11.1.-) ydJP - Bacillus subtilis dbj BAA22772.1 (AB007638) peroxidase [Bacillus subtilis] emb CAB12447.1 (Z99107) similar to arylesterase [Bacillus subtilis] Length = 271
SEQ ID n°2430	Prot n°PL-3181.1	Contig33	4832	5660	37%	Identities = 54/170 (31%), Positives = 91/170 (52%), Gaps = 1/170 (0%) pir D70329 hypothetical protein aq_327 - Aquifex aeolicus gb AAC06628.1 (AE000684) putative protein [Aquifex aeolicus] Length = 256
SEQ ID n°2431	Prot n°PL-3182.1	Contig33	2500	3405	77%	Identities = 184/284 (64%), Positives = 233/284 (81%), Gaps = 2/284 (0%) pir E64818 probable membrane protein ybIF - Escherichia coli gb AAC73900.1 (AE000183) putative transmembrane subunit [Escherichia coli] dbj BAA35485.1 (D90718) Hypothetical protein 1 [Escherichia coli] dbj BAA35495.1 (D90719) Hypothetical protein 1 [Escherichia coli] Length = 295
SEQ ID n°2432	Prot n°PL-3183.1	Contig33	1269	1832	74%	Identities = 118/184 (64%), Positives = 151/184 (81%) (AP001517) unknown conserved protein [Bacillus halodurans] Length = 187
SEQ ID n°2433	Prot n°PL-3184.1	Contig41	1100879	1101527	73%	Identities = 161/279 (57%), Positives = 210/279 (74%), Gaps = 3/279 (1%) gb AAF33488.1 (AF233324) 83% identity with E. coli hypothetical protein (YIFA) (SP:P22788) and 95% identity with amino acids 1-80 of E. coli possible regulatory protein (PSSR) (SP:P27826) [Salmonella typhimurium LT2] Length = 282
SEQ ID n°2434	Prot n°PL-3185.1	Contig41	1098657	1100180	77%	Identities = 319/510 (62%), Positives = 405/510 (78%), Gaps = 1/510 (0%) pir S30663 hypothetical protein f516 - Escherichia coli gb AA67569.1 (M87049) similar to Mg chelatase subunit of Rhodobacter capsulata [Escherichia coli] Length = 516
SEQ ID n°2435	Prot n°PL-3186.1	Contig21	1005	2033	No Hits found	
SEQ ID n°2436	Prot n°PL-3187.1	Contig21	2	712	No Hits found	
SEQ ID n°2437	Prot n°PL-3188.1	Contig20	1125	1811	No Hits found	

TABLEAU I

SEQ ID n°2438	Prot n°PL-3189.1	Contig19	5493	6254	88%	Identities = 216/237 (91%), Positives = 226/237 (95%) gblAAB58155.1 (U82621) hypothetical protein [Shigella flexneri] Length = 272
SEQ ID n°2439	Prot n°PL-319.1	Contig41	552408	553418	No Hits found	Identities = 61/68 (89%), Positives = 63/68 (91%) embICAB54974.1 (AL117189) putative transposase [Yersinia pestis] Length = 308
SEQ ID n°2440	Prot n°PL-3190.1	Contig19	3633	4619	19%	Identities = 229/391 (58%), Positives = 284/391 (72%), Gaps = 3/391 (0%) spIP19780YIS1_STRCO INSERTION ELEMENT IS110 HYPOTHETICAL 43.6 KDA PROTEIN pirJA26848 probable transposase/integrase - Streptomyces coelicolor transposon IS110 embICAA19602.1 (AL023861) putative IS110 transposase/integrase [Streptomyces coelicolor A3(2)] embICAB51528.1 (Y00434) major ORF 1215 (AA 1-420) [Streptomyces coelicolor A3(2)] embICAB66288.1 (AL136519) probable transposase. [Streptomyces coelicolor A3(2)] Length = 405
SEQ ID n°2441	Prot n°PL-3191.1	Contig19	2346	3542	69%	Identities = 314/321 (97%), Positives = 318/321 (97%) pirJT14972 probable transposase a - Yersinia pestis plasmid pMT1 gblAAC44981.1 (U59875) ORFA; putative transposase [Yersinia pestis] gblAAC62541.1 (AF053945) transposase [Yersinia pestis] gblAAC62546.1 (AF053946) transposase [Yersinia pestis] gblAAC13168.1 (AF053947) putative transposase [Yersinia pestis] gblAAC82715.1 (AF074811) IS transposase [Yersinia pestis] gblAAC82751.1 (AF074611) transposase [Yersinia pestis] embICAA21335.1 (AL031866) ORF12, len: 340 aa, IS100, identical to YPU59875.1 Yersinia pestis, transposase embICAA21403.1 (AL031868) ORF 78, len=340 aa, IS 100, probable transposase, 100.0% identity in 340 aa overlap, with YPU59875_1 Y. pestis pesticin plasmid (340 aa), Fast scores: opt: 2328, E0: 0 [Yersinia pestis] embICAB46599.1 (AJ236887) IS100 transposase [Yersinia pseudotuberculosis] embICAB53164.1 (AL109969) putative transposase [Yersinia pestis] embICAB54878.1 (AL117189) putative
SEQ ID n°2442	Prot n°PL-3192.1	Contig19	1150	2154	90%	
SEQ ID n°2443	Prot n°PL-3193.1	Contig18	2675	3349	No Hits found	Identities = 29/100 (29%), Positives = 51/100 (51%), Gaps = 9/100 (9%) gblAAC32470.1 (AF044501) unknown [Escherichia coli] Length = 150
SEQ ID n°2444	Prot n°PL-3194.1	Contig18	1578	2249	22%	Identities = 58/181 (32%), Positives = 77/181 (42%), Gaps = 20/181 (11%) gblAAC98393.1 (M17282) elastin [Homo sapiens] Length = 687
SEQ ID n°2445	Prot n°PL-3195.1	Contig18	681	1301	32%	
SEQ ID n°2446	Prot n°PL-3196.1	Contig17	5245	6303	No Hits found	Identities = 82/205 (40%), Positives = 112/205 (54%), Gaps = 13/205 (6%) dbjBAA84884.1 (AB024946) orf29 [Escherichia coli] dbjBAA84884.1 (AB024946) orf49 [Escherichia coli] Length = 216
SEQ ID n°2447	Prot n°PL-3197.1	Contig17	4033	4719	48%	Identities = 231/340 (67%), Positives = 267/340 (77%) dbjBAA84886.1 (AB024946) orf51 [Escherichia coli] Length = 523
SEQ ID n°2448	Prot n°PL-3198.1	Contig17	2093	3241	69%	

TABLEAU I

SEQ ID n°2448	Prot n°PL-3199.1	Contig30	96292	97275	44%	Identities = 79/310 (25%), Positives = 145/310 (46%), Gaps = 19/310 (6%) gb AAC38751.1 (AF030373) galactosyl transferase [Streptococcus pneumoniae] gb AAC69531.1 (AF057294) Cps23H [Streptococcus pneumoniae] Length = 323
SEQ ID n°2450	Prot n°PL-32.1	Contig41	59016	60209	61%	Identities = 185/346 (53%), Positives = 245/346 (70%), Gaps = 2/346 (0%) gb AAC46212.1 (AF035922) PepB [Pseudomonas aeruginosa] Length = 390
SEQ ID n°2451	Prot n°PL-320.1	Contig41	553979	555361	57%	Identities = 206/489 (42%), Positives = 269/489 (54%), Gaps = 47/489 (9%) pdb 1F3 A Chain A, Crystal Structure Of Tn5 Transposase Complexed With Transposon End Dna Length = 481
SEQ ID n°2452	Prot n°PL-3200.1	Contig30	95325	96188	37%	Identities = 62/212 (29%), Positives = 108/212 (50%), Gaps = 20/212 (9%) gb AAB49823.1 (U58147) LOS biosynthesis enzyme LBG [Haemophilus ducreyi] gb AAC45592.1 (AF004712) LosA [Haemophilus ducreyi] Length = 224
SEQ ID n°2453	Prot n°PL-3201.1	Contig30	94395	95174	No Hits found	Identities = 77/196 (39%), Positives = 116/196 (58%), Gaps = 2/196 (1%) ref NP_037719.1 Gp29 gb AAF31112.1 (AF066529) Gp28 [Bacteriophage HK97] Length = 202
SEQ ID n°2454	Prot n°PL-3202.1	Contig30	91429	92076	53%	Identities = 54/214 (25%), Positives = 94/214 (43%), Gaps = 9/214 (4%) gb AAG04736.1 (AE004564_5) (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°2455	Prot n°PL-3203.1	Contig16	4668	5351	41%	Identities = 61/225 (27%), Positives = 102/225 (45%), Gaps = 11/225 (4%) gb AAF96971.1 (AE004433) transcriptional regulator, LuxR family [Vibrio cholerae] Length = 319
SEQ ID n°2456	Prot n°PL-3204.1	Contig16	3749	4510	40%	Identities = 56/208 (26%), Positives = 93/208 (43%), Gaps = 9/208 (4%) gb AAG04736.1 (AE004564_5) (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°2457	Prot n°PL-3205.1	Contig16	3102	3800	39%	Identities = 58/212 (27%), Positives = 98/212 (45%), Gaps = 16/212 (7%) gb AAF96971.1 (AE004433) transcriptional regulator, LuxR family [Vibrio cholerae] Length = 319
SEQ ID n°2458	Prot n°PL-3206.1	Contig16	2328	3089	38%	Identities = 60/219 (27%), Positives = 98/219 (44%), Gaps = 10/219 (4%) gb AAF96971.1 (AE004433) transcriptional regulator, LuxR family [Vibrio cholerae] Length = 319
SEQ ID n°2459	Prot n°PL-3207.1	Contig16	1681	2379	42%	Identities = 55/208 (26%), Positives = 97/208 (46%), Gaps = 9/208 (4%) gb AAG04736.1 (AE004564_5) (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°2460	Prot n°PL-3208.1	Contig16	940	1668	39%	Identities = 56/216 (25%), Positives = 94/216 (42%), Gaps = 10/216 (4%) gb AAG04736.1 (AE004564_5) (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°2461	Prot n°PL-3209.1	Contig16	2	727	38%	
SEQ ID n°2462	Prot n°PL-321.1	Contig41	555362	555978	No Hits found	
SEQ ID n°2463	Prot n°PL-3210.1	Contig15	613	1404	No Hits found	

TABLEAU I

SEQ ID n°2464	Prot n°PL-3211.1	Contig15	1	939	15%	Identities = 38/69 (55%), Positives = 47/69 (68%) gb AAF84988.1 AE004032.7 (AE004032) hypothetical protein [Xylella fastidiosa] Length = 109
SEQ ID n°2465	Prot n°PL-3212.1	Contig10	224	1966	96%	Identities = 579/580 (99%), Positives = 579/580 (99%) sp P18011 JPAB_SHIFL 62 KD MEMBRANE ANTIGEN pIr A34965 62K membrane antigen ipaB - Shigella flexneri plasmid gb AA98424.1 (M34849) antigen [Plasmid pWR100] Length = 580
SEQ ID n°2466	Prot n°PL-3213.2	Contig37	372	2042		Identities = 217/217 (100%), Positives = 217/217 (100%) sp Q04641 MXID_SHIFL OUTER MEMBRANE PROTEIN MXID PRECURSOR pIr S28068 mxID protein - Shigella flexneri emb CAA47644.1 (X67206) MXID [Shigella flexneri] Length = 586
SEQ ID n°2467	Prot n°PL-3214.1	Contig9	1309	1959	100%	Identities = 198/329 (60%), Positives = 245/329 (74%) db BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] Length = 345
SEQ ID n°2468	Prot n°PL-3215.2	Contig40	694820	695464	72%	
SEQ ID n°2469	Prot n°PL-3216.1	Contig40	695583	696596		
SEQ ID n°2470	Prot n°PL-3217.1	Contig41	1204850	1205437		
SEQ ID n°2471	Prot n°PL-3218.1	Contig41	1199341	1199835		
SEQ ID n°2472	Prot n°PL-3219.1	Contig41	1198640	1199098		
SEQ ID n°2473	Prot n°PL-322.1	Contig41	555967	558615	No Hits found	
SEQ ID n°2474	Prot n°PL-3220.1	Contig41	1193210	1193617		
SEQ ID n°2475	Prot n°PL-3221.1	Contig41	1190186	1190874		
SEQ ID n°2476	Prot n°PL-3222.1	Contig41	1180385	1180894		
SEQ ID n°2477	Prot n°PL-3223.1	Contig41	1177349	1177789		
SEQ ID n°2478	Prot n°PL-3225.1	Contig41	1161137	1161718		
SEQ ID n°2479	Prot n°PL-3227.1	Contig41	1148528	1149076		
SEQ ID n°2480	Prot n°PL-3228.1	Contig41	1138286	1138861		
SEQ ID n°2481	Prot n°PL-3229.1	Contig41	1131575	1132051		
SEQ ID n°2482	Prot n°PL-323.1	Contig41	560569	561261	34%	Identities = 55/199 (27%), Positives = 79/199 (39%), Gaps = 7/198 (3%) gb AAG21430.1 AC008054_1 (AC008054) L8453.1 [Leishmania major] Length = 1514
SEQ ID n°2483	Prot n°PL-3231.1	Contig41	1126676	1127158		
SEQ ID n°2484	Prot n°PL-3232.1	Contig41	1124878	1125415		
SEQ ID n°2485	Prot n°PL-3234.1	Contig41	1122706	1123206		
SEQ ID n°2486	Prot n°PL-3235.1	Contig41	1117536	1118093		
SEQ ID n°2487	Prot n°PL-3236.1	Contig41	1117027	1117443		
SEQ ID n°2488	Prot n°PL-3237.1	Contig41	1112133	1112645		
SEQ ID n°2489	Prot n°PL-3238.1	Contig41	1109727	1110296		
SEQ ID n°2490	Prot n°PL-3239.1	Contig41	1108115	1108660		
SEQ ID n°2491	Prot n°PL-324.1	Contig41	562366	563049	31%	Identities = 53/194 (27%), Positives = 71/194 (36%), Gaps = 12/194 (6%) gb AAG21430.1 AC008054_1 (AC008054) L8453.1 [Leishmania major] Length = 1514
SEQ ID n°2492	Prot n°PL-3240.1	Contig41	1102357	1102812		

TABLEAU I

SEQ ID n°2532	Prot n°PL-3284.1	Contig41	719748	720167	
SEQ ID n°2533	Prot n°PL-3285.1	Contig41	709165	709755	
SEQ ID n°2534	Prot n°PL-3286.1	Contig41	699529	699951	
SEQ ID n°2535	Prot n°PL-3287.1	Contig41	689918	690310	
SEQ ID n°2536	Prot n°PL-3288.1	Contig41	658505	658963	
SEQ ID n°2537	Prot n°PL-3289.1	Contig41	645448	645816	
SEQ ID n°2538	Prot n°PL-329.1	Contig41	566664	567683	No Hits found
SEQ ID n°2539	Prot n°PL-3291.1	Contig41	635989	636513	
SEQ ID n°2540	Prot n°PL-3293.1	Contig41	608416	608886	
SEQ ID n°2541	Prot n°PL-3294.1	Contig41	606481	606894	
SEQ ID n°2542	Prot n°PL-3295.1	Contig41	606066	606512	
SEQ ID n°2543	Prot n°PL-3296.1	Contig41	595900	596355	
SEQ ID n°2544	Prot n°PL-3297.1	Contig41	589581	590141	
SEQ ID n°2545	Prot n°PL-33.1	Contig41	60694	61614	67%
Identities = 161/319 (50%), Positives = 228/319 (71%), Gaps = 20/319 (6%) sp P21206 LCRV_YERPE VIRULENCE-ASSOCIATED V ANTIGEN (LOW CALCIUM RESPONSE LOCUS PROTEIN V) pir B33601 lcrV protein - Yersinia pestis Length = 326					
SEQ ID n°2546	Prot n°PL-330.1	Contig41	567671	570325	No Hits found
SEQ ID n°2547	Prot n°PL-3301.1	Contig41	558674	559165	
SEQ ID n°2548	Prot n°PL-3302.1	Contig41	546288	546824	
SEQ ID n°2549	Prot n°PL-3304.1	Contig41	543739	544143	
SEQ ID n°2550	Prot n°PL-3306.1	Contig41	513631	514110	
SEQ ID n°2551	Prot n°PL-3307.1	Contig41	513055	513522	
SEQ ID n°2552	Prot n°PL-3308.1	Contig41	512479	512946	
SEQ ID n°2553	Prot n°PL-3309.1	Contig41	511910	512371	
SEQ ID n°2554	Prot n°PL-331.1	Contig41	570271	571314	No Hits found
SEQ ID n°2555	Prot n°PL-3310.1	Contig41	511333	511800	
SEQ ID n°2556	Prot n°PL-3311.1	Contig41	510774	511241	
SEQ ID n°2557	Prot n°PL-3312.1	Contig41	510198	510665	
SEQ ID n°2558	Prot n°PL-3319.1	Contig41	492247	492675	
SEQ ID n°2559	Prot n°PL-332.1	Contig41	571322	573712	41%
Identities = 209/746 (28%), Positives = 333/746 (44%), Gaps = 53/746 (7%) gb AAG04900.1 AE004579_12 (AE004579) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 842					
SEQ ID n°2560	Prot n°PL-3320.1	Contig41	490277	490705	
SEQ ID n°2561	Prot n°PL-3321.1	Contig41	489717	490028	
SEQ ID n°2562	Prot n°PL-3322.1	Contig41	488035	488538	
SEQ ID n°2563	Prot n°PL-3324.1	Contig41	457730	458218	
SEQ ID n°2564	Prot n°PL-3325.1	Contig41	451168	451734	
SEQ ID n°2565	Prot n°PL-3326.1	Contig41	450628	450942	
SEQ ID n°2566	Prot n°PL-3327.1	Contig41	438252	438683	
SEQ ID n°2567	Prot n°PL-3328.1	Contig41	436090	436683	

TABLEAU I

SEQ ID n°2568	Prot n°PL-3329.1	Contig41	433169	433651		
SEQ ID n°2568	Prot n°PL-333.1	Contig41	573697	576378	60%	Identities = 414/870 (47%), Positives = 545/870 (62%), Gaps = 48/870 (5%) gb AAG05759.1 AE004663_5 (AE004663) probable CipA/B-type protease [Pseudomonas aeruginosa] Length = 849
SEQ ID n°2570	Prot n°PL-3331.1	Contig41	392044	392514		
SEQ ID n°2571	Prot n°PL-3332.1	Contig41	391562	392014		
SEQ ID n°2572	Prot n°PL-3333.1	Contig41	387136	387624		
SEQ ID n°2573	Prot n°PL-3334.1	Contig41	386383	386970		
SEQ ID n°2574	Prot n°PL-3335.1	Contig41	378263	378727		
SEQ ID n°2575	Prot n°PL-3336.1	Contig41	374147	374701		
SEQ ID n°2576	Prot n°PL-3337.1	Contig41	370477	371013		
SEQ ID n°2577	Prot n°PL-3339.1	Contig41	366405	366815		
SEQ ID n°2578	Prot n°PL-334.1	Contig41	576627	578375	11%	Identities = 461/117 (39%), Positives = 681/117 (57%), Gaps = 1/117 (0%) gb AAF83163.1 AE003886_12 (AE003886) outer membrane protein [Xylella fastidiosa] Length = 389
SEQ ID n°2579	Prot n°PL-3340.1	Contig41	364530	365009		
SEQ ID n°2580	Prot n°PL-3341.1	Contig41	361360	361905		
SEQ ID n°2581	Prot n°PL-3342.1	Contig41	360813	361391		
SEQ ID n°2582	Prot n°PL-3343.1	Contig41	360229	360792		
SEQ ID n°2583	Prot n°PL-3345.1	Contig41	355908	358414		
SEQ ID n°2584	Prot n°PL-3347.1	Contig41	350347	350892		
SEQ ID n°2585	Prot n°PL-3348.1	Contig41	342619	343191		
SEQ ID n°2586	Prot n°PL-335.1	Contig41	578320	578973	36%	Identities = 47/185 (25%), Positives = 79/185 (42%), Gaps = 21/185 (11%) gb AAF96029.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 257
SEQ ID n°2587	Prot n°PL-3350.1	Contig41	337003	337464		
SEQ ID n°2588	Prot n°PL-3351.1	Contig41	335556	336071		
SEQ ID n°2589	Prot n°PL-3352.1	Contig41	335130	335504		
SEQ ID n°2590	Prot n°PL-3353.1	Contig41	322852	323442		
SEQ ID n°2591	Prot n°PL-3354.1	Contig41	305869	308402		
SEQ ID n°2592	Prot n°PL-3356.1	Contig41	275344	275757		
SEQ ID n°2593	Prot n°PL-3357.1	Contig41	266008	266670		
SEQ ID n°2594	Prot n°PL-3358.1	Contig41	261474	261962		
SEQ ID n°2595	Prot n°PL-3359.1	Contig41	246558	247097		
SEQ ID n°2596	Prot n°PL-336.1	Contig41	578007	580509	41%	Identities = 133/450 (29%), Positives = 206/450 (45%), Gaps = 18/450 (4%) gb AAG03469.1 AE004447_2 (AE004447) hypothetical protein [Pseudomonas aeruginosa] Length = 444
SEQ ID n°2597	Prot n°PL-3361.1	Contig41	228973	229461		
SEQ ID n°2598	Prot n°PL-3365.1	Contig41	204716	205165		
SEQ ID n°2599	Prot n°PL-3366.1	Contig41	203005	203475		
SEQ ID n°2600	Prot n°PL-3367.1	Contig41	200988	201479		

TABLEAU I

SEQ ID n°2601	Prot n°PL-3368.1	Contig41	199204	199677		
SEQ ID n°2602	Prot n°PL-3369.1	Contig41	198542	199066		
SEQ ID n°2603	Prot n°PL-337.1	Contig41	580385	581917	57%	Identities = 203/451 (45%), Positives = 294/451 (65%), Gaps = 5/451 (1%) gb AAAF96022.1 (AE004353) conserved hypothetical protein [Vibrio cholerae] Length = 492
SEQ ID n°2604	Prot n°PL-3370.1	Contig41	191123	191614		
SEQ ID n°2605	Prot n°PL-3371.1	Contig41	170926	171300		
SEQ ID n°2606	Prot n°PL-3372.1	Contig41	167964	168425		
SEQ ID n°2607	Prot n°PL-3373.1	Contig41	160873	161319		
SEQ ID n°2608	Prot n°PL-3374.1	Contig41	151659	152407		
SEQ ID n°2609	Prot n°PL-3375.1	Contig41	150416	150931		
SEQ ID n°2610	Prot n°PL-3376.1	Contig41	149555	150097		
SEQ ID n°2611	Prot n°PL-3377.1	Contig41	148860	149411		
SEQ ID n°2612	Prot n°PL-3378.1	Contig41	128307	128783		
SEQ ID n°2613	Prot n°PL-3379.1	Contig41	122841	123296		
SEQ ID n°2614	Prot n°PL-338.1	Contig41	583544	584785	43%	Identities = 108/375 (28%), Positives = 182/375 (47%), Gaps = 8/375 (2%) gb AAF63418.1 (AF146029) putative multidrug-resistance protein [Aeromonas hydrophila] Length = 409
SEQ ID n°2615	Prot n°PL-3380.1	Contig41	106583	107113		
SEQ ID n°2616	Prot n°PL-3381.1	Contig41	105208	105702		
SEQ ID n°2617	Prot n°PL-3382.1	Contig41	92363	92812		
SEQ ID n°2618	Prot n°PL-3384.1	Contig41	76407	76829		
SEQ ID n°2619	Prot n°PL-3385.1	Contig41	68438	68899		
SEQ ID n°2620	Prot n°PL-3386.1	Contig41	60181	60684		
SEQ ID n°2621	Prot n°PL-3387.1	Contig41	53256	53705		
SEQ ID n°2622	Prot n°PL-3388.1	Contig41	52835	53167		
SEQ ID n°2623	Prot n°PL-3389.1	Contig41	39379	39687		
SEQ ID n°2624	Prot n°PL-339.1	Contig41	585115	586110	19%	Identities = 39/109 (35%), Positives = 65/109 (58%), Gaps = 7/109 (6%) gb AAG06749.1 AE004758_6 (AE004758) hypothetical protein [Pseudomonas aeruginosa] Length = 115
SEQ ID n°2625	Prot n°PL-3390.1	Contig41	29298	29864		
SEQ ID n°2626	Prot n°PL-3391.1	Contig41	8498	8968		
SEQ ID n°2627	Prot n°PL-3392.1	Contig41	5668	6061		
SEQ ID n°2628	Prot n°PL-3396.1	Contig40	670291	670770		
SEQ ID n°2629	Prot n°PL-3397.1	Contig40	666355	666834		
SEQ ID n°2630	Prot n°PL-34.1	Contig41	62370	64487	88%	Identities = 580/700 (82%), Positives = 647/700 (91%), Gaps = 2/700 (0%) dbj BAA01770.1 (D10998) low calcium response protein [Yersinia enterocolitica] Length = 704
SEQ ID n°2631	Prot n°PL-340.1	Contig41	586488	587531	18%	Identities = 39/109 (35%), Positives = 86/109 (59%), Gaps = 7/109 (6%) gb AAG06749.1 AE004758_6 (AE004758) hypothetical protein [Pseudomonas aeruginosa] Length = 115

TABLEAU I

SEQ ID n°2632	Prot n°PL-3404.1	Contig40	601533	601961		
SEQ ID n°2633	Prot n°PL-3405.1	Contig40	599074	599553		
SEQ ID n°2634	Prot n°PL-3406.1	Contig40	598440	598964		
SEQ ID n°2635	Prot n°PL-3407.1	Contig40	584845	585351		
SEQ ID n°2636	Prot n°PL-3408.1	Contig40	563229	563780		
SEQ ID n°2637	Prot n°PL-341.1	Contig41	588071	589519	68%	Identities = 258/484 (53%), Positives = 334/484 (68%), Gaps = 6/484 (1%) pir G70852 hypothetical protein Rv3083 - Mycobacterium tuberculosis (strain H37RV) emb CAA16141.1 (AL021309) hypothetical protein Rv3083 [Mycobacterium tuberculosis] Length = 495
SEQ ID n°2638	Prot n°PL-3410.1	Contig40	550444	550980		
SEQ ID n°2639	Prot n°PL-3414.1	Contig40	502951	503490		
SEQ ID n°2640	Prot n°PL-3415.1	Contig40	495630	496142		
SEQ ID n°2641	Prot n°PL-3416.1	Contig40	495066	495578		
SEQ ID n°2642	Prot n°PL-342.1	Contig41	591527	592537	66%	Identities = 163/337 (48%), Positives = 231/337 (68%), Gaps = 28/337 (8%) gb AAAF81206.1 AF247502.1 (AF247502) Y12 [Salmonella dublin] Length = 316
SEQ ID n°2643	Prot n°PL-3420.1	Contig40	475396	475908		
SEQ ID n°2644	Prot n°PL-3421.1	Contig40	474832	475344		
SEQ ID n°2645	Prot n°PL-3422.1	Contig40	474265	474780		
SEQ ID n°2646	Prot n°PL-3423.1	Contig40	473240	473611		
SEQ ID n°2647	Prot n°PL-3427.1	Contig40	458185	458676		
SEQ ID n°2648	Prot n°PL-343.1	Contig41	593276	594241	22%	Identities = 44/108 (40%), Positives = 71/108 (65%), Gaps = 2/108 (1%) gb AAG06749.1 AE004758.6 (AE004758) hypothetical protein [Pseudomonas aeruginosa] Length = 115
SEQ ID n°2649	Prot n°PL-3431.1	Contig40	450004	450501		
SEQ ID n°2650	Prot n°PL-3433.1	Contig40	429509	429991		
SEQ ID n°2651	Prot n°PL-3434.1	Contig40	417222	417743		
SEQ ID n°2652	Prot n°PL-3435.1	Contig40	414582	415076		
SEQ ID n°2653	Prot n°PL-3437.1	Contig40	373475	373996		
SEQ ID n°2654	Prot n°PL-3438.1	Contig40	372151	372597		
SEQ ID n°2655	Prot n°PL-3439.1	Contig40	371759	372271		
SEQ ID n°2656	Prot n°PL-344.1	Contig41	594560	595354	No Hits found	
SEQ ID n°2657	Prot n°PL-3440.1	Contig40	365377	365847		
SEQ ID n°2658	Prot n°PL-3442.1	Contig40	358247	358747		
SEQ ID n°2659	Prot n°PL-3444.1	Contig40	342238	342702		
SEQ ID n°2660	Prot n°PL-3445.1	Contig40	340017	340586		
SEQ ID n°2661	Prot n°PL-3446.1	Contig40	335541	336014		
SEQ ID n°2662	Prot n°PL-3447.1	Contig40	335098	335616		
SEQ ID n°2663	Prot n°PL-3448.1	Contig40	332740	333333		
SEQ ID n°2664	Prot n°PL-3449.1	Contig40	329076	329609		
SEQ ID n°2665	Prot n°PL-345.1	Contig41	596856	597773	No Hits found	

TABLEAU I

SEQ ID n°2666	Prot n°PL-3450.1	Contig40	320122	320852		
SEQ ID n°2667	Prot n°PL-3451.1	Contig40	315837	316427		
SEQ ID n°2668	Prot n°PL-3452.1	Contig40	312610	313173		
SEQ ID n°2669	Prot n°PL-3453.1	Contig40	308604	309038		
SEQ ID n°2670	Prot n°PL-3454.1	Contig40	307985	308447		
SEQ ID n°2671	Prot n°PL-3455.1	Contig40	301635	301915		
SEQ ID n°2672	Prot n°PL-3456.1	Contig40	300301	300918		
SEQ ID n°2673	Prot n°PL-3457.1	Contig40	298759	299223		
SEQ ID n°2674	Prot n°PL-3458.1	Contig40	295173	295610		
SEQ ID n°2675	Prot n°PL-3459.1	Contig40	292337	292785		
SEQ ID n°2676	Prot n°PL-346.1	Contig41	598062	599756	24%	Identities = 94/368 (25%), Positives = 136/368 (36%), Gaps = 67/368 (18%) p rl A40774 phosphocholine-binding protein - Atlantic horseshoe crab Length = 484
SEQ ID n°2677	Prot n°PL-3460.1	Contig40	290046	290522		
SEQ ID n°2678	Prot n°PL-3461.1	Contig40	283108	283620		
SEQ ID n°2679	Prot n°PL-3462.1	Contig40	281174	281746		
SEQ ID n°2680	Prot n°PL-3463.1	Contig40	280848	281097		
SEQ ID n°2681	Prot n°PL-3464.1	Contig40	279291	279836		
SEQ ID n°2682	Prot n°PL-3465.1	Contig40	278690	279247		
SEQ ID n°2683	Prot n°PL-3466.1	Contig40	266716	267240		
SEQ ID n°2684	Prot n°PL-3467.1	Contig40	264623	265090		
SEQ ID n°2685	Prot n°PL-3468.1	Contig40	264174	264623		
SEQ ID n°2686	Prot n°PL-3469.1	Contig40	261105	261554		
SEQ ID n°2687	Prot n°PL-347.1	Contig41	599847	600872	19%	Identities = 34/106 (32%), Positives = 65/106 (61%), Gaps = 2/106 (1%) gb AAG06749.1 AE004758_6 (AE004758) hypothetical protein [Pseudomonas aeruginosa] Length = 115
SEQ ID n°2688	Prot n°PL-3470.1	Contig40	256743	257288		
SEQ ID n°2689	Prot n°PL-3471.1	Contig40	252934	253458		
SEQ ID n°2690	Prot n°PL-3473.1	Contig40	244710	245183		
SEQ ID n°2691	Prot n°PL-3474.1	Contig40	242820	243413		
SEQ ID n°2692	Prot n°PL-3475.1	Contig40	240932	241504		
SEQ ID n°2693	Prot n°PL-3476.1	Contig40	238454	239038		
SEQ ID n°2694	Prot n°PL-3477.1	Contig40	231201	231698		
SEQ ID n°2695	Prot n°PL-3478.1	Contig40	226887	227297		
SEQ ID n°2696	Prot n°PL-348.1	Contig41	601277	601975	No Hits found	
SEQ ID n°2697	Prot n°PL-3480.1	Contig40	224356	224892		
SEQ ID n°2698	Prot n°PL-3481.1	Contig40	219968	220480		
SEQ ID n°2699	Prot n°PL-3482.1	Contig40	217130	217612		
SEQ ID n°2700	Prot n°PL-3483.1	Contig40	216520	217050		
SEQ ID n°2701	Prot n°PL-3486.1	Contig40	212901	213356		
SEQ ID n°2702	Prot n°PL-3487.1	Contig40	209931	210392		

TABLEAU I

SEQ ID n°2703	Prot n°PL-3488.1	Contig40	194953	195486		
SEQ ID n°2704	Prot n°PL-3489.1	Contig40	148514	148989		
SEQ ID n°2705	Prot n°PL-349.1	Contig41	602353	603360	88%	Identities = 204/307 (66%), Positives = 246/307 (79%), Gaps = 3/307 (0%) sp P39407 YJUJ_ECOLI HYPOTHETICAL 39.8 KD PROTEIN IN OSMY-DEOC INTERGENIC REGION (O357) pi S5660.1 hypothetical 39.8K protein (osmY-deoC intergenic region) - Escherichia coli gb AA97273.1 (U14003) ORF_o357 [Escherichia coli] gb AAC77330.1 (AE000508) orf, hypothetical protein [Escherichia coli] Length = 357
SEQ ID n°2706	Prot n°PL-3490.1	Contig40	125676	126197		
SEQ ID n°2707	Prot n°PL-3491.1	Contig40	121507	122013		
SEQ ID n°2708	Prot n°PL-3492.1	Contig40	120079	120537		
SEQ ID n°2709	Prot n°PL-3493.1	Contig40	106534	106992		
SEQ ID n°2710	Prot n°PL-3494.1	Contig40	106377	106978		
SEQ ID n°2711	Prot n°PL-3495.1	Contig40	106363	106986		
SEQ ID n°2712	Prot n°PL-3496.1	Contig40	101053	101556		
SEQ ID n°2713	Prot n°PL-3497.1	Contig40	93796	95178		
SEQ ID n°2714	Prot n°PL-35.1	Contig41	65814	66686	75%	Identities = 172/291 (59%), Positives = 220/291 (75%), Gaps = 4/291 (1%) gb AAC45939.1 (AF010150) PopN [Pseudomonas aeruginosa] gb AAG05087.1 (AE004597) outer membrane protein PopN [Pseudomonas aeruginosa] Length = 288
SEQ ID n°2715	Prot n°PL-350.1	Contig41	604320	605918	92%	Identities = 467/529 (88%), Positives = 497/529 (93%) sp Q56121 RF3_SALTY PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3) dbj BAA09090.1 (D50496) peptide release factor 3/RF3 [Salmonella typhimurium] Length = 529
SEQ ID n°2716	Prot n°PL-3501.1	Contig40	70114	70689		
SEQ ID n°2717	Prot n°PL-3502.1	Contig40	65116	65670		
SEQ ID n°2718	Prot n°PL-3503.1	Contig40	59634	60182		
SEQ ID n°2719	Prot n°PL-3504.1	Contig40	43726	44304		
SEQ ID n°2720	Prot n°PL-3505.1	Contig40	36347	36769		
SEQ ID n°2721	Prot n°PL-3506.1	Contig40	28042	28500		
SEQ ID n°2722	Prot n°PL-351.1	Contig41	607025	608041	66%	Identities = 191/334 (57%), Positives = 248/334 (74%) sp P39406 RSMC_ECOLI RIBOSOMAL RNA SMALL SUBUNIT METHYLTRANSFERASE C (RRNA (GUANINE-N2)-METHYLTRANSFERASE) (16S RNA M2G1207 METHYLTRANSFERASE) pi S56595 hypothetical 37.6K protein (dnaT-hold intergenic region) - Escherichia coli gb AA97267.1 (U14003) ORF_f343b [Escherichia coli] gb AAC77324.1 (AE000507) putative enzyme [Escherichia coli] Length = 343
SEQ ID n°2723	Prot n°PL-3511.1	Contig40	9486	9944		
SEQ ID n°2724	Prot n°PL-3512.1	Contig40	7268	7759		
SEQ ID n°2725	Prot n°PL-3513.1	Contig40	4191	4667		
SEQ ID n°2726	Prot n°PL-3514.1	Contig40	1485	2054		

TABLEAU I

SEQ ID n°2727	Prot n°PL-3516.1	Contig39	700326	700778		
SEQ ID n°2728	Prot n°PL-3517.1	Contig39	699495	699950		
SEQ ID n°2728	Prot n°PL-352.1	Contig41	609242	610465	48%	Identities = 97/363 (26%), Positives = 189/363 (51%), Gaps = 10/363 (2%) pir D71676 bicyclomycin resistance protein (bcr2) RP698 - Rickettsia prowazekii emb CAA15134.1 (AJ235272) BICYCLOMYCIN RESISTANCE PROTEIN (bcr2) [Rickettsia prowazekii] Length = 391
SEQ ID n°2730	Prot n°PL-3525.1	Contig39	669863	670363		
SEQ ID n°2731	Prot n°PL-3526.1	Contig39	664339	664929		
SEQ ID n°2732	Prot n°PL-3527.1	Contig39	661241	661807		
SEQ ID n°2733	Prot n°PL-3528.1	Contig39	660468	660962		
SEQ ID n°2734	Prot n°PL-353.1	Contig41	610806	612140	78%	Identities = 327/490 (66%), Positives = 389/490 (78%), Gaps = 5/490 (1%) gb AAC73486.1 (AE000145) alkaline phosphatase [Escherichia coli] Length = 494
SEQ ID n°2735	Prot n°PL-3531.1	Contig39	640522	640988		
SEQ ID n°2736	Prot n°PL-3534.1	Contig39	634171	634641		
SEQ ID n°2737	Prot n°PL-3535.1	Contig39	627864	628349		
SEQ ID n°2738	Prot n°PL-3536.1	Contig39	617260	617714		
SEQ ID n°2739	Prot n°PL-3537.1	Contig39	616718	617176		
SEQ ID n°2740	Prot n°PL-3538.1	Contig39	610955	611545		
SEQ ID n°2741	Prot n°PL-354.1	Contig41	612353	613984	22%	Identities = 85/199 (42%), Positives = 125/199 (62%), Gaps = 5/199 (2%) gb AAG05838.1(AE004672.7 (AE004672) hypothetical protein [Pseudomonas aeruginosa] Length = 199
SEQ ID n°2742	Prot n°PL-3540.1	Contig39	590314	590628		
SEQ ID n°2743	Prot n°PL-3541.1	Contig39	588718	589245		
SEQ ID n°2744	Prot n°PL-3542.1	Contig39	582106	582594		
SEQ ID n°2745	Prot n°PL-3543.1	Contig39	577009	577518		
SEQ ID n°2746	Prot n°PL-3544.1	Contig39	570027	570473		
SEQ ID n°2747	Prot n°PL-3547.1	Contig39	565441	565827		
SEQ ID n°2748	Prot n°PL-3548.1	Contig39	563357	563839		
SEQ ID n°2749	Prot n°PL-3549.1	Contig39	550011	550529		
SEQ ID n°2750	Prot n°PL-355.1	Contig41	614276	615727	52%	Identities = 172/456 (37%), Positives = 261/456 (56%), Gaps = 18/456 (3%) gb AAF66548.1(AF140605.2 (AF140605) phenol 2-hydroxylase component A [Bacillus thermoglucosidasius] Length = 504
SEQ ID n°2751	Prot n°PL-3550.1	Contig39	493849	494361		
SEQ ID n°2752	Prot n°PL-3552.1	Contig39	488647	489128		
SEQ ID n°2753	Prot n°PL-3553.1	Contig39	486393	486866		
SEQ ID n°2754	Prot n°PL-3554.1	Contig39	479584	480054		
SEQ ID n°2755	Prot n°PL-3555.1	Contig39	473039	473617		
SEQ ID n°2756	Prot n°PL-3556.1	Contig39	465817	466095		
SEQ ID n°2757	Prot n°PL-3557.1	Contig39	452981	453416		
SEQ ID n°2758	Prot n°PL-3558.1	Contig39	413595	414023		

TABLEAU I

SEQ ID n°2758	Prot n°PL-3559.1	Contig39	412442	413014	80%	Identities = 142/206 (68%), Positives = 173/206 (83%) gb AAG04574.1 AE004549_1 (AE004549) probable glutathione S-transferase [Pseudomonas aeruginosa] Length = 209
SEQ ID n°2760	Prot n°PL-356.1	Contig41	615936	616559		
SEQ ID n°2761	Prot n°PL-3560.1	Contig39	412015	412482		
SEQ ID n°2762	Prot n°PL-3561.1	Contig39	411060	411470		
SEQ ID n°2763	Prot n°PL-3562.1	Contig39	410472	410924		
SEQ ID n°2764	Prot n°PL-3563.1	Contig39	409938	410390		
SEQ ID n°2765	Prot n°PL-3564.1	Contig39	400841	401377		
SEQ ID n°2766	Prot n°PL-3565.1	Contig39	400299	400847		
SEQ ID n°2767	Prot n°PL-3566.1	Contig39	398436	398891		
SEQ ID n°2768	Prot n°PL-3567.1	Contig39	395309	395824		
SEQ ID n°2769	Prot n°PL-3568.1	Contig39	387764	388315		
SEQ ID n°2770	Prot n°PL-3569.1	Contig39	386992	387444		
SEQ ID n°2771	Prot n°PL-357.1	Contig41	617058	617996	63%	Identities = 148/292 (50%), Positives = 199/292 (67%) gb AAG04573.1 AE004548_7 (AE004548) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 286
SEQ ID n°2772	Prot n°PL-3570.1	Contig39	386250	386750		
SEQ ID n°2773	Prot n°PL-3571.1	Contig39	385201	385746		
SEQ ID n°2774	Prot n°PL-3572.1	Contig39	382998	383525		
SEQ ID n°2775	Prot n°PL-3573.1	Contig39	376265	376834		
SEQ ID n°2776	Prot n°PL-3574.1	Contig39	374714	375253		
SEQ ID n°2777	Prot n°PL-3575.1	Contig39	368640	369179		
SEQ ID n°2778	Prot n°PL-3576.1	Contig39	363108	363590		
SEQ ID n°2779	Prot n°PL-3579.1	Contig39	356438	356848		
SEQ ID n°2780	Prot n°PL-358.1	Contig41	618388	619356	66%	Identities = 155/313 (49%), Positives = 214/313 (67%), Gaps = 3/313 (0%) gb AAG04575.1 AE004549_2 (AE004549) hypothetical protein [Pseudomonas aeruginosa] Length = 339
SEQ ID n°2781	Prot n°PL-3580.1	Contig39	302853	303446		
SEQ ID n°2782	Prot n°PL-3581.1	Contig39	302139	302711		
SEQ ID n°2783	Prot n°PL-3582.1	Contig39	300758	301318		
SEQ ID n°2784	Prot n°PL-3585.1	Contig39	294254	294826		
SEQ ID n°2785	Prot n°PL-3586.1	Contig39	292851	293417		
SEQ ID n°2786	Prot n°PL-3587.1	Contig39	290268	290813		
SEQ ID n°2787	Prot n°PL-3588.1	Contig39	289774	290256		
SEQ ID n°2788	Prot n°PL-3589.1	Contig39	289259	289750		
SEQ ID n°2789	Prot n°PL-359.1	Contig41	619409	620734	52%	Identities = 143/437 (32%), Positives = 234/437 (52%), Gaps = 29/437 (6%) gb AAG05774.1 AE004665_1 (AE004665) L-ornithine N5-oxygenase [Pseudomonas aeruginosa] Length = 443
SEQ ID n°2790	Prot n°PL-3591.1	Contig39	284541	285116		
SEQ ID n°2791	Prot n°PL-3592.1	Contig39	257755	258336		

TABLEAU I

SEQ ID n°2792	Prot n°PL-3593.1	Contig39	250807	251358		
SEQ ID n°2793	Prot n°PL-3594.1	Contig39	247814	248323		
SEQ ID n°2794	Prot n°PL-3596.1	Contig39	230432	230737		
SEQ ID n°2795	Prot n°PL-3597.1	Contig39	217843	218416		
SEQ ID n°2796	Prot n°PL-3598.1	Contig39	202343	202885		
SEQ ID n°2797	Prot n°PL-36.1	Contig41	67116	68438	89%	Identities = 375/438 (85%), Positives = 398/438 (90%) spiP40290 YSCN_YEREN PROBABLE ATP SYNTHASE YSCN (YOPS SECRETION ATPASE) pir J55520 yscN protein - Yersinia enterocolitica gb AAD16824.1 (AF102980) ATPase YscN [Yersinia enterocolitica] Length = 439
SEQ ID n°2798	Prot n°PL-360.1	Contig41	620691	622103	56%	Identities = 180/426 (42%), Positives = 265/426 (61%), Gaps = 11/426 (2%) db BAB06343.1 (AP001516) aminotransferase [Bacillus halodurans] Length = 454
SEQ ID n°2799	Prot n°PL-3600.1	Contig39	182383	182973		
SEQ ID n°2800	Prot n°PL-3601.1	Contig39	181090	181584		
SEQ ID n°2801	Prot n°PL-3602.1	Contig39	170478	171035		
SEQ ID n°2802	Prot n°PL-3603.1	Contig39	161630	162079		
SEQ ID n°2803	Prot n°PL-3605.1	Contig39	157884	158538		
SEQ ID n°2804	Prot n°PL-3607.1	Contig39	149788	150120		
SEQ ID n°2805	Prot n°PL-3608.1	Contig39	142283	142738		
SEQ ID n°2806	Prot n°PL-361.1	Contig41	622384	623964	40%	Identities = 124/455 (27%), Positives = 212/455 (46%), Gaps = 20/455 (4%) pir T35923 probable tRNA synthetase - Streptomyces coelicolor emb CAA22745.1 (AL035206) putative tRNA synthetase [Streptomyces coelicolor A3(2)] Length = 506
SEQ ID n°2807	Prot n°PL-3610.1	Contig39	131458	131919		
SEQ ID n°2808	Prot n°PL-3611.1	Contig39	129038	129559		
SEQ ID n°2809	Prot n°PL-3612.1	Contig39	128420	128989		
SEQ ID n°2810	Prot n°PL-3613.1	Contig39	128015	128419		
SEQ ID n°2811	Prot n°PL-3614.1	Contig39	127261	127839		
SEQ ID n°2812	Prot n°PL-3615.1	Contig39	126681	127250		
SEQ ID n°2813	Prot n°PL-3616.1	Contig39	126101	126670		
SEQ ID n°2814	Prot n°PL-3617.1	Contig39	125579	126100		
SEQ ID n°2815	Prot n°PL-3618.1	Contig39	108374	108786		
SEQ ID n°2816	Prot n°PL-362.1	Contig41	623916	625094	38%	Identities = 91/352 (25%), Positives = 153/352 (42%), Gaps = 24/352 (6%) pir G75122 sarcosine oxidase, chain beta (soxB) PAB1843 - Pyrococcus abyssi (strain Orsay) emb CAB48686.1 (AJ248285) sarcosine oxidase, subunit beta (soxB) [Pyrococcus abyssi] Length = 382
SEQ ID n°2817	Prot n°PL-3620.1	Contig39	107001	107552		
SEQ ID n°2818	Prot n°PL-3622.1	Contig39	101309	101839		
SEQ ID n°2819	Prot n°PL-3623.1	Contig39	84789	85274		
SEQ ID n°2820	Prot n°PL-3624.1	Contig39	70694	71152		

TABLEAU I

SEQ ID n°2821	Prot n°PL-3625.1	Contig39	70173	70676		
SEQ ID n°2822	Prot n°PL-3628.1	Contig39	50318	50887		
SEQ ID n°2823	Prot n°PL-3629.1	Contig39	41142	41702		
SEQ ID n°2824	Prot n°PL-363.1	Contig41	625015	626070	33%	Identities = 65/287 (22%), Positives = 118/287 (40%), Gaps = 39/287 (13%) pir J36125 branched-chain amino acid transport protein BraC - Pseudomonas aeruginosa (strain PAO) dbj BAA14254.1 (D90223) BraC (periplasmic protein) [Pseudomonas aeruginosa] gb AA04483.1 AE004539_5 (AE004539) branched-chain amino acid transport protein BraC [Pseudomonas aeruginosa] Length = 373
SEQ ID n°2825	Prot n°PL-3630.1	Contig39	40429	41004		
SEQ ID n°2826	Prot n°PL-3633.1	Contig39	29362	29847		
SEQ ID n°2827	Prot n°PL-3634.1	Contig39	26874	27404		
SEQ ID n°2828	Prot n°PL-3638.1	Contig39	3678	4175		
SEQ ID n°2829	Prot n°PL-364.1	Contig41	626058	627374	48%	Identities = 124/417 (29%), Positives = 206/417 (48%), Gaps = 8/417 (1%) pir T36416 probable peptide monooxygenase - Streptomyces coelicolor emb CAB53328.1 (AL109974) putative peptide monooxygenase [Streptomyces coelicolor A3(2)] Length = 451
SEQ ID n°2830	Prot n°PL-3640.1	Contig38	591204	591683		
SEQ ID n°2831	Prot n°PL-3641.1	Contig38	586003	586467		
SEQ ID n°2832	Prot n°PL-3643.1	Contig38	582588	583103		
SEQ ID n°2833	Prot n°PL-3644.1	Contig38	579890	580420		
SEQ ID n°2834	Prot n°PL-3645.1	Contig38	578582	579084		
SEQ ID n°2835	Prot n°PL-3647.1	Contig38	571643	572215		
SEQ ID n°2836	Prot n°PL-3648.1	Contig38	558807	559340		
SEQ ID n°2837	Prot n°PL-3649.1	Contig38	558324	558794		
SEQ ID n°2838	Prot n°PL-365.1	Contig41	627375	628847	32%	Identities = 100/347 (28%), Positives = 162/347 (45%), Gaps = 6/347 (1%) emb CAB71551.1 (AJ270937) aromatic amino acid decarboxylase [Sorangium cellulosum] Length = 512
SEQ ID n°2839	Prot n°PL-3650.1	Contig38	558740	557117		
SEQ ID n°2840	Prot n°PL-3651.1	Contig38	552785	553225		
SEQ ID n°2841	Prot n°PL-3652.1	Contig38	552232	552693		
SEQ ID n°2842	Prot n°PL-3655.1	Contig38	531435	531950		
SEQ ID n°2843	Prot n°PL-3656.1	Contig38	531007	531519		
SEQ ID n°2844	Prot n°PL-3658.1	Contig38	521390	521869		
SEQ ID n°2845	Prot n°PL-3659.1	Contig38	512461	512982		
SEQ ID n°2846	Prot n°PL-366.1	Contig41	629190	630152	No Hits found	
SEQ ID n°2847	Prot n°PL-3660.1	Contig38	510594	511064		
SEQ ID n°2848	Prot n°PL-3661.1	Contig38	509978	510532		
SEQ ID n°2849	Prot n°PL-3663.1	Contig38	496035	496502		
SEQ ID n°2850	Prot n°PL-3664.1	Contig38	482251	482721		
SEQ ID n°2851	Prot n°PL-3665.1	Contig38	479969	480466		

TABLEAU I

SEQ ID n°2852	Prot n°PL-3666.1	Contig38	479496	479834		
SEQ ID n°2853	Prot n°PL-3667.1	Contig38	471600	471935		
SEQ ID n°2854	Prot n°PL-3668.1	Contig38	470704	471135		
SEQ ID n°2855	Prot n°PL-3669.1	Contig38	457864	458460		
SEQ ID n°2856	Prot n°PL-367.1	Contig41	630628	631299	34%	Identities = 48/175 (27%), Positives = 78/175 (44%), Gaps = 2/175 (1%) gb AA07458.1 AE004823.4 (AE004823) hypothetical protein [Pseudomonas aeruginosa] Length = 192
SEQ ID n°2857	Prot n°PL-3670.1	Contig38	455061	455534		
SEQ ID n°2858	Prot n°PL-3671.1	Contig38	450178	450678		
SEQ ID n°2859	Prot n°PL-3673.1	Contig38	443087	443483		
SEQ ID n°2860	Prot n°PL-3674.1	Contig38	427684	428259		
SEQ ID n°2861	Prot n°PL-3675.1	Contig38	413488	413904		
SEQ ID n°2862	Prot n°PL-3676.1	Contig38	407058	407546		
SEQ ID n°2863	Prot n°PL-3677.1	Contig38	400209	401057		
SEQ ID n°2864	Prot n°PL-3678.1	Contig38	399683	400219		
SEQ ID n°2865	Prot n°PL-3679.1	Contig38	399141	399689		
SEQ ID n°2866	Prot n°PL-368.1	Contig41	631199	632692	79%	Identities = 324/479 (67%), Positives = 394/479 (81%), Gaps = 2/479 (0%) gb AA07459.1 AE004823.5 (AE004823) probable amino acid permease [Pseudomonas aeruginosa] Length = 496
SEQ ID n°2867	Prot n°PL-3680.1	Contig38	391639	392214		
SEQ ID n°2868	Prot n°PL-3681.1	Contig38	388864	389337		
SEQ ID n°2869	Prot n°PL-3682.1	Contig38	387867	388391		
SEQ ID n°2870	Prot n°PL-3683.1	Contig38	386605	386907		
SEQ ID n°2871	Prot n°PL-3684.1	Contig38	380011	380484		
SEQ ID n°2872	Prot n°PL-3686.1	Contig38	368733	369224		
SEQ ID n°2873	Prot n°PL-3687.1	Contig38	367772	368317		
SEQ ID n°2874	Prot n°PL-3688.1	Contig38	358340	358849		
SEQ ID n°2875	Prot n°PL-3689.1	Contig38	310040	310540		
SEQ ID n°2876	Prot n°PL-369.1	Contig41	633266	633925	61%	Identities = 119/214 (55%), Positives = 162/214 (75%), Gaps = 3/214 (1%) sp P54794 MOAR_KLEAE MONOAMINE REGULON TRANSCRIPTIONAL REGULATOR pir J36937 monoamine regulon positive regulator MoaR - Klebsiella pneumoniae db JBAA03667.1 (D15072) regulator protein [Klebsiella aerogenes] Length = 227
SEQ ID n°2877	Prot n°PL-3690.1	Contig38	309534	310100		
SEQ ID n°2878	Prot n°PL-3691.1	Contig38	295970	296425		
SEQ ID n°2879	Prot n°PL-3692.1	Contig38	291024	291479		
SEQ ID n°2880	Prot n°PL-3693.1	Contig38	289240	289812		
SEQ ID n°2881	Prot n°PL-3694.1	Contig38	266460	266921		
SEQ ID n°2882	Prot n°PL-3695.1	Contig38	264250	264822		
SEQ ID n°2883	Prot n°PL-3697.1	Contig38	256474	257067		
SEQ ID n°2884	Prot n°PL-3698.1	Contig38	246898	247385		

TABLEAU I

SEQ ID n°2885	Prot n°PL-3699.1	Contig38	244413	244901		Identities = 112/402 (27%), Positives = 170/402 (41%), Gaps = 60/402 (14%) gb AAG05084.1 AE004596_10 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa] Length = 369
SEQ ID n°2886	Prot n°PL-37.1	Contig41	68848	70041	42%	
SEQ ID n°2887	Prot n°PL-370.1	Contig41	634375	635259	59%	Identities = 126/284 (44%), Positives = 188/284 (65%), Gaps = 4/284 (1%) gb AAC26596.1 U83895 putative protease [Pseudomonas gingivalis] Length = 300
SEQ ID n°2888	Prot n°PL-3700.1	Contig38	243914	244420		
SEQ ID n°2889	Prot n°PL-3702.1	Contig38	234963	235436		
SEQ ID n°2890	Prot n°PL-3703.1	Contig38	232404	232844		
SEQ ID n°2891	Prot n°PL-3704.1	Contig38	228060	228527		
SEQ ID n°2892	Prot n°PL-3705.1	Contig38	226300	226857		
SEQ ID n°2893	Prot n°PL-3708.1	Contig38	220869	221577		
SEQ ID n°2894	Prot n°PL-3708.1	Contig38	220562	220981		
SEQ ID n°2895	Prot n°PL-371.1	Contig41	635362	635976	No Hits found	
SEQ ID n°2896	Prot n°PL-3710.1	Contig38	215661	216113		
SEQ ID n°2897	Prot n°PL-3711.1	Contig38	212908	213465		
SEQ ID n°2898	Prot n°PL-3712.1	Contig38	209269	209751		
SEQ ID n°2899	Prot n°PL-3713.1	Contig38	203895	204461		
SEQ ID n°2900	Prot n°PL-3714.1	Contig38	197292	197789		
SEQ ID n°2901	Prot n°PL-3715.1	Contig38	195873	196391		
SEQ ID n°2902	Prot n°PL-3718.1	Contig38	189324	189842		
SEQ ID n°2903	Prot n°PL-372.1	Contig41	636927	641213	32%	Identities = 323/1220 (26%), Positives = 463/1220 (37%), Gaps = 207/1220 (16%) gb AAG06072.1 AE004696_6 (AE004696) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 1317
SEQ ID n°2904	Prot n°PL-3720.1	Contig38	174075	174844		
SEQ ID n°2905	Prot n°PL-3721.1	Contig38	172801	173376		
SEQ ID n°2906	Prot n°PL-3722.1	Contig38	162925	163404		
SEQ ID n°2907	Prot n°PL-3723.1	Contig38	160190	160642		
SEQ ID n°2908	Prot n°PL-3724.1	Contig38	156880	157419		
SEQ ID n°2909	Prot n°PL-3725.1	Contig38	155146	155652		
SEQ ID n°2910	Prot n°PL-3727.1	Contig38	150388	150954		
SEQ ID n°2911	Prot n°PL-3728.1	Contig38	141767	142141		
SEQ ID n°2912	Prot n°PL-3729.1	Contig38	141199	141669		
SEQ ID n°2913	Prot n°PL-373.1	Contig41	642623	643720	67%	Identities = 188/370 (50%), Positives = 251/370 (67%), Gaps = 10/370 (2%) gb AAG03963.1 AE004493_8 (AE004493) hypothetical protein [Pseudomonas aeruginosa] Length = 373
SEQ ID n°2914	Prot n°PL-3730.1	Contig38	136548	137093		
SEQ ID n°2915	Prot n°PL-3731.1	Contig38	135958	136386		
SEQ ID n°2916	Prot n°PL-3732.1	Contig38	134430	134936		
SEQ ID n°2917	Prot n°PL-3734.1	Contig38	77823	78308		

TABLEAU I

SEQ ID n°2918	Prot n°PL-3735.1	Contig38	77035	77511		
SEQ ID n°2919	Prot n°PL-3736.1	Contig38	66657	67247		
SEQ ID n°2920	Prot n°PL-3737.1	Contig38	62017	62499		
SEQ ID n°2921	Prot n°PL-3738.1	Contig38	56623	57117		
SEQ ID n°2922	Prot n°PL-3739.1	Contig38	53885	54424		
SEQ ID n°2923	Prot n°PL-374.1	Contig41	643802	645295	65%	Identities = 227/495 (45%), Positives = 326/495 (65%), Gaps = 2/495 (0%) emb CAA66106.1 (X87453) phenylacetaldehyde dehydrogenase [Escherichia coli] Length = 499
SEQ ID n°2924	Prot n°PL-3741.1	Contig38	15523	16065		
SEQ ID n°2925	Prot n°PL-3743.1	Contig38	15217	15702		
SEQ ID n°2926	Prot n°PL-3745.1	Contig38	7711	8241		
SEQ ID n°2927	Prot n°PL-3746.1	Contig38	7001	7516		
SEQ ID n°2928	Prot n°PL-3749.1	Contig37	529036	529761		
SEQ ID n°2929	Prot n°PL-375.1	Contig41	645881	647185	80%	Identities = 294/431 (68%), Positives = 355/431 (82%), Gaps = 1/431 (0%) gb AAG05705.1 AE004657_12 (AE004657) probable oxidoreductase [Pseudomonas aeruginosa] Length = 432
SEQ ID n°2930	Prot n°PL-3750.1	Contig37	528467	529054		
SEQ ID n°2931	Prot n°PL-3751.1	Contig37	520714	521313		
SEQ ID n°2932	Prot n°PL-3752.1	Contig37	514140	514688		
SEQ ID n°2933	Prot n°PL-3753.1	Contig37	510154	510582		
SEQ ID n°2934	Prot n°PL-3754.1	Contig37	508939	509376		
SEQ ID n°2935	Prot n°PL-3756.1	Contig37	483291	483981		
SEQ ID n°2936	Prot n°PL-3757.1	Contig37	435931	436515		
SEQ ID n°2937	Prot n°PL-3758.1	Contig37	428049	428627		
SEQ ID n°2938	Prot n°PL-3759.1	Contig37	427367	427735		
SEQ ID n°2939	Prot n°PL-376.1	Contig41	647418	648173	47%	Identities = 82/248 (33%), Positives = 119/248 (47%), Gaps = 15/248 (6%) gb AAG04873.1 AE004577_8 (AE004577) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 268
SEQ ID n°2940	Prot n°PL-3761.1	Contig37	416832	417353		
SEQ ID n°2941	Prot n°PL-3762.1	Contig37	401226	401642		
SEQ ID n°2942	Prot n°PL-3763.1	Contig37	399665	400135		
SEQ ID n°2943	Prot n°PL-3764.1	Contig37	374138	374617		
SEQ ID n°2944	Prot n°PL-3765.1	Contig37	366827	367357		
SEQ ID n°2945	Prot n°PL-3768.1	Contig37	342980	343456		
SEQ ID n°2946	Prot n°PL-3769.1	Contig37	328362	328802		

TABLEAU I

SEQ ID n°2947	Prot n°PL-377.1	Contig41	648439	649369	77%	<p>Identities = 208/311 (67%), Positives = 248/311 (79%), Gaps = 1/311 (0%) pdbj2MASIA Chain A, Purine Nucleoside Hydrolase With A Transition State Inhibitor pdbj2MASIB Chain B, Purine Nucleoside Hydrolase With A Transition State Inhibitor State With A Transition State Nucleoside Hydrolase With A Transition State Chain A, Purine Nucleoside Hydrolase Inhibitor pdbj2MASID Chain D, Purine Nucleoside Hydrolase Inhibitor State Inhibitor pdbj1MASIA Chain A, Purine Nucleoside Hydrolase Inhibitor State Inhibitor pdbj1MASIB Chain B, Purine Nucleoside Hydrolase Inhibitor State Inhibitor State Length = 314</p>
SEQ ID n°2948	Prot n°PL-3770.1	Contig37	316832	317224		
SEQ ID n°2949	Prot n°PL-3771.1	Contig37	312469	312924		
SEQ ID n°2950	Prot n°PL-3772.1	Contig37	302772	303332		
SEQ ID n°2951	Prot n°PL-3773.1	Contig37	286421	286888		
SEQ ID n°2952	Prot n°PL-3774.1	Contig37	265362	265866		
SEQ ID n°2953	Prot n°PL-3775.1	Contig37	244527	244988		
SEQ ID n°2954	Prot n°PL-3776.1	Contig37	235067	235438		
SEQ ID n°2955	Prot n°PL-3777.1	Contig37	233382	233852		
SEQ ID n°2956	Prot n°PL-3778.1	Contig37	215572	216168		
SEQ ID n°2957	Prot n°PL-3779.1	Contig37	209700	210194		
SEQ ID n°2958	Prot n°PL-378.1	Contig41	649443	650432	71%	<p>Identities = 194/323 (60%), Positives = 244/323 (75%) gbJAAD37770.1(AF146532_10 (AF146532) glycosyltransferase [Klebsiella pneumoniae]) Length = 329</p>
SEQ ID n°2959	Prot n°PL-3780.1	Contig37	203294	203596		
SEQ ID n°2960	Prot n°PL-3781.1	Contig37	155489	155923		
SEQ ID n°2961	Prot n°PL-3783.1	Contig37	136612	137085		
SEQ ID n°2962	Prot n°PL-3784.1	Contig37	134358	134804		
SEQ ID n°2963	Prot n°PL-3785.1	Contig37	133891	134361		
SEQ ID n°2964	Prot n°PL-3786.1	Contig37	126784	127185		
SEQ ID n°2965	Prot n°PL-3787.1	Contig37	124584	125048		
SEQ ID n°2966	Prot n°PL-3788.1	Contig37	124250	124843		
SEQ ID n°2967	Prot n°PL-3789.1	Contig37	119484	120065		
SEQ ID n°2968	Prot n°PL-379.1	Contig41	650737	652008	No Hits found	
SEQ ID n°2969	Prot n°PL-3792.1	Contig37	110174	110623		
SEQ ID n°2970	Prot n°PL-3793.1	Contig37	105976	106452		
SEQ ID n°2971	Prot n°PL-3794.1	Contig37	102681	103097		
SEQ ID n°2972	Prot n°PL-3795.1	Contig37	86809	87279		
SEQ ID n°2973	Prot n°PL-3796.1	Contig37	74304	74783		
SEQ ID n°2974	Prot n°PL-3797.1	Contig37	63233	63712		
SEQ ID n°2975	Prot n°PL-3799.1	Contig37	39450	40007		
SEQ ID n°2976	Prot n°PL-38.1	Contig41	70023	70970	60%	<p>Identities = 146/307 (47%), Positives = 191/307 (61%), Gaps = 7/307 (2%) gbJAAD16827.1(AF102990) YscQ [Yersinia enterocolitica] Length =</p>
SEQ ID n°2977	Prot n°PL-380.1	Contig41	652178	652801	No Hits found	

TABLEAU I

SEQ ID n°2978	Prot n°PL-3800.1	Contig37	37356	37904		
SEQ ID n°2979	Prot n°PL-3801.1	Contig37	36895	37275		
SEQ ID n°2980	Prot n°PL-3802.1	Contig37	32227	32823		
SEQ ID n°2981	Prot n°PL-3803.1	Contig37	7308	7886		
SEQ ID n°2982	Prot n°PL-3804.1	Contig36	456260	456772		
SEQ ID n°2983	Prot n°PL-3805.1	Contig36	446844	447395		
SEQ ID n°2984	Prot n°PL-3806.1	Contig36	442062	442472		
SEQ ID n°2985	Prot n°PL-3808.1	Contig36	433290	433799		
SEQ ID n°2986	Prot n°PL-3809.1	Contig36	431005	431484		
SEQ ID n°2987	Prot n°PL-381.1	Contig41	654074	655063	52%	Identities = 123/318 (38%), Positives = 177/318 (54%), Gaps = 15/318 (4%) pir T35271 probable transcription regulator - Streptomyces coelicolor emb CAB40696.1 (AL049587) putative transcriptional regulator [Streptomyces coelicolor A3(2)] Length = 325
SEQ ID n°2988	Prot n°PL-3811.1	Contig36	428475	428933		
SEQ ID n°2989	Prot n°PL-3812.1	Contig36	427860	428330		
SEQ ID n°2990	Prot n°PL-3813.1	Contig36	400462	400932		
SEQ ID n°2991	Prot n°PL-3814.1	Contig36	398560	398973		
SEQ ID n°2992	Prot n°PL-3815.1	Contig36	397384	397680		
SEQ ID n°2993	Prot n°PL-3816.1	Contig36	376674	377054		
SEQ ID n°2994	Prot n°PL-3817.1	Contig36	353647	354057		
SEQ ID n°2995	Prot n°PL-3818.1	Contig36	352311	352766		
SEQ ID n°2996	Prot n°PL-382.1	Contig41	655022	655619	51%	Identities = 104/214 (48%), Positives = 136/214 (62%), Gaps = 1/214 (0%) emb CAB56727.1 (AL121600) hypothetical protein SCF76.07 [Streptomyces coelicolor A3(2)] Length = 247
SEQ ID n°2997	Prot n°PL-3820.1	Contig36	339426	339826		
SEQ ID n°2998	Prot n°PL-3821.1	Contig36	338730	339272		
SEQ ID n°2999	Prot n°PL-3822.1	Contig36	335846	336331		
SEQ ID n°3000	Prot n°PL-3823.1	Contig36	325767	326297		
SEQ ID n°3001	Prot n°PL-3824.1	Contig36	321149	321691		
SEQ ID n°3002	Prot n°PL-3828.1	Contig36	262736	263278		
SEQ ID n°3003	Prot n°PL-3829.1	Contig36	260998	261546		
SEQ ID n°3004	Prot n°PL-383.1	Contig41	656643	657443	47%	Identities = 93/207 (44%), Positives = 127/207 (60%), Gaps = 2/207 (0%) emb CAB61681.1 (AL133213) putative GntR-family transcriptional regulator. [Streptomyces coelicolor A3(2)] Length = 231
SEQ ID n°3005	Prot n°PL-3830.1	Contig36	254751	255248		
SEQ ID n°3006	Prot n°PL-3831.1	Contig36	253138	253491		
SEQ ID n°3007	Prot n°PL-3832.1	Contig36	250958	251461		
SEQ ID n°3008	Prot n°PL-3833.1	Contig36	246478	247041		
SEQ ID n°3009	Prot n°PL-3834.1	Contig36	241015	241473		
SEQ ID n°3010	Prot n°PL-3837.1	Contig36	209549	210010		
SEQ ID n°3011	Prot n°PL-3838.1	Contig36	202423	202965		

TABLEAU I

SEQ ID n°3012	Prot n°PL-384.1	Contig41	657887	658603	80%	Identities = 100/221 (45%), Positives = 147/221 (66%), Gaps = 2/221 (0%) emb[CAB56670.1] (AL121596) possible integral membrane protein [Streptomyces coelicolor A3(2)] Length = 239
SEQ ID n°3013	Prot n°PL-3840.1	Contig36	183780	184325		
SEQ ID n°3014	Prot n°PL-3841.1	Contig36	183283	183753		
SEQ ID n°3015	Prot n°PL-3842.1	Contig36	170477	171040		
SEQ ID n°3016	Prot n°PL-3844.1	Contig36	134886	135275		
SEQ ID n°3017	Prot n°PL-3845.1	Contig36	134129	134599		
SEQ ID n°3018	Prot n°PL-3846.1	Contig36	125221	125805		
SEQ ID n°3019	Prot n°PL-3847.1	Contig36	117585	118127		
SEQ ID n°3020	Prot n°PL-3848.1	Contig36	114386	114856		
SEQ ID n°3021	Prot n°PL-3849.1	Contig36	94129	94731		
SEQ ID n°3022	Prot n°PL-385.1	Contig41	658603	659619	60%	Identities = 140/341 (41%), Positives = 206/341 (60%), Gaps = 30/341 (8%) emb[CAB75189.1] (AL139075) putative integral membrane protein [Campylobacter jejuni] Length = 317
SEQ ID n°3023	Prot n°PL-3850.1	Contig36	75709	76233		
SEQ ID n°3024	Prot n°PL-3852.1	Contig36	38198	38716		
SEQ ID n°3025	Prot n°PL-3853.1	Contig36	19989	20420		
SEQ ID n°3026	Prot n°PL-3854.1	Contig36	17255	17740		
SEQ ID n°3027	Prot n°PL-3855.1	Contig36	10034	10483		
SEQ ID n°3028	Prot n°PL-3856.1	Contig36	8100	8510		
SEQ ID n°3029	Prot n°PL-3857.1	Contig36	2059	2565		
SEQ ID n°3030	Prot n°PL-3858.1	Contig35	241967	242536		
SEQ ID n°3031	Prot n°PL-386.1	Contig41	659629	660291	66%	Identities = 118/218 (54%), Positives = 148/218 (67%), Gaps = 9/218 (4%) spIP42673]PCP_PSEFL PYRROLIDONE-CARBOXYLATE PEPTIDASE (5- OXOPROPYL-PEPTIDASE) (PYROGLUTAMYL-PEPTIDASE I) (PGP-I) (PYRASE) pir JA55583 pyroglutamyl-peptidase I (EC 3.4.19.3) - Pseudomonas fluorescens emb CAA53519.1] (X75919) TRANSFERRED ENTRY: 3.4.19.3 [Pseudomonas fluorescens] Length = 213
SEQ ID n°3032	Prot n°PL-3860.1	Contig35	220862	221407		
SEQ ID n°3033	Prot n°PL-3862.1	Contig35	201157	201750		
SEQ ID n°3034	Prot n°PL-3863.1	Contig35	200582	201130		
SEQ ID n°3035	Prot n°PL-3864.1	Contig35	179215	179811		
SEQ ID n°3036	Prot n°PL-3865.1	Contig35	174041	174502		
SEQ ID n°3037	Prot n°PL-3866.1	Contig35	147137	147858		
SEQ ID n°3038	Prot n°PL-3867.1	Contig35	146888	147268		
SEQ ID n°3039	Prot n°PL-3868.1	Contig35	142088	142651		
SEQ ID n°3040	Prot n°PL-3869.1	Contig35	139435	139917		
SEQ ID n°3041	Prot n°PL-387.1	Contig41	660378	661154	62%	Identities = 139/249 (55%), Positives = 176/249 (69%), Gaps = 1/249 (0%) (AL121596) hypothetical protein SCF51A.19 [Streptomyces coelicolor A3(2)] Length = 250

TABLEAU I

SEQ ID n°3042	Prot n°PL-3870.1	Contig35	135581	136081		
SEQ ID n°3043	Prot n°PL-3871.1	Contig35	128004	128465		
SEQ ID n°3044	Prot n°PL-3872.1	Contig35	123350	123874		
SEQ ID n°3045	Prot n°PL-3875.1	Contig35	111471	111986		
SEQ ID n°3046	Prot n°PL-3877.1	Contig35	108751	107308		
SEQ ID n°3047	Prot n°PL-3878.1	Contig35	99122	99568		
SEQ ID n°3048	Prot n°PL-3879.1	Contig35	76097	76624		
SEQ ID n°3049	Prot n°PL-388.1	Contig41	661073	662785	43%	Identities = 169/529 (31%), Positives = 247/529 (45%), Gaps = 68/529 (12%) gb AAC46262.1 (AF006000) unknown [Bordetella pertussis] Length =
SEQ ID n°3050	Prot n°PL-3880.1	Contig35	64574	65141		
SEQ ID n°3051	Prot n°PL-3881.1	Contig35	63785	64169		
SEQ ID n°3052	Prot n°PL-3882.1	Contig35	55489	55959		
SEQ ID n°3053	Prot n°PL-3883.1	Contig35	52815	53363		
SEQ ID n°3054	Prot n°PL-3885.1	Contig35	43369	43836		
SEQ ID n°3055	Prot n°PL-3886.1	Contig35	24140	24589		
SEQ ID n°3056	Prot n°PL-3887.1	Contig35	18478	19008		
SEQ ID n°3057	Prot n°PL-3888.1	Contig35	9959	10420		
SEQ ID n°3058	Prot n°PL-389.1	Contig41	662794	664572	72%	Identities = 341/585 (58%), Positives = 438/585 (74%), Gaps = 4/585 (0%) p S71006 biotin carboxylase protein A1 - Saccharopolyspora erythraea emb CAA63308.1 (X92556) biotin carboxylase and biotin carboxyl carrier protein [Saccharopolyspora erythraea] Length = 587
SEQ ID n°3059	Prot n°PL-3891.1	Contig34	235932	236369		
SEQ ID n°3060	Prot n°PL-3892.1	Contig34	234530	234838		
SEQ ID n°3061	Prot n°PL-3893.1	Contig34	220872	221363		
SEQ ID n°3062	Prot n°PL-3894.1	Contig34	198591	199103		
SEQ ID n°3063	Prot n°PL-3895.1	Contig34	179864	180358		
SEQ ID n°3064	Prot n°PL-3896.1	Contig34	162622	163074		
SEQ ID n°3065	Prot n°PL-3897.1	Contig34	155173	155876		
SEQ ID n°3066	Prot n°PL-3899.1	Contig34	104959	105450		
SEQ ID n°3067	Prot n°PL-39.1	Contig41	70967	71620	87%	Identities = 180/216 (83%), Positives = 205/216 (94%) gb AAG05082.1 AE004596.8 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa] Length = 217
SEQ ID n°3068	Prot n°PL-390.1	Contig41	665829	667055	81%	Identities = 296/404 (73%), Positives = 340/404 (83%), Gaps = 2/404 (0%) gb AAG07971.1 AE004872.2 (AE004872) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 404
SEQ ID n°3069	Prot n°PL-3900.1	Contig34	102044	102502		
SEQ ID n°3070	Prot n°PL-3902.1	Contig34	80787	81233		
SEQ ID n°3071	Prot n°PL-3903.1	Contig34	77872	78330		
SEQ ID n°3072	Prot n°PL-3905.1	Contig34	56844	57335		
SEQ ID n°3073	Prot n°PL-3906.1	Contig34	53887	54387		
SEQ ID n°3074	Prot n°PL-3908.1	Contig34	44198	44719		

TABLEAU I

SEQ ID n°3076	Prot n°PL-391.1	Contig41	667081	667891	52%	Identities = 118/231 (51%), Positives = 161/231 (69%) gb AAG07972.1 AE004872.3 (AE004872) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 270
SEQ ID n°3076	Prot n°PL-3910.1	Contig34	28151	28654		
SEQ ID n°3077	Prot n°PL-3912.1	Contig34	17487	18011		
SEQ ID n°3078	Prot n°PL-3913.1	Contig34	13608	14150		
SEQ ID n°3079	Prot n°PL-3914.1	Contig33	207474	207944		
SEQ ID n°3080	Prot n°PL-3916.1	Contig33	187191	187616		
SEQ ID n°3081	Prot n°PL-3917.1	Contig33	185312	185713		
SEQ ID n°3082	Prot n°PL-3918.1	Contig33	174658	175089		
SEQ ID n°3083	Prot n°PL-3919.1	Contig33	174117	174533		
SEQ ID n°3084	Prot n°PL-392.1	Contig41	668116	669282	70%	Identities = 226/387 (58%), Positives = 287/387 (73%), Gaps = 2/387 (0%) sp P24196 YGIC_ECOLI_HYPOTHETICAL_45.0_KD_PROTEIN_IN_TOLC-RIBB INTERGENIC_REGION (ORF) (O386) pir S22361 hypothetical protein A - Escherichia coli gb AA71876.1 (M77129) ORF [Escherichia coli] gb AAA69206.1 (U28377) ORF_o388; alternate name ygiC; orfA of M77129 [Escherichia coli] gb AAC76074.1 (AE000385) putative synthetase/amidase [Escherichia coli] Length = 386 "
SEQ ID n°3085	Prot n°PL-3921.1	Contig33	167391	167900		
SEQ ID n°3086	Prot n°PL-3923.1	Contig33	154747	155337		
SEQ ID n°3087	Prot n°PL-3924.1	Contig33	150360	150884		
SEQ ID n°3088	Prot n°PL-3925.1	Contig33	134822	135403		
SEQ ID n°3089	Prot n°PL-3926.1	Contig33	128904	129362		
SEQ ID n°3090	Prot n°PL-3928.1	Contig33	101253	101717		
SEQ ID n°3091	Prot n°PL-3929.1	Contig33	89465	100007		
SEQ ID n°3092	Prot n°PL-393.1	Contig41	669402	670301	26%	Identities = 54/177 (30%), Positives = 79/177 (44%), Gaps = 18/177 (10%) sp P24196 YGIB_ECOLI_HYPOTHETICAL_24.9_KD_PROTEIN_IN_TOLC-RIBB INTERGENIC_REGION (ORF) (O234) pir S22360 hypothetical protein D - Escherichia coli gb AA71875.1 (M77129) ORF [Escherichia coli] gb AAA69205.1 (U28377) ORF_o234; alternate name ygiB; orfD of M77129 [Escherichia coli] gb AAC76073.1 (AE000385) orf, hypothetical protein [Escherichia coli] Length = 234 "
SEQ ID n°3093	Prot n°PL-3930.1	Contig33	94558	94962		
SEQ ID n°3094	Prot n°PL-3931.1	Contig33	90261	90761		
SEQ ID n°3095	Prot n°PL-3935.1	Contig33	40112	40591		
SEQ ID n°3096	Prot n°PL-3936.1	Contig33	39414	39866		
SEQ ID n°3097	Prot n°PL-3937.1	Contig33	25845	26435		
SEQ ID n°3098	Prot n°PL-3938.1	Contig33	16092	16796		
SEQ ID n°3099	Prot n°PL-3939.1	Contig33	15403	15975		
SEQ ID n°3100	Prot n°PL-3940.1	Contig33	540	950		
SEQ ID n°3101	Prot n°PL-3941.1	Contig32	182117	182623		

TABLEAU I

SEQ ID n°3102	Prot n°PL-3943.1	Contig32	164225	164776		
SEQ ID n°3103	Prot n°PL-3944.1	Contig32	163758	164228		
SEQ ID n°3104	Prot n°PL-3945.1	Contig32	163187	163657		
SEQ ID n°3105	Prot n°PL-3947.1	Contig32	126953	127357		
SEQ ID n°3106	Prot n°PL-3948.1	Contig32	125617	126114		
SEQ ID n°3107	Prot n°PL-395.1	Contig41	670740	671432	37%	Identities = 54/185 (29%), Positives = 86/185 (46%), Gaps = 11/185 (5%) spiP39293YJFK_ECOLI HYPOTHETICAL 25.0 KD PROTEIN IN VACB-AIDB INTERGENIC REGION (0219) p[IS56408 hypothetical 25.0K protein (vacB- aidB intergenic region) - Escherichia coli gb AAA97079.1 (U14003) ORF_o219 [Escherichia coli] gb AAC77140.1 (AE000490) orf, hypothetical protein [Escherichia coli] Length = 219
SEQ ID n°3108	Prot n°PL-3950.1	Contig32	118473	118901		
SEQ ID n°3109	Prot n°PL-3951.1	Contig32	111029	111526		
SEQ ID n°3110	Prot n°PL-3952.1	Contig32	106318	106999		
SEQ ID n°3111	Prot n°PL-3953.1	Contig32	99787	100305		
SEQ ID n°3112	Prot n°PL-3954.1	Contig32	82543	83043		
SEQ ID n°3113	Prot n°PL-3955.1	Contig32	53705	54193		
SEQ ID n°3114	Prot n°PL-3956.1	Contig32	53222	53704		
SEQ ID n°3115	Prot n°PL-3957.1	Contig32	52017	52571		
SEQ ID n°3116	Prot n°PL-3958.1	Contig32	42891	43430		
SEQ ID n°3117	Prot n°PL-3959.1	Contig32	37798	38373		
SEQ ID n°3118	Prot n°PL-396.1	Contig41	671468	672151	59%	Identities = 102/228 (44%), Positives = 139/228 (60%), Gaps = 1/228 (0%) gb AAG07118.1 AE004792_3 (AE004792) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 231
SEQ ID n°3119	Prot n°PL-3960.1	Contig32	36783	37196		
SEQ ID n°3120	Prot n°PL-3961.1	Contig32	36202	36660		
SEQ ID n°3121	Prot n°PL-3962.1	Contig32	30228	30665		
SEQ ID n°3122	Prot n°PL-3963.1	Contig32	27832	28287		
SEQ ID n°3123	Prot n°PL-3964.1	Contig32	25293	25811		
SEQ ID n°3124	Prot n°PL-3965.1	Contig32	22982	23533		
SEQ ID n°3125	Prot n°PL-3966.1	Contig32	9689	10234		
SEQ ID n°3126	Prot n°PL-3968.1	Contig31	83498	83938		
SEQ ID n°3127	Prot n°PL-3969.1	Contig31	91738	92151		
SEQ ID n°3128	Prot n°PL-397.1	Contig41	672957	673841	59%	Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300
SEQ ID n°3129	Prot n°PL-3970.1	Contig31	67816	68160		
SEQ ID n°3130	Prot n°PL-3971.1	Contig31	65808	66284		
SEQ ID n°3131	Prot n°PL-3972.1	Contig31	63863	64308		
SEQ ID n°3132	Prot n°PL-3973.1	Contig31	56281	56658		
SEQ ID n°3133	Prot n°PL-3974.1	Contig31	51561	52073		

TABLEAU I

SEQ ID n°3156	Prot n°PL-40.1	Contig41	71886	72674	86%	Identities = 193/262 (73%), Positives = 232/262 (87%) gb AAG06080.1 AE004596.6 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa] Length = 262
SEQ ID n°3156	Prot n°PL-400.1	Contig41	678238	679335	58%	Identities = 153/408 (37%), Positives = 215/408 (52%), Gaps = 52/408 (12%) pir 41084 type I site-specific deoxyribonuclease (EC 3.1.21.3) EcoDXXI chain hsdS - Escherichia coli emb CAA52162.1 (X73984) hsdS [Escherichia coli] Length = 408
SEQ ID n°3157	Prot n°PL-4001.1	Contig30	5897	6352		
SEQ ID n°3158	Prot n°PL-4003.1	Contig29	51338	51766		
SEQ ID n°3159	Prot n°PL-4006.1	Contig29	23891	24397		
SEQ ID n°3160	Prot n°PL-401.1	Contig41	679337	680491	70%	Identities = 218/389 (56%), Positives = 275/389 (70%), Gaps = 17/389 (4%) gb AAF41243.1 (AE002436) antitoxin nuclease [Neisseria meningitidis MC58] Length = 380
SEQ ID n°3161	Prot n°PL-4010.1	Contig29	1218	1676		
SEQ ID n°3162	Prot n°PL-4011.1	Contig28	68660	67172		
SEQ ID n°3163	Prot n°PL-4012.1	Contig28	49029	49598		
SEQ ID n°3164	Prot n°PL-4013.1	Contig28	41929	42474		
SEQ ID n°3165	Prot n°PL-4014.1	Contig28	36550	37029		
SEQ ID n°3166	Prot n°PL-4015.1	Contig28	24667	25224		
SEQ ID n°3167	Prot n°PL-4016.1	Contig28	16201	16623		
SEQ ID n°3168	Prot n°PL-4017.1	Contig27	64218	64769		
SEQ ID n°3169	Prot n°PL-4018.1	Contig27	63405	63875		
SEQ ID n°3170	Prot n°PL-4019.1	Contig27	57553	58059		
SEQ ID n°3171	Prot n°PL-402.1	Contig41	680517	683633	88%	Identities = 817/1031 (79%), Positives = 917/1031 (88%), Gaps = 1/1031 (0%) sp P10486 T1R1_ECOLI TYPE I RESTRICTION ENZYME ECOR124II R PROTEIN pir S02168 type I site-specific deoxyribonuclease (EC 3.1.21.3) EcoR124/3 chain hsdR - Escherichia coli plasmid R124/3 emb CAA31543.1 (X13145) hsdR protein (AA 1-1033) [Escherichia coli] Length = 1033
SEQ ID n°3172	Prot n°PL-4020.1	Contig27	53699	54175		
SEQ ID n°3173	Prot n°PL-4021.1	Contig27	53192	53829		
SEQ ID n°3174	Prot n°PL-4023.1	Contig27	50056	50484		
SEQ ID n°3175	Prot n°PL-4024.1	Contig27	34999	35484		
SEQ ID n°3176	Prot n°PL-4026.1	Contig27	24784	25242		
SEQ ID n°3177	Prot n°PL-4028.1	Contig27	20232	20736		
SEQ ID n°3178	Prot n°PL-4029.1	Contig27	17696	18214		
SEQ ID n°3179	Prot n°PL-403.2	Contig41	684405	686030		
SEQ ID n°3180	Prot n°PL-4030.1	Contig27	1	687		
SEQ ID n°3181	Prot n°PL-4031.1	Contig26	70219	71013		
SEQ ID n°3182	Prot n°PL-4032.1	Contig26	69733	70218		
SEQ ID n°3183	Prot n°PL-4034.1	Contig26	62000	62527		

TABLEAU I

SEQ ID n°3184	Prot n°PL-4035.1	Contig26	60950	61483		
SEQ ID n°3185	Prot n°PL-4036.1	Contig26	58166	58701		
SEQ ID n°3186	Prot n°PL-4037.1	Contig26	57656	58087		
SEQ ID n°3187	Prot n°PL-4039.1	Contig26	34999	35490		
SEQ ID n°3188	Prot n°PL-404.1	Contig41	686860	687741	17%	Identities = 38/119 (31%), Positives = 62/119 (42%), Gaps = 9/119 (7%) pir C75394 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb AAAF11086.1 AE001997_2 (AE001997) conserved hypothetical protein [Deinococcus radiodurans] Length = 299
SEQ ID n°3189	Prot n°PL-4040.1	Contig26	24517	24984		
SEQ ID n°3190	Prot n°PL-4041.1	Contig26	6699	7133		
SEQ ID n°3191	Prot n°PL-4043.1	Contig26	2376	2824		
SEQ ID n°3192	Prot n°PL-4044.1	Contig25	18020	18589		
SEQ ID n°3193	Prot n°PL-4045.1	Contig25	11802	12281		
SEQ ID n°3194	Prot n°PL-4048.1	Contig23	387	815		
SEQ ID n°3195	Prot n°PL-405.1	Contig41	687930	689921	48%	Identities = 194/678 (28%), Positives = 325/678 (47%), Gaps = 48/678 (7%) gb AAB91579.2 (AF242881) yme [Agrobacterium tumefaciens] Length = 660
SEQ ID n°3196	Prot n°PL-4050.1	Contig20	3234	3767		
SEQ ID n°3197	Prot n°PL-4051.1	Contig20	2814	3281		
SEQ ID n°3198	Prot n°PL-4052.1	Contig20	2001	2456		
SEQ ID n°3199	Prot n°PL-4053.1	Contig20	45	503		
SEQ ID n°3200	Prot n°PL-4054.1	Contig19	6142	6558		
SEQ ID n°3201	Prot n°PL-4055.1	Contig19	5814	6359		
SEQ ID n°3202	Prot n°PL-4056.1	Contig19	3875	4306		
SEQ ID n°3203	Prot n°PL-4057.1	Contig18	129	668		
SEQ ID n°3204	Prot n°PL-4058.1	Contig17	3848	4414		
SEQ ID n°3205	Prot n°PL-406.1	Contig41	690403	691620	38%	Identities = 94/407 (23%), Positives = 158/407 (38%), Gaps = 47/407 (11%) gb AAF93665.1 (AE004135) hypothetical protein [Vibrio cholerae] Length = 388
SEQ ID n°3206	Prot n°PL-4060.1	Contig17	3117	3689		
SEQ ID n°3207	Prot n°PL-4061.1	Contig17	16	501		
SEQ ID n°3208	Prot n°PL-4062.1	Contig10	1972	2439		
SEQ ID n°3209	Prot n°PL-4063.1	Contig10	603	1196		
SEQ ID n°3210	Prot n°PL-4064.1	Contig9	728	1322		
SEQ ID n°3211	Prot n°PL-4065.1	Contig9	131	559		
SEQ ID n°3212	Prot n°PL-407.1	Contig41	693216	694325	91%	Identities = 330/369 (89%), Positives = 354/369 (95%) gb AAD46162.1 AF130307_1 (AF130307) glutathione-dependent formaldehyde dehydrogenase [Acinetobacter baumannii] Length = 176/274 (64%), Positives = 211/274 (76%) pir S75249 esterase sil0992 - Synecocystis sp. (strain PCC 6803) dbj BAA17163.1 (D90904) esterase [Synecocystis sp.] Length = 276
SEQ ID n°3213	Prot n°PL-408.1	Contig41	694448	695296	70%	

TABLEAU I

SEQ ID n°3214	Prot n°PL-409.1	Contig41	696786	698369	46%	Identities = 155/477 (32%), Positives = 245/477 (51%), Gaps = 34/477 (7%) pir S76169 hypothetical protein - <i>Synechocystis</i> sp. (strain PCC 6803) dbj BAA18428.1 (D90914) ignostibene-alpha,beta-dioxygenase [<i>Synechocystis</i> sp.] Length = 490
SEQ ID n°3215	Prot n°PL-41.1	Contig41	72671	73726	79%	Identities = 245/349 (70%), Positives = 295/349 (84%) gb AA05079.1 AE004596_5 (AE004596) translocation protein in type III secretion [<i>Pseudomonas aeruginosa</i>] Length = 349
SEQ ID n°3216	Prot n°PL-410.1	Contig41	698511	699506	55%	Identities = 139/282 (49%), Positives = 185/282 (65%), Gaps = 1/282 (0%) sp P21684 CRTE_PANAN GERANYLGERANYL PYROPHOSPHATE SYNTHETASE (GGPP SYNTHETASE) (FARNESYLTRANSFERASE) pir A37802 crtE protein - <i>Erwinia</i> uredovora dbj BAA14124.1 (D90087) crtE [Pantoea ananas] Length = Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U83995) putative protease [<i>Porphyromonas gingivalis</i>] Length = 300
SEQ ID n°3217	Prot n°PL-411.1	Contig41	699964	700848	59%	Identities = 132/200 (66%), Positives = 165/200 (82%) sp Q01335 YCR6_ERWHE HYPOTHETICAL 37.2 KD PROTEIN IN CRTE- CRTX INTERGENIC REGION (ORF6) pir S52979 hypothetical protein 6 - <i>Erwinia herbicola</i> gb AA64978.1 (M87280) gene not found in <i>Erwinia</i> uredovora crt gene cluster, ORF6 [Erwinia herbicola] Length = Identities = 204/381 (53%), Positives = 256/381 (66%), Gaps = 5/381 (1%) pir S52585 dycopene cyclase - <i>Erwinia herbicola</i> gb AAA21262.1 (M90698) dycopene cyclase [Erwinia herbicola] Length = 382
SEQ ID n°3218	Prot n°PL-413.1	Contig41	701670	702845	63%	Identities = 377/486 (77%), Positives = 419/486 (85%) sp P21685 CRTL_PANAN PHYTOENE DEHYDROGENASE (PHYTOENE DESATURASE) pir D37802 phytoene dehydrogenase (EC 1.3.-.-) crtI - <i>Erwinia uredovora</i> dbj BAA14127.1 (D90087) crtI [Pantoea ananas] emb CAC07574.1 (AX014697) unnamed protein product [Pantoea ananas]
SEQ ID n°3220	Prot n°PL-414.1	Contig41	702838	704319	82%	Identities = 177/295 (60%), Positives = 216/295 (73%) sp P21683 CRTB_PANAN PHYTOENE SYNTHASE pir E37802 crtB protein - <i>Erwinia uredovora</i> dbj BAA14128.1 (D90087) crtB [Pantoea ananas] Length = 296
SEQ ID n°3222	Prot n°PL-416.2	Contig41	706006	708164	No Hits found	
SEQ ID n°3223	Prot n°PL-417.1	Contig39	698619	699494	No Hits found	
SEQ ID n°3224	Prot n°PL-418.1	Contig39	697300	698262	No Hits found	
SEQ ID n°3225	Prot n°PL-419.1	Contig39	696138	697016	No Hits found	
SEQ ID n°3226	Prot n°PL-42.1	Contig41	74626	75444	75%	Identities = 173/273 (63%), Positives = 212/273 (77%), Gaps = 1/273 (0%) gb AA05102.1 AE004598_1 (AE004598) transcriptional regulator ExsA [<i>Pseudomonas aeruginosa</i>] Length = 278

TABLEAU I

SEQ ID n°3227	Prot n°PL-420.1	Contig39	684412	695286	59%	Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U63995) putative protease [Porphyrionomonas gingivalis] Length = 300	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°3228	Prot n°PL-421.1	Contig39	689024	694389	56%	Identities = 785/1615 (48%), Positives = 1015/1615 (62%), Gaps = 40/1615 (2%) pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] Length = 9376	
SEQ ID n°3229	Prot n°PL-422.1	Contig39	687641	689023	57%	Identities = 206/489 (42%), Positives = 269/489 (54%), Gaps = 47/489 (9%) pdb 1F31A Chain A, Crystal Structure Of TrnS Transposase Complexed With Transposon End Dna Length = 481	
SEQ ID n°3230	Prot n°PL-423.1	Contig39	672679	687630	54%	Identities = 2086/4554 (45%), Positives = 2728/4554 (59%), Gaps = 241/4554 (5%) pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] Length = 9376	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°3231	Prot n°PL-424.1	Contig39	671493	672113	31%	Identities = 51/100 (51%), Positives = 65/100 (65%), Gaps = 1/100 (1%) gb AAC82519.1 (AF027768) RetA [Serratia marcescens] Length = 495	
SEQ ID n°3232	Prot n°PL-425.1	Contig39	670120	671556	59%	Identities = 220/405 (54%), Positives = 285/405 (70%), Gaps = 1/405 (0%) pir S50828 hypothetical protein - Escherichia coli emb CAA54637.1 (X77508) Intron associated [Escherichia coli] Length = 416	
SEQ ID n°3233	Prot n°PL-426.1	Contig39	669104	669769	58%	Identities = 105/185 (56%), Positives = 130/185 (69%), Gaps = 2/185 (1%) gb AAC82519.1 (AF027768) RetA [Serratia marcescens] Length = 495	
SEQ ID n°3234	Prot n°PL-427.1	Contig39	667789	668436	40%	Identities = 59/162 (36%), Positives = 88/162 (53%), Gaps = 1/162 (0%) dbj BAB16031.1 (AB030747) transposase [Streptococcus pyogenes] Length = 428	
SEQ ID n°3235	Prot n°PL-428.1	Contig39	666472	667635	67%	Identities = 233/374 (62%), Positives = 287/374 (76%) spiP20932MDLB_PSEPU L(+)-MANDELATE DEHYDROGENASE (S-MANDELATE DEHYDROGENASE) (MDH) pir B44767 L-mandelate dehydrogenase (EC 1.1.2.-) - Pseudomonas putida gb AAC15503.1 (J05293) S-mandelate dehydrogenase [Pseudomonas putida] Length = 393	
SEQ ID n°3236	Prot n°PL-429.1	Contig39	664939	666243	54%	Identities = 164/415 (39%), Positives = 238/415 (56%), Gaps = 10/415 (2%) pir T36319 probable aminotransferase - Streptomyces coelicolor (fragment) emb CAB38598.1 (AL035654) putative aminotransferase [Streptomyces coelicolor A3(2)] Length = 431	
SEQ ID n°3237	Prot n°PL-43.1	Contig41	75559	76392	53%	Identities = 102/276 (36%), Positives = 151/276 (53%), Gaps = 1/276 (0%) gb AA05103.1 (AE004598.2) (AE004598) hypothetical protein [Pseudomonas aeruginosa] Length = 276	
SEQ ID n°3238	Prot n°PL-430.1	Contig39	658105	659652	No Hits found		
SEQ ID n°3239	Prot n°PL-432.1	Contig39	656325	657767	No Hits found		
SEQ ID n°3240	Prot n°PL-433.1	Contig39	655395	656351	No Hits found		
SEQ ID n°3241	Prot n°PL-434.1	Contig39	655281	656324	No Hits found		

TABLEAU I

SEQ ID n°3242	Prot n°PL-435.1	Contig39	652025	654922	18%	Identities = 89/433 (22%), Positives = 176/433 (39%), Gaps = 80/433 (18%) gb AAD03958.1 (AF079317) sex pilus assembly and synthesis protein [Sphingomonas aromaticivorans] Length = 856
SEQ ID n°3243	Prot n°PL-436.1	Contig39	650132	651628	No Hits found	
SEQ ID n°3244	Prot n°PL-437.1	Contig39	649174	650160	No Hits found	
SEQ ID n°3245	Prot n°PL-438.1	Contig39	645669	646739	66%	Identities = 173/340 (50%), Positives = 245/340 (71%), Gaps = 12/340 (3%) db BAA89622.1 (AB036665) similar to E.coli hypothetical protein o375 [bacteriophage WO] Length = 343
SEQ ID n°3246	Prot n°PL-44.1	Contig41	76708	76670	73%	Identities = 397/590 (67%), Positives = 482/590 (81%), Gaps = 10/590 (1%) sp Q01244 YSCC_YEREN YOP PROTEINS TRANSLOCATION PROTEIN C PRECURSOR pil C40361 virC-region hypothetical protein yscC precursor - Yersinia enterocolitica plasmid pYV gb AAC37020.1 (M74011) yscC gene product [Yersinia enterocolitica] gb AAD16836.1 (AF102990) secretin YscC [Yersinia enterocolitica] Length = 607
SEQ ID n°3247	Prot n°PL-440.1	Contig39	644686	645459	No Hits found	
SEQ ID n°3248	Prot n°PL-441.1	Contig39	643005	644387	57%	Identities = 206/489 (42%), Positives = 269/489 (54%), Gaps = 47/489 (9%) pdb 1F3 A Chain A, Crystal Structure Of Tn5 Transposase Complexed With Transposon End Dna Length = 481
SEQ ID n°3249	Prot n°PL-442.1	Contig39	641072	643030	37%	Identities = 143/598 (23%), Positives = 245/598 (40%), Gaps = 51/598 (8%) gb AAF69957.1 (AF250878_118 (AF250878)orf; hypothetical protein [Salmonella typhi] Length = 894 "
SEQ ID n°3250	Prot n°PL-443.1	Contig39	639800	640426	35%	Identities = 49/143 (34%), Positives = 74/143 (51%), Gaps = 11/143 (7%) pir G71704 hypothetical protein RP457 - Rickettsia prowazekii emb CAA14913.1 (AJ235271) unknown [Rickettsia prowazekii] Length = 290
SEQ ID n°3251	Prot n°PL-444.1	Contig39	639000	639824	No Hits found	
SEQ ID n°3252	Prot n°PL-445.1	Contig39	638263	639084	No Hits found	
SEQ ID n°3253	Prot n°PL-446.1	Contig39	634627	636132	53%	Identities = 201/511 (39%), Positives = 274/511 (53%), Gaps = 38/511 (7%) db BAA84886.1 (AB024946)orf51 [Escherichia coli] Length = 523
SEQ ID n°3254	Prot n°PL-447.1	Contig39	632397	633575	64%	Identities = 213/411 (51%), Positives = 279/411 (67%), Gaps = 28/411 (6%) sp P09750 SHU8_ECOLI SHUFFLON PROTEIN C' pir F26421 shufflon C' - Escherichia coli plasmid R64 Length = 433
SEQ ID n°3255	Prot n°PL-448.1	Contig39	631666	632331	60%	Identities = 93/224 (41%), Positives = 134/224 (59%), Gaps = 9/224 (4%) db BAA77981.1 (AB027308) prelin peptidase [Plasmid R64] 218
SEQ ID n°3256	Prot n°PL-449.1	Contig39	631036	631665	66%	Identities = 114/186 (61%), Positives = 140/186 (74%) db BAA77979.1 (AB027308) type IV prelin [Plasmid R64] Length = 204
SEQ ID n°3257	Prot n°PL-45.1	Contig41	78667	79935	65%	Identities = 208/417 (49%), Positives = 279/417 (66%), Gaps = 3/417 (0%) gb AAG05106.1 (AE004598_5 (AE004598) type III export protein PscD [Pseudomonas aeruginosa] Length = 432

TABLEAU I

SEQ ID n°3258	Prot n°PL-450.1	Contig39	629909	630994	69%	Identities = 184/360 (51%), Positives = 253/360 (70%), Gaps = 3/360 (0%) dbj BAA75181.1 (AB021076) Integral membrane protein [Plasmid Colib-P9] dbj BAA77978.1 (AB027308) Integral membrane protein [Plasmid R64] gnl PID d1038915 integral membrane protein Length = 365 Identities = 317/511 (62%), Positives = 386/511 (75%), Gaps = 8/511 (1%) gb AAF81213.1 AF247502_8 (AF247502) PilQ [Salmonella dublin] Length = 571
SEQ ID n°3259	Prot n°PL-451.1	Contig39	628363	629916	72%	Identities = 167/438 (38%), Positives = 247/438 (56%), Gaps = 22/438 (5%) gb AAF14815.2 (AF000001) PilO [Salmonella typhi] gb AAF81211.1 AF247502_6 (AF247502) PilO [Salmonella dublin] Length = 428
SEQ ID n°3260	Prot n°PL-452.1	Contig39	626561	627877	52%	Identities = 338/553 (61%), Positives = 415/553 (74%), Gaps = 15/553 (2%) dbj BAA75185.1 (AB021078) lipoprotein [Plasmid Colib-P9] dbj BAA77974.1 (AB027308) lipoprotein [Plasmid R64] gnl PID d1038919 lipoprotein Length = 560
SEQ ID n°3261	Prot n°PL-453.1	Contig39	624816	626537	72%	Identities = 187/416 (44%), Positives = 237/416 (56%), Gaps = 70/416 (16%) gb AAF14812.2 (AF000001) PilL [Salmonella typhi] gb AAF81207.1 AF247502_2 (AF247502) PilL [Salmonella dublin] Length = 414
SEQ ID n°3262	Prot n°PL-454.1	Contig39	623322	624371	65%	
SEQ ID n°3263	Prot n°PL-455.1	Contig39	619994	620926	No Hits found	
SEQ ID n°3264	Prot n°PL-456.1	Contig39	619094	619990	No Hits found	
SEQ ID n°3265	Prot n°PL-457.1	Contig39	618439	619119	33%	Identities = 44/176 (25%), Positives = 75/176 (42%), Gaps = 11/176 (6%) gb AAG05059.1 AE004594_11 (AE004594) serine/threonine phosphoprotein phosphatase Sip1 [Pseudomonas aeruginosa] Length = 242
SEQ ID n°3266	Prot n°PL-458.1	Contig39	615879	616502	No Hits found	
SEQ ID n°3267	Prot n°PL-459.1	Contig39	614028	616058	76%	Identities = 420/670 (62%), Positives = 518/670 (76%), Gaps = 8/670 (1%) gb AAF14809.1 (AF000001) topoisomerase B [Salmonella typhi] Length = 684
SEQ ID n°3268	Prot n°PL-46.1	Contig41	80671	81306	38%	Identities = 55/136 (40%), Positives = 82/136 (59%), Gaps = 8/136 (5%) sp Q00929 YSC_H_YERPS YOP PROTEINS TRANSLOCATION PROTEIN H (LOW CALCIUM RESPONSE LOCUS PROTEIN P) gb AA27649.1 (M83986) lcrP [Yersinia pseudotuberculosis] gb AAC62547.1 (AF053946) Yop proteins translocation protein H homolog [Yersinia pestis] gb AAC69828.1 (AF074612) secreted protein [Yersinia pestis] emb CAB54934.1 (AL117189) putative type III secretion protein [Yersinia pestis] Length = 165
SEQ ID n°3269	Prot n°PL-460.1	Contig39	613281	614024	46%	Identities = 64/225 (28%), Positives = 116/225 (51%), Gaps = 14/225 (6%) gb AAF84588.1 AE004000_5 (AE004000) hypothetical protein [Xylella fastidiosa] Length = 249

TABLEAU I

SEQ ID n°3270	Prot n°PL-461.1	Contig39	611771	613057	43%	Identities = 120/369 (32%), Positives = 188/369 (49%), Gaps = 31/369 (8%) gb AAF84588.1 AE004000_6 (AE004000) hypothetical protein [Xylella fastidiosa] Length = 418
SEQ ID n°3271	Prot n°PL-462.1	Contig39	608905	610647	23%	Identities = 99/194 (50%), Positives = 135/194 (69%), Gaps = 4/194 (2%) gb AAF84592.1 AE004000_9 (AE004000) hypothetical protein [Xylella fastidiosa] Length = 253
SEQ ID n°3272	Prot n°PL-463.1	Contig39	607538	608920	67%	Identities = 225/444 (50%), Positives = 313/444 (69%), Gaps = 8/444 (1%) sp P10338 DNAB_SALTY REPLICATIVE DNA HELICASE Length = 471
SEQ ID n°3273	Prot n°PL-464.1	Contig39	606664	607548	57%	Identities = 115/294 (39%), Positives = 173/294 (58%), Gaps = 18/294 (6%) gb AAF84593.1 AE004000_10 (AE004000) chromosome partitioning related protein [Xylella fastidiosa] Length = 291
SEQ ID n°3274	Prot n°PL-465.1	Contig39	605113	606129	47%	Identities = 112/305 (36%), Positives = 162/305 (52%), Gaps = 8/305 (2%) gb AAG02084.1 AF285416_2 (AF285416) XerC [Pseudomonas aeruginosa] Length = 427
SEQ ID n°3275	Prot n°PL-466.1	Contig39	603425	605050	20%	Identities = 67/220 (30%), Positives = 113/220 (50%), Gaps = 3/220 (1%) gb AAF84562.1 AE003998_4 (AE003998) hypothetical protein [Xylella fastidiosa] Length = 618
SEQ ID n°3276	Prot n°PL-467.1	Contig39	601886	602809	47%	Identities = 108/311 (34%), Positives = 165/311 (52%), Gaps = 8/311 (2%) dbj BAA75117.1 (AB021078) yccB [Plasmid Colib-P8] gnl PID1038851 yccB Length = 308
SEQ ID n°3277	Prot n°PL-468.1	Contig39	600442	601458	No Hits found	Identities = 170/252 (67%), Positives = 193/252 (76%) protein - Escherichia coli plasmid pO157 Length = 279
SEQ ID n°3278	Prot n°PL-469.1	Contig39	599784	600611	63%	Identities = 180/243 (78%), Positives = 215/243 (88%) (U56077) PscJ [Pseudomonas aeruginosa] Length = 248
SEQ ID n°3279	Prot n°PL-471.1	Contig41	81727	82484	86%	Identities = 177/298 (59%), Positives = 214/298 (71%), Gaps = 3/298 (1%) gb AAC82519.1 (AF027768) RelA [Serratia marcescens] Length = 495
SEQ ID n°3280	Prot n°PL-470.1	Contig39	597524	598450	69%	Identities = 24/54 (44%), Positives = 37/54 (68%) gb AAC82519.1 (AF027768) RelA [Serratia marcescens] Length = 495
SEQ ID n°3281	Prot n°PL-471.1	Contig39	596943	597527	14%	Identities = 96/200 (48%), Positives = 136/200 (68%), Gaps = 3/200 (1%) sp P55606 Y4OU_RHISN HYPOTHETICAL PROTEIN Y4OU PRECURSOR Length = 200
SEQ ID n°3282	Prot n°PL-472.1	Contig39	596500	597120	No Hits found	gb AAB91807.1 (AE000089) Y4OU [Rhizobium sp. NGR234] Length = 200
SEQ ID n°3283	Prot n°PL-473.1	Contig39	596634	596458	49%	Identities = 199/399 (49%), Positives = 270/399 (68%), Gaps = 3/399 (0%) sp P55606 Y4OU_RHISN HYPOTHETICAL PROTEIN Y4OU PRECURSOR Length = 200
SEQ ID n°3284	Prot n°PL-474.1	Contig39	593284	593904	No Hits found	gb AAB91807.1 (AE000089) Y4OU [Rhizobium sp. NGR234] Length = 200
SEQ ID n°3285	Prot n°PL-475.1	Contig39	591899	593143	60%	Identities = 169/270 (62%), Positives = 205/270 (75%) sp P55607 Y4OV_RHISN HYPOTHETICAL 30.2 KD PROTEIN Y4OV Length = 270
SEQ ID n°3286	Prot n°PL-476.1	Contig39	591085	591933	72%	gb AAB91808.1 (AE000089) Y4OV [Rhizobium sp. NGR234] Length = 270

THIS PAGE BLANK (USPTO)

TABLEAU I

SEQ ID n°3287	Prot n°PL-477.1	Contig39	586468	587820	60%	Identities = 190/430 (44%), Positives = 282/430 (65%), Gaps = 8/430 (1%) gb AAG03624.1 AE004461_7 (AE004461) 4-hydroxybenzoate transporter PcaK [Pseudomonas aeruginosa] Length = 448
SEQ ID n°3288	Prot n°PL-478.1	Contig39	585466	586413	50%	Identities = 106/281 (37%), Positives = 162/281 (58%), Gaps = 5/281 (1%) sp P37610 TAUD_ECOLI_ALPHA-KETOGLUTARATE-DEPENDENT TAURINE DIOXYGENASE (SULFATE STARVATION-INDUCED PROTEIN 3) (SS13) pir H64764 probable taurine dioxygenase (EC 1.-.-) - Escherichia coli dbj BAA12841.1 (D85613) dioxygenase [Escherichia coli] gb AAB18091.1 (U73857) dioxygenase [Escherichia coli] gb AAC73471.1 (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli] Length = 283
SEQ ID n°3289	Prot n°PL-479.1	Contig39	584193	585431	41%	Identities = 86/384 (22%), Positives = 173/384 (44%), Gaps = 17/384 (4%) gb AAB18085.1 (U73857) cyanate transport protein [Escherichia coli] Length = 393
SEQ ID n°3290	Prot n°PL-48.1	Contig41	82464	83090	45%	Identities = 96/205 (46%), Positives = 125/205 (60%), Gaps = 2/205 (0%) gb AAG05113.1 AE004598_12 (AE004598) type III export protein PscK [Pseudomonas aeruginosa] Length = 208
SEQ ID n°3291	Prot n°PL-480.1	Contig39	582911	584095	56%	Identities = 152/405 (37%), Positives = 228/405 (56%), Gaps = 18/405 (4%) gb AAG03835.1 AE004482_2 (AE004482) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 407
SEQ ID n°3292	Prot n°PL-481.1	Contig39	580884	582116	63%	Identities = 176/410 (42%), Positives = 260/410 (62%), Gaps = 18/410 (4%) gb AAD12607.1 (AF036894) salicylate-5-hydroxylase large oxygenase component [Ralstonia sp. U2] Length = 423
SEQ ID n°3293	Prot n°PL-482.1	Contig39	579800	580897	29%	Identities = 75/201 (37%), Positives = 107/201 (52%), Gaps = 5/201 (2%) pir C71664 hypothetical protein RP592 - Rickettsia prowazekii emb CAA15037.1 (AJ235272) unknown [Rickettsia prowazekii] Length = 204
SEQ ID n°3294	Prot n°PL-483.1	Contig39	576284	576952	54%	Identities = 87/217 (40%), Positives = 128/217 (58%), Gaps = 8/217 (3%) sp P42914 YRAI_ECOLI_HYPOTHETICAL_25.7_KD_FIMBRIAL_CHAPERONE IN AGAI-MTR INTERGENIC REGION PRECURSOR pir C65104 hypothetical 25.7 kD fimbrial chaperone in agai-mtr intergeni - Escherichia coli (strain K-12) gb AAA57946.1 (U18997) ORF_0231 [Escherichia coli] gb AAC76177.1 (AE000395) putative chaperone Length = 302/819 (36%), Positives = 476/819 (57%), Gaps = 32/819 (3%)
SEQ ID n°3295	Prot n°PL-484.1	Contig39	573765	576287	56%	Identities = 302/819 (36%), Positives = 476/819 (57%), Gaps = 32/819 (3%) sp P42915 YRAJ_ECOLI_HYPOTHETICAL_OUTER_MEMBRANE_USHER PROTEIN IN AGAI-MTR INTERGENIC REGION PRECURSOR pir D65104 probable outer membrane usher protein precursor (agal-mtr intergenic region) - Escherichia coli (strain K-12) gb AAC76178.1 (AE000395) putative outer membrane protein [Escherichia coli] Length = 838

TABLEAU I

SEQ ID n°3296	Prot n°PL-485.1	Contig39	572757	573755	18%	<p>Identities = 39/135 (28%), Positives = 61/135 (44%), Gaps = 12/135 (8%) sp P21648 MRKD_KLEPN_FIMBRIA_ADHESIN_PROTEIN_PRECURSOR pi I B32801 fimbrial adhesin precursor, type 3 - Klebsiella pneumoniae gb AA25096.1 (M55912) mrkD [Klebsiella pneumoniae] gb AA25098.1 (M24538) fimbrial adhesin [Klebsiella pneumoniae] Length = 321</p> <p>Identities = 47/133 (35%), Positives = 69/133 (51%), Gaps = 7/133 (5%) sp P12903 FM12_KLEPN_FIMBRIAL_SUBUNIT_TYPE_1_PRECURSOR pi Y QKB1 type 1 fimbrial protein precursor - Klebsiella pneumoniae (strain IA565) gb AA25091.1 (M20917) major fimbrial subunit precursor [Klebsiella pneumoniae] Length = 182</p> <p>Identities = 72/214 (33%), Positives = 108/214 (49%), Gaps = 2/214 (0%) gb AAG04554.1 AE004546_9 (AE004546) hypothetical protein [Pseudomonas aeruginosa] Length = 242</p>
SEQ ID n°3297	Prot n°PL-486.1	Contig39	571339	572367	20%	<p>Identities = 143/210 (68%), Positives = 165/210 (78%) sp Q9RPU5 HPAG_SALDU_4-HYDROXYPHENYLACETATE_DEGRADATION BIFUNCTIONAL ISOMERASE/DECARBOXYLASE [INCLUDES: 2-HYDROXYHEPTA-2,4-DIENE-1,7-DIOATE ISOMERASE (HHDD ISOMERASE), 5-CARBOXYMETHYL-2-OXO-HEX-3-ENE-1,7-DIOATE DECARBOXYLASE (OPET DECARBOXYLASE)] gb AAD53501.1 AF144422_8 (AF144422) HpaG [Salmonella dublin] Identities = 176/249 (70%), Positives = 206/249 (82%) gb AAG07509.1 AE004828_10 (AE004828) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 259</p> <p>Identities = 138/200 (69%), Positives = 167/200 (83%), gb AAC37030.1 (M74011) putative [Yersinia enterocolitica] Length = 212</p> <p>Identities = 447/488 (91%), Positives = 471/488 (96%) emb CAA86041.1 (Z37980) 5-carboxy-2-hydroxymuconate semialdehyde dehydrogenase [Escherichia coli] Length = 488</p> <p>Identities = 251/282 (89%), Positives = 268/282 (95%) gb AAD53498.1 AF144422_6 (AF144422) HpaD [Salmonella dublin] Length = 283</p>
SEQ ID n°3298	Prot n°PL-487.1	Contig39	570550	571326	41%	<p>Identities = 168/384 (43%), Positives = 234/384 (60%), Gaps = 7/384 (1%) gb AAG07523.1 AE004830_4 (AE004830) probable MFS transporter [Pseudomonas aeruginosa] Length = 402</p> <p>Identities = 323/480 (67%), Positives = 395/480 (82%), Gaps = 1/480 (0%) gb AAG03654.1 AE004464_7 (AE004464) succinate-semialdehyde dehydrogenase [Pseudomonas aeruginosa] Length = 483</p> <p>Identities = 230/267 (86%), Positives = 244/267 (91%) emb CAA86044.1 (Z37980) 2-oxo-hept-3-ene-1,7-dioate hydratase [Escherichia coli] gb AAB91474.1 (AF038583) 2-oxo-hept-4-ene-1,7-dioate hydratase [Escherichia coli] Length = 267</p>
SEQ ID n°3299	Prot n°PL-488.1	Contig39	569008	569640	76%	
SEQ ID n°3300	Prot n°PL-489.1	Contig39	568250	568011	68%	
SEQ ID n°3301	Prot n°PL-49.1	Contig41	83069	83686	79%	
SEQ ID n°3302	Prot n°PL-490.1	Contig39	566784	568250	95%	
SEQ ID n°3303	Prot n°PL-491.1	Contig39	565841	566719	80%	
SEQ ID n°3304	Prot n°PL-492.1	Contig39	564209	565447	56%	
SEQ ID n°3305	Prot n°PL-493.1	Contig39	562747	564219	79%	
SEQ ID n°3306	Prot n°PL-494.1	Contig39	561939	562742	88%	

TABLEAU I

SEQ ID n°3307	Prot n°PL-495.1	Contig39	561121	561954	78%	Identities = 201/265 (75%), Positives = 229/265 (85%), Gaps = 2/265 (0%) sp Q8RPV0 HPIA1_SALDU 2,4-DIHYDROXYHEPT-2-ENE-1,7-DIOIC ACID ALDOLASE (HEDD ALDOLASE) gb AAD53496.1 AF144422_3 (AF144422) HpaI [Salmonella dublin] Length = 263
SEQ ID n°3308	Prot n°PL-496.1	Contig39	559648	561024	88%	Identities = 356/458 (77%), Positives = 409/458 (88%) gb AAD53495.1 AF144422_2 (AF144422) HpaX [Salmonella dublin] Length = 458
SEQ ID n°3309	Prot n°PL-497.1	Contig39	558732	559622	77%	Identities = 201/293 (68%), Positives = 234/293 (79%) gb AAD53494.1 AF144422_1 (AF144422) HpaA [Salmonella dublin] Length = 298
SEQ ID n°3310	Prot n°PL-498.1	Contig39	555580	556326	76%	Identities = 164/245 (66%), Positives = 196/245 (79%) sp P52037 YGF_ECOLI_HYPOTHETICAL_OXIDOREDUCTASE_IN_BGLA- GCVP_INTERGENIC_REGION_pir F65074 hypothetical oxidoreductase - Escherichia coli (strain K-12) gb AAC75940.1 AE000373 putative oxidoreductase [Escherichia coli] Length = 247
SEQ ID n°3311	Prot n°PL-499.1	Contig39	552433	555312	61%	Identities = 519/691 (75%), Positives = 591/691 (85%), Gaps = 5/691 (0%) gb AAC38630.1 AF047028 insecticidal toxin complex protein TccC [Photobacterium luminescens] Length = 1043
SEQ ID n°3312	Prot n°PL-5.1	Contig41	13475	14407	No Hits found	Identities = 163/301 (54%), Positives = 209/301 (69%), Gaps = 10/301 (3%) gb AAC62582.1 AF053946 unknown [Yersinia pestis] gb AAC69833.1 (AF074612) Yop targeted effector [Yersinia pestis] emb CAB54897.1 (AL117189) putative cytotoxic effector protein [Yersinia pestis] Length =
SEQ ID n°3313	Prot n°PL-50.1	Contig41	83838	84824	63%	Identities = 493/520 (94%), Positives = 507/520 (98%) gb AAC08739.1 (AF021839) 4-hydroxyphenylacetic acid hydroxylase [Photobacterium luminescens] Length = 520
SEQ ID n°3314	Prot n°PL-500.1	Contig39	550549	552111	94%	Identities = 378/483 (78%), Positives = 434/483 (89%) sp P36837 YHIP_ECOLI_HYPOTHETICAL_53.7_KD_PROTEIN_IN_USPA-PRLC INTERGENIC_REGION_pir C65147 hypothetical 53.7 kD protein in uspa-prlc intergenic region - Escherichia coli (strain K-12) gb AAC76521.1 (AE000426) putative transport protein [Escherichia coli] Length = 489
SEQ ID n°3315	Prot n°PL-501.1	Contig39	548072	549541	86%	Identities = 62/229 (27%), Positives = 97/228 (42%), Gaps = 19/229 (8%) pir T33131 hypothetical protein C23H6.1 - Caenorhabditis elegans gb AAC17532.1 AF067609 contains similarity to methyltransferases [Caenorhabditis elegans] Length = 365
SEQ ID n°3316	Prot n°PL-502.1	Contig39	547214	547936	40%	Identities = 686/1176 (58%), Positives = 848/1176 (71%), Gaps = 117/1176 (9%) gb AAF05542.1 AF180483_1 (AF180483) toxin A [Photobacterium luminescens] Length = 2516
SEQ ID n°3317	Prot n°PL-503.1	Contig39	539762	546427	38%	Identities = 1451/2152 (67%), Positives = 1688/2152 (78%), Gaps = 98/2152 (4%) gb AAF05542.1 AF180483_1 (AF180483) toxin A [Photobacterium luminescens] Length = 2516
SEQ ID n°3318	Prot n°PL-504.1	Contig39	531955	539451	67%	Unknown, similar to insecticidal toxins

TABLEAU I

SEQ ID n°3318	Prot n°PL-505.1	Contig39	527471	531898	72%	Identities = 861/1488 (57%), Positives = 1084/1488 (71%), Gaps = 28/1488 (1%) gb AAC38625.1 (AF046867) insecticidal toxin complex protein TcaC [Photorhabdus luminescens] Length = 1485	Unknown, similar to insecticidal toxins
SEQ ID n°3320	Prot n°PL-506.1	Contig39	524037	526949	61%	Identities = 508/725 (70%), Positives = 601/725 (82%), Gaps = 17/725 (2%) gb AAC38630.1 (AF047028) insecticidal toxin complex protein TccC [Photorhabdus luminescens] Length = 1043	Unknown, similar to insecticidal toxins
SEQ ID n°3321	Prot n°PL-507.1	Contig39	522980	523927	13%	Identities = 29/75 (39%), Positives = 42/75 (55%) gb AAC48441.1 (AF009224) LysR-type transcriptional activator [Achromobacter sp. ADP1] Length = 304	
SEQ ID n°3322	Prot n°PL-508.1	Contig39	515266	522663	68%	Identities = 1457/2113 (68%), Positives = 1679/2113 (78%), Gaps = 58/2113 (2%) gb AAF05542.1 (AF188483) toxin A [Photorhabdus luminescens] Length = 2516	Unknown, similar to insecticidal toxins
SEQ ID n°3323	Prot n°PL-509.1	Contig39	512257	515073	61%	Identities = 497/685 (72%), Positives = 579/685 (83%), Gaps = 13/685 (1%) gb AAC38630.1 (AF047028) insecticidal toxin complex protein TccC [Photorhabdus luminescens] Length = 1043	Unknown, similar to insecticidal toxins
SEQ ID n°3324	Prot n°PL-51.1	Contig41	87125	87976	No Hits found		
SEQ ID n°3325	Prot n°PL-510.1	Contig39	511171	512094	18%	Identities = 34/109 (31%), Positives = 57/109 (52%), Gaps = 8/109 (7%) sp P52044 YGF_L_ECOLI HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN SBM-FBA INTERGENIC REGION pir H65078 hypothetical protein b2921 - Escherichia coli (strain K-12) gb AAA69088.1 (U28377) ORF_f303 [Escherichia coli] gb AAC75958.1 (AE000375) putative transcriptional regulator LYSR-type [Escherichia coli] Length = 303	
SEQ ID n°3326	Prot n°PL-511.1	Contig39	502909	510486	91%	Identities = 2213/2530 (87%), Positives = 2334/2530 (91%), Gaps = 19/2530 (0%) gb AAF05542.1 (AF188483) toxin A [Photorhabdus luminescens] Length = 2516	Unknown, similar to insecticidal toxins
SEQ ID n°3327	Prot n°PL-512.1	Contig39	498426	502856	73%	Identities = 880/1486 (59%), Positives = 1089/1486 (73%), Gaps = 18/1486 (1%) gb AAC38625.1 (AF046867) insecticidal toxin complex protein TcaC [Photorhabdus luminescens] Length = 1485	Unknown, similar to insecticidal toxins
SEQ ID n°3328	Prot n°PL-513.1	Contig39	495088	497845	60%	Identities = 466/684 (68%), Positives = 556/684 (81%), Gaps = 18/684 (2%) gb AAC38630.1 (AF047028) insecticidal toxin complex protein TccC [Photorhabdus luminescens] Length = 1043	Unknown, similar to insecticidal toxins
SEQ ID n°3329	Prot n°PL-514.1	Contig39	492705	493781	90%	Identities = 313/358 (87%), Positives = 339/358 (94%) sp O52402 ALF_EDWIC FRUCTOSE-BISPHOSPHATE ALDOLASE gb AA892572.1 (AF037440) fructose 1,6-bisphosphate aldolase [Edwardsiella] Length = 358	
SEQ ID n°3330	Prot n°PL-515.1	Contig39	491479	492642	92%	Identities = 334/387 (86%), Positives = 367/387 (94%) sp P11665 PGK_ECOLI PHOSPHOGLYCERATE KINASE pir TVECG phosphoglycerate kinase (EC 2.7.2.3) - Escherichia coli emb CAA32604.1 (X14436) phosphoglycerate kinase (AA 1-387) [Escherichia coli] gb AAA69093.1 (U28377) phosphoglycerate kinase [Escherichia coli] gb AAC75963.1 (AE000376) phosphoglycerate kinase [Escherichia coli] Length = 387	

TABLEAU I

SEQ ID n°3331	Prot n°PL-516.1	Contig39	490376	491395	86%	<p>Identities = 266/339 (78%), Positives = 301/339 (88%) sp P11603 E4PD_ECOLI D-ERYTHROSE 4-PHOSPHATE DEHYDROGENASE (E4PDH) pir DEECGB glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) B - Escherichia coli emb CAA32603.1 (X14436) glyceraldehyde 3-phosphate dehydrogenase (AA 1-339) [Escherichia coli] gb AA69084.1 (U28377) glyceraldehyde 3-phosphate dehydrogenase [Escherichia coli] gb AAC75984.1 (AE000376) D- erythrose 4-phosphate dehydrogenase [Escherichia coli] Length = 339 Identities = 78/219 (35%), Positives = 119/219 (53%), Gaps = 8/218 (3%) emb CAB84355.1 (AJ243941) eugenol hydroxylase flavoprotein subunit [Pseudomonas sp.] Length = 517</p>
SEQ ID n°3332	Prot n°PL-517.1	Contig39	487935	488726	45%	<p>Identities = 83/196 (42%), Positives = 119/196 (60%), Gaps = 1/196 (0%) gb AAG06319.1 AE004719_5 (AE004719) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 196</p>
SEQ ID n°3333	Prot n°PL-518.1	Contig39	487164	487757	59%	<p>Identities = 542/663 (81%), Positives = 601/663 (89%) sp P27302 TKT1_ECOLI TRANSKETOLASE 1 (TK 1) pir XJECTK transketolase (EC 2.2.1.1) A - Escherichia coli gb AAC75972.1 (AE000376) transketolase 1 isozyme [Escherichia coli] Length = 663</p>
SEQ ID n°3335	Prot n°PL-52.1	Contig41	90847	91893	No Hits found	
SEQ ID n°3336	Prot n°PL-520.1	Contig39	482144	482898	32%	<p>Identities = 55/214 (25%), Positives = 92/214 (42%), Gaps = 9/214 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230</p>
SEQ ID n°3337	Prot n°PL-521.1	Contig39	480112	480858	84%	<p>Identities = 183/242 (75%), Positives = 213/242 (87%) sp P14566 DPP3E_SALTY DNA POLYMERASE III, EPSILON CHAIN gb AA86422.1 (U44090) dnaQ [Salmonella typhimurium] gb AAC44792.1 (U77466) DNA polymerase III epsilon chain [Salmonella typhimurium]</p>
SEQ ID n°3338	Prot n°PL-522.1	Contig39	478870	478583	72%	<p>Identities = 139/242 (57%), Positives = 175/242 (71%), Gaps = 1/242 (0%) pir G64745 probable membrane protein yafS - Escherichia coli gb AAC73318.1 (AE000130) orf, hypothetical protein [Escherichia coli] Length = 246</p>
SEQ ID n°3339	Prot n°PL-523.1	Contig39	478073	478825	70%	<p>Identities = 136/251 (54%), Positives = 180/251 (71%), Gaps = 1/251 (0%) sp Q47677 GLO2_ECOLI PROBABLE HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II) (GLX II) pir F64745 probable hydroxyacylglutathione hydrolase (EC 3.1.2.6) glbB - Escherichia coli gb AAB08634.1 (U70214) hypothetical protein [Escherichia coli] gb AAC73317.1 (AE000130) probable hydroxyacylglutathione hydrolase [Escherichia coli] db BAA77883.1 (D83536) Hypothetical protein 1 [Escherichia coli] Length = 251</p>

TABLEAU I

SEQ ID n°3340	Prot n°PL-524.1	Contig39	476640	478001	71%	Identities = 250/457 (54%), Positives = 329/457 (71%), Gaps = 24/457 (5%) sp P23931 MLTD_ECOLI MEMBRANE-BOUND LYTIC MUREIN HYDROLASE D) (REGULATORY PROTEIN DNIR) p j E64745 regulatory protein dnir - Escherichia coli gb AA080833.1 (U70214) DnIR [Escherichia coli] gb AAC73316.1 (AE000130) transcriptional regulator for nitrite reductase (cytochrome c552) [Escherichia coli] Length = 452
SEQ ID n°3341	Prot n°PL-525.1	Contig39	475056	476027	17%	Identities = 32/120 (26%), Positives = 57/120 (46%), Gaps = 15/120 (12%) dbj BAA97424.1 (AB025638) 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana] Length = 362
SEQ ID n°3342	Prot n°PL-526.1	Contig39	473643	474848	38%	Identities = 70/325 (21%), Positives = 154/325 (46%), Gaps = 30/325 (9%) dbj BAB06758.1 (AP001514) unknown conserved protein in others [Bacillus halodurans] Length = 418
SEQ ID n°3343	Prot n°PL-527.1	Contig39	471777	472952	27%	Identities = 60/254 (23%), Positives = 108/254 (41%), Gaps = 14/254 (5%) p j S77024 hypothetical protein sil0785 - Synecocystis sp. (strain PCC 6803) dbj BAA10716.1 (D64005) hypothetical protein [Synecocystis sp.] Length = 362
SEQ ID n°3344	Prot n°PL-528.1	Contig39	470965	471816	40%	Identities = 70/235 (29%), Positives = 116/235 (48%), Gaps = 22/235 (9%) sp Q57573 Y109_METJA HYPOTHETICAL PROTEIN MJ0109 p j E64313 hypothetical protein MJ0109 - Methanococcus jannaschii gb AAB98091.1 (U67468) extragenic suppressor (subB) [Methanococcus jannaschii] Length = 252
SEQ ID n°3345	Prot n°PL-529.1	Contig39	469889	470974	No Hits found	Identities = 150/365 (41%), Positives = 233/365 (63%), Gaps = 2/365 (0%) p j S48408 hypothetical protein - Aeromonas salmonicida gb AAA72049.1 (L27156) [Aeromonas salmonicida gene, complete cds.] gene product Length = 371
SEQ ID n°3346	Prot n°PL-53.1	Contig41	93459	94556	62%	
SEQ ID n°3347	Prot n°PL-530.1	Contig39	468888	469934	No Hits found	Identities = 42/167 (25%), Positives = 74/167 (44%), Gaps = 25/167 (14%) emb CAB87851.1 (AL163832) leucoanthocyanidin dioxygenase-like protein [Arabidopsis thaliana] Length = 363
SEQ ID n°3348	Prot n°PL-531.1	Contig39	466218	467186	22%	Identities = 228/389 (58%), Positives = 283/389 (72%), Gaps = 3/389 (0%) gb AAG08933.1 AE004967_4 (AE004967) probable MFS transporter [Pseudomonas aeruginosa] Length = 401
SEQ ID n°3349	Prot n°PL-532.1	Contig39	463861	465033	71%	
SEQ ID n°3350	Prot n°PL-533.2	Contig39	462354	463739		
SEQ ID n°3351	Prot n°PL-534.1	Contig39	460476	461378	29%	Identities = 56/202 (27%), Positives = 88/202 (42%), Gaps = 9/202 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°3352	Prot n°PL-535.1	Contig39	459593	460465	30%	Identities = 53/202 (26%), Positives = 88/202 (43%), Gaps = 9/202 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230

TABLEAU I

SEQ ID n°3353	Prot n°PL-536.1	Contig39	458709	459473	33%	Identities = 49/202 (24%), Positives = 85/202 (41%), Gaps = 9/202 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°3354	Prot n°PL-537.1	Contig39	457701	458564	30%	Identities = 56/202 (27%), Positives = 88/202 (42%), Gaps = 9/202 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°3355	Prot n°PL-538.1	Contig39	456661	457434	33%	Identities = 54/202 (26%), Positives = 87/202 (42%), Gaps = 9/202 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°3356	Prot n°PL-539.1	Contig39	455638	456453	33%	Identities = 57/202 (28%), Positives = 91/202 (44%), Gaps = 9/202 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°3357	Prot n°PL-54.1	Contig41	95390	96478	No Hits found	
SEQ ID n°3358	Prot n°PL-540.1	Contig39	454594	455367	34%	Identities = 54/202 (26%), Positives = 88/202 (42%), Gaps = 9/202 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°3359	Prot n°PL-541.1	Contig39	453711	454676	27%	Identities = 55/202 (27%), Positives = 89/202 (43%), Gaps = 9/202 (4%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230
SEQ ID n°3360	Prot n°PL-542.1	Contig39	451422	452618	38%	Identities = 79/372 (21%), Positives = 152/372 (40%), Gaps = 25/372 (6%) dbj BAB05798.1 (AP01514) unknown conserved protein in others [Bacillus halodurans] Length = 392
SEQ ID n°3361	Prot n°PL-543.1	Contig39	450221	451402	65%	Identities = 185/387 (47%), Positives = 260/387 (66%), Gaps = 4/387 (1%) pir A71692 iron-sulfur cofactor synthesis protein RP486 - Rickettsia prowazekii emb CAA14939.1 (A1235272) NIFS PROTEIN HOMOLOG (spi1) [Rickettsia prowazekii] Length = 410
SEQ ID n°3362	Prot n°PL-544.1	Contig39	449257	450030	No Hits found	
SEQ ID n°3363	Prot n°PL-545.1	Contig39	447438	448658	42%	Identities = 95/387 (24%), Positives = 171/387 (43%), Gaps = 7/387 (1%) pir C75251 phosphopyruvate hydratase - Deinococcus radiodurans (strain R1) Length = 499
SEQ ID n°3364	Prot n°PL-546.1	Contig39	447339	448640	93%	Identities = 386/434 (88%), Positives = 414/434 (94%), Gaps = 3/434 (0%) sp P08324 ENO_ECOLI ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) pir INOC phosphopyruvate hydratase (EC 4.2.1.11) - Escherichia coli (strain K-12) gb AA69289.1 (U29580) enolase [Escherichia coli] gb AAC75821.1 (AE000361) enolase [Escherichia coli] Length = 432
SEQ ID n°3365	Prot n°PL-547.1	Contig39	445628	447265	94%	Identities = 479/545 (87%), Positives = 518/545 (94%) sp P08399 PYRG_ECOLI CTP SYNTHASE (UTP--AMMONIA LIGASE) (CTP SYNTHETASE) pir SYECTP CTP synthase (EC 6.3.4.2) - Escherichia coli gb AA69289.1 (U29580) CTP synthetase [Escherichia coli] gb AAC75822.1 (AE000361) CTP synthetase [Escherichia coli] Length = 545

TABLEAU I

SEQ ID n°3366	Prot n°PL-548.1	Contig39	444627	445406	78%	<p>Identities = 178/260 (68%), Positives = 208/260 (78%)</p> <p>sp P33646 MAZG_ECOLI_MAZG_PROTEIN_pir J65060 mazG protein - Escherichia coli (strain K-12) gb AA69291.1 (U29580) CG Site No. 33299 [Escherichia coli]</p> <p>Identities = 598/744 (80%), Positives = 670/744 (89%), Gaps = 1/744 (0%)</p> <p>sp P11585 RELA_ECOLI_GTP_PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) ((PPPPGPP SYNTHETASE) pir KIECG GTP pyrophosphokinase (EC 2.7.6.5) - Escherichia coli gb AA69294.1 (U29580) GTP pyrophosphokinase [Escherichia coli] gb AAC75826.1 (AE000362) (p)ppGpp synthetase I (GTP pyrophosphokinase); regulation of RNA synthesis; stringent factor [Escherichia coli] Length = 744 "</p>
SEQ ID n°3367	Prot n°PL-549.1	Contig39	442328	444559	89%	<p>Identities = 155/220 (70%), Positives = 184/220 (83%)</p> <p>sp P76458 ATOD_ECOLI_ACETATE_COA-TRANSFERASE ALPHA SUBUNIT (ACETYL-COA-ACETOACETATE COA TRANSFERASE) pir C64892 atoD protein - Escherichia coli (strain K-12) dbj BAA16017.1 (D90851) Acetyl-CoA:acetoacetyl-CoA transferase a subunit (EC 2.8.3.-) [Escherichia coli] gb AAC75821.1 (AE000311) acetyl-CoA:acetoacetyl-CoA transferase alpha subunit [Escherichia coli] Length = 220</p>
SEQ ID n°3368	Prot n°PL-550.1	Contig41	97104	97763	82%	<p>Identities = 262/438 (59%), Positives = 328/438 (74%), Gaps = 7/438 (1%)</p> <p>sp P55135 YGCA_ECOLI_HYPOTHETICAL_RNA_METHYLTRANSFERASE IN RELA-BARA INTERGENIC REGION pir E65060 ygcA protein - Escherichia coli (strain K-12) gb AAA69295.1 (U29580) alternate gene name ygcA; ORF_f433 [Escherichia coli] gb AAC75827.1 (AE000382) putative enzyme [Escherichia coli] Length = 433 "</p>
SEQ ID n°3370	Prot n°PL-551.1	Contig39	438589	440916	62%	<p>Identities = 347/770 (45%), Positives = 485/770 (62%), Gaps = 39/770 (5%)</p> <p>sp P26607 BARA_ECOLI_SENSOR_PROTEIN_BARA_pir S20550 sensor-regulator protein barA (EC 2.7.3.-) - Escherichia coli dbj BAA01710.1 (D10888) sensor-regulator protein [Escherichia coli] gb AAC75828.1 (AE000362) sensor-regulator, activates OmpR by phosphorylation [Escherichia coli] Length = 918</p>
SEQ ID n°3371	Prot n°PL-552.1	Contig39	437048	438574	73%	<p>Identities = 293/510 (57%), Positives = 376/510 (73%), Gaps = 6/510 (1%)</p> <p>sp P15723 DGTP_ECOLI_DEOXYGUANOSINETRIPHOSPHATE TRIPHOSPHOHYDROLASE (DGTPASE) pir J35993 dGTPase (EC 3.1.5.1) - Escherichia coli gb AAA23679.1 (M31772) dGTP triphosphohydrolase [Escherichia coli] dbj BAA05607.1 (D26562) deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli] gb AAB08590.1 (U70214) deoxyguanosine triphosphate [Escherichia coli] gb AAC73271.1 (AE000125) deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli] Length = 505</p>

TABLEAU I

SEQ ID n°3372	Prot n°PL-553.1	Contig39	436219	436820	81%	Identities = 170/230 (73%), Positives = 198/230 (86%) sp P24247 PFS_ECOLI_MTA/SAH NUCLEOSIDASE (P48) [INCLUDES: 5'-METHYLTHIOADENOSINE NUCLEOSIDASE; S-ADENOSYLHOMOCYSTEINE NUCLEOSIDASE] pir S45227 pfs protein - Escherichia coli dbj BA05606.1 (D26562) 'ORF' [Escherichia coli] gb AAB08589.1 (U70214) similar to purine nucleoside phosphorylase (deoD) [Escherichia coli] gb AAC73270.1 (AE000125) orf, hypothetical protein [Escherichia coli] gb AAC38291.1 (U24438) MTA/SAH nucleosidase [Escherichia coli] Length = 232 "	
SEQ ID n°3373	Prot n°PL-554.1	Contig39	435186	436097	60%	Identities = 137/247 (55%), Positives = 185/247 (74%), Gaps = 3/247 (1%) sp P37028 YADT_ECOLI HYPOTHETICAL 29.4 KD PROTEIN IN HEML-PFS INTERGENIC REGION PRECURSOR pir F64739 yadT protein - Escherichia coli gb AAB08588.1 (U70214) hypothetical [Escherichia coli] gb AAC73269.1 (AE000125) orf, hypothetical protein [Escherichia coli] Length = 263	
SEQ ID n°3374	Prot n°PL-555.1	Contig39	433659	434492	58%	Identities = 112/262 (42%), Positives = 162/262 (61%), Gaps = 3/262 (1%) gb AAF94488.1 (AE004213) hypothetical protein [Vibrio cholerae] Length = 275	
SEQ ID n°3375	Prot n°PL-556.1	Contig39	432325	433608	90%	Identities = 362/426 (84%), Positives = 391/426 (90%) sp P23893 GSA_ECOLI GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) pir B64739 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Escherichia coli gb AAB08584.1 (U70214) glutamine-1-semialdehyde aminotransferase [Escherichia coli] gb AAC73265.1 (AE000125) glutamate-1-semialdehyde aminotransferase (aminomutase) [Escherichia coli] Length = 426	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°3376	Prot n°PL-557.1	Contig39	425251	431283	41%	Identities = 568/1506 (37%), Positives = 842/1506 (55%), Gaps = 70/1506 (4%) emb CAC01604.1 (AJ269505) peptide synthetase [Anabaena sp. 90] Length = 5060	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°3377	Prot n°PL-558.1	Contig39	420521	425257	53%	Identities = 587/1505 (39%), Positives = 852/1505 (56%), Gaps = 78/1505 (5%) emb CAC01604.1 (AJ269505) peptide synthetase [Anabaena sp. 90] Length = 5060	Unknown, similar to proteins involved in antibiotic biosynthesis
SEQ ID n°3378	Prot n°PL-559.1	Contig39	416994	420527	56%	Identities = 479/1096 (43%), Positives = 670/1096 (60%), Gaps = 62/1096 (5%) gb AAF17281.1 (AF204805) NosD [Nostoc sp. GSV224] Length = 2450	Unknown, similar to proteins involved in antibiotic biosynthesis

TABLEAU I

SEQ ID n°3378	Prot n°PL-56.1	Contig41	97766	98425	72%	<p>sp P76459 ATOA_ECOLI_ACETATE_COA-TRANSFERASE BETA SUBUNIT (ACETYL-COA:ACETOACETATE COA TRANSFERASE) pir D64992 atoA protein - Escherichia coli (strain K-12) dbj BAA16018.1 (D90851) Acetyl-CoA:acetoacetyl-CoA transferase b subunit (EC 2.8.3.-). [Escherichia coli] gb AAC75282.1 (AE000311) acetyl-CoA:acetoacetyl-CoA transferase beta subunit [Escherichia coli] Length = 216</p> <p>Identities = 148/209 (70%), Positives = 177/209 (83%)</p>
SEQ ID n°3380	Prot n°PL-560.1	Contig39	414897	416228	27%	<p>sp P39410 YJJJ_ECOLI_HYPOTHETICAL_49.8_KD_PROTEIN_IN_DEOD-LPLA INTERGENIC REGION (O443) pir S56609 yjjj protein - Escherichia coli gb AAA97281.1 (U14003) yjjj gene product [Escherichia coli] gb AAC77338.1 (AE000508) orf, hypothetical protein [Escherichia coli]</p> <p>Identities = 83/317 (26%), Positives = 124/317 (38%), Gaps = 52/317 (16%)</p>
SEQ ID n°3381	Prot n°PL-561.1	Contig39	408262	409938	27%	<p>Identities = 114/283 (40%), Positives = 151/283 (53%), Gaps = 12/283 (4%)</p> <p>pir A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] Length = 766</p>
SEQ ID n°3382	Prot n°PL-562.1	Contig39	405324	407780	83%	<p>Identities = 576/845 (68%), Positives = 688/845 (81%), Gaps = 31/845 (3%)</p> <p>pir ZPECPB penicillin-binding protein 1B - Escherichia coli gb AAC73260.1 (AE000124) peptidoglycan synthetase; penicillin-binding protein 1B [Escherichia coli] Length = 844 "</p>
SEQ ID n°3383	Prot n°PL-563.1	Contig39	402741	405230	74%	<p>Identities = 511/829 (61%), Positives = 626/829 (74%), Gaps = 5/829 (0%)</p> <p>pir D64738 ATP-dependent helicase hrpB - Escherichia coli gb AAC73259.1 (AE000124) helicase, ATP-dependent [Escherichia coli] Length = 824</p>
SEQ ID n°3384	Prot n°PL-564.1	Contig39	401367	402209	61%	<p>Identities = 131/255 (51%), Positives = 174/255 (67%), Gaps = 5/255 (1%)</p> <p>gb AAD38234.1 (U17224) CarF [Pectobacterium carotovorum] Length = 288</p>
SEQ ID n°3385	Prot n°PL-565.1	Contig38	398019	398690	No Hits found	
SEQ ID n°3386	Prot n°PL-566.1	Contig38	396894	397796	45%	<p>Identities = 75/272 (27%), Positives = 138/272 (49%), Gaps = 9/272 (3%)</p> <p>gb AAF93929.1 (AE004161) hypothetical protein [Vibrio cholerae] Length = 305</p>
SEQ ID n°3387	Prot n°PL-567.1	Contig38	394554	396056	84%	<p>Identities = 368/500 (77%), Positives = 430/500 (85%), Gaps = 1/500 (0%)</p> <p>sp P13035 GLPD_ECOLI_AEROBIC_GLYCEROL-3-PHOSPHATE DEHYDROGENASE pir DEECGD glycerol-3-phosphate dehydrogenase (EC 1.1.99.5), aerobic - Escherichia coli gb AA24636.1 (M55989) glycarophosphate dehydrogenase [Escherichia coli] gb AAC76451.1 (AE000418) sn-glycerol-3-phosphate dehydrogenase (aerobic) [Escherichia coli] Length = 501</p>

TABLEAU I

SEQ ID n°3388	Prot n°PL-588.1	Contig38	393555	394313	87%	Identities = 194/252 (76%), Positives = 224/252 (87%) pir B65138 glpR protein - Escherichia coli (strain K-12) gb AAA58221.1 (U18997) CG Site No. 688 [Escherichia coli] gb AAC28167.1 (M96795) repressor protein [Escherichia coli] gb AAC76448.1 (AE000418) repressor of the glp operon [Escherichia coli] Length = 252
SEQ ID n°3389	Prot n°PL-589.1	Contig38	392689	393537	66%	Identities = 136/277 (49%), Positives = 192/277 (69%), Gaps = 4/277 (1%) pir BVCECG glpG protein - Escherichia coli gb AAC28166.1 (M96795) the translation start site has been verified [Escherichia coli] gb AAC76449.1 (AE000418) protein of glp regulon [Escherichia coli]
SEQ ID n°3390	Prot n°PL-57.1	Contig41	99269	100273	35%	Identities = 73/267 (27%), Positives = 120/267 (44%), Gaps = 19/267 (7%) pir T36184 probable oxygenase - Streptomyces coelicolor emb CAB38880.1 (AL035707) putative oxygenase [Streptomyces coelicolor A3(2)] Length = 333
SEQ ID n°3391	Prot n°PL-570.1	Contig38	390898	391579	51%	Identities = 109/234 (46%), Positives = 151/234 (63%) pir H65136 hypothetical 27.7 kD protein in bioh-gntt intergenic region - Escherichia coli (strain K-12) gb AAA58211.1 (U18997) ORF_o243 [Escherichia coli] gb AAC76438.1 (AE000417) orf, hypothetical protein [Escherichia coli]
SEQ ID n°3392	Prot n°PL-571.1	Contig38	389348	390556	81%	Identities = 176/377 (46%), Positives = 248/377 (65%), Gaps = 2/377 (0%) pir S16426 tyrosine-tRNA ligase (EC 6.1.1.1) TyrZ - Bacillus subtilis emb CAA51565.1 (X73124) ipa-9r [Bacillus subtilis] emb CAB15872.1 (Z99123) tyrosyl-tRNA synthetase [Bacillus subtilis] Length = 413
SEQ ID n°3393	Prot n°PL-572.1	Contig38	387309	388094	74%	Identities = 164/255 (64%), Positives = 202/255 (78%) sp P13001 BIOH_EC01 BIOH PROTEIN pir BVCEBH bioH protein - Escherichia coli emb CAA33612.1 (X15587) bioH protein (AA 1-256) [Escherichia coli] gb AAA58210.1 (U18997) CG Site No. 954; alternate name bioB [Escherichia coli] gb AAC76437.1 (AE000417) biotin biosynthesis; reaction prior to pimeloyl CoA [Escherichia coli] Length = 256
SEQ ID n°3394	Prot n°PL-573.1	Contig38	383921	386233	85%	Identities = 568/774 (73%), Positives = 660/774 (84%), Gaps = 5/774 (0%) sp P33650 FEOB_EC01 FERROUS IRON TRANSPORT PROTEIN B pir A36932 iron(I) transport system protein feoB - Escherichia coli emb CAA50387.1 (X71063) ferrous iron transport protein B [Escherichia coli] gb AAC76434.1 (AE000416) ferrous iron transport protein B [Escherichia coli] Length = 773
SEQ ID n°3395	Prot n°PL-574.1	Contig38	380907	383237	88%	Identities = 648/776 (83%), Positives = 698/776 (89%), Gaps = 4/776 (0%) sp P46837 YHGF_EC01 85.1 KDA PROTEIN IN GREB-FEOA INTERGENIC REGION Length = 773

TABLEAU I

SEQ ID n°3396	Prot n°PL-575.1	Contig38	378438	378157	75%	<p>Identities = 194/238 (82%), Positives = 216/238 (91%)</p> <p>spiP03025 OMPR_ECOLI TRANSCRIPTIONAL REGULATORY PROTEIN OMPR pir IRGECOR osmosensor response regulator ompR - Escherichia coli gb AAA16241.1 (J01656) OmpR protein [Escherichia coli] emb CAA54510.1 (X77305) ompR [Salmonella typhi] gb AAA58202.1 (U18987) CG Site No. 434; alternate name ompB [Escherichia coli] gb AAC76430.1 (AE000446) response regulator (sensor, EnvZ) affecting transcription of ompC and ompF; outer membrane protein synthesis [Escherichia coli]</p>
SEQ ID n°3397	Prot n°PL-576.1	Contig38	377110	378441	76%	<p>Identities = 293/438 (66%), Positives = 358/438 (80%)</p> <p>spiP08982 ENVZ_SALTY OSMOLARITY SENSOR PROTEIN ENVZ pir S01367 inner membrane protein envZ - Salmonella typhimurium emb CAA30935.1 (X12374) envZ inner membrane protein (AA 1 - 450) [Salmonella typhimurium] Length = 450</p>
SEQ ID n°3398	Prot n°PL-577.1	Contig38	375731	376771	85%	<p>Identities = 271/346 (78%), Positives = 309/346 (88%)</p> <p>spiP08128 PSTS_ECOLI PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR (PBP) pir BYECPR phosphate-repressible phosphate-binding protein precursor - Escherichia coli gb AA24378.1 (K01992) phosphate-binding protein [Escherichia coli] gb AAC76751.1 (AE000449) high-affinity phosphate-specific transport system; periplasmic phosphate-binding protein [Escherichia coli] Length = 346 "</p>
SEQ ID n°3399	Prot n°PL-579.1	Contig38	374643	375599	89%	<p>Identities = 271/317 (85%), Positives = 292/317 (91%) dbj BAA22862.1 (D89963) peripheral membrane protein C [Enterobacter cloacae] Length = 319</p>
SEQ ID n°3400	Prot n°PL-58.1	Contig41	100274	101203	58%	<p>Identities = 105/306 (34%), Positives = 182/306 (59%), Gaps = 6/306 (1%)</p> <p>pir E71694 hypothetical protein RP372 - Rickettsia prowazekii emb CAA14831.1 (AJ235271) unknown [Rickettsia prowazekii] Length = 323</p>
SEQ ID n°3401	Prot n°PL-580.1	Contig38	373757	374641	89%	<p>Identities = 255/295 (86%), Positives = 273/295 (92%), Gaps = 1/295 (0%)</p> <p>dbj BAA22863.1 (D89963) Integral membrane protein A [Enterobacter cloacae] Length = 296</p>
SEQ ID n°3402	Prot n°PL-581.1	Contig38	372954	373730	92%	<p>Identities = 226/253 (89%), Positives = 240/253 (94%)</p> <p>spiP07656 PSTB_ECOLI PHOSPHATE TRANSPORT ATP-BINDING PROTEIN PSTB pir BVECBZ phosphate transport ATP-binding protein PetB - Escherichia coli emb CAA26509.1 (X02723) pstB gene product (aa 1-257) [Escherichia coli] gb AAA24381.1 (K01992) peripheral membrane protein B [Escherichia coli] gb AAA62076.1 (L10328) peripheral membrane protein B [Escherichia coli] gb AAC76748.1 (AE000449) ATP-binding component of high-affinity phosphate-specific transport system [Escherichia coli]</p>

TABLEAU I

SEQ ID n°3403	Prot n°PL-582.1	Contig38	372220	372951	88%	Identities = 205/241 (85%), Positives = 224/241 (92%), Gaps = 1/241 (0%) sp P07666 PHOU_ECOLI PHOSPHATE TRANSPORT SYSTEM REGULATORY PROTEIN pir JBEVEPU peripheral membrane protein U - Escherichia coli emb CAA26510.1 (X02723) phoU gene product (aa 1-241) [Escherichia coli] gb AAA24382.1 (K01992) peripheral membrane protein U [Escherichia coli] gb AAC76747.1 (AE000449) negative regulator for pho regulon and putative enzyme in phosphate metabolism [Escherichia regulon and putative enzyme in phosphate metabolism]
SEQ ID n°3404	Prot n°PL-583.1	Contig38	371215	372051	70%	Identities = 151/264 (57%), Positives = 202/264 (76%), Gaps = 4/264 (1%) gb AAG05592.1 AE004647_1 (AE004647) probable binding protein component of ABC transporter [Pseudomonas aeruginosa] Length = 268
SEQ ID n°3405	Prot n°PL-584.1	Contig38	370396	371133	69%	Identities = 143/230 (62%), Positives = 171/230 (74%), Gaps = 4/230 (1%) gb AAG05591.1 AE004646_12 (AE004646) probable amino acid permease [Pseudomonas aeruginosa] Length = 238
SEQ ID n°3406	Prot n°PL-585.1	Contig38	369651	370394	71%	Identities = 140/222 (63%), Positives = 181/222 (81%) gb AAG05590.1 AE004646_11 (AE004646) probable amino acid permease [Pseudomonas aeruginosa] Length = 225
SEQ ID n°3407	Prot n°PL-586.1	Contig38	364424	365185	No Hits found	
SEQ ID n°3408	Prot n°PL-587.1	Contig38	362523	367766	40%	Identities = 437/1707 (25%), Positives = 704/1707 (40%), Gaps = 275/1707 (16%) gb AAAF42119.1 (AE002527) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58] Length = 1995
SEQ ID n°3409	Prot n°PL-588.1	Contig38	360898	362577	60%	Identities = 239/555 (43%), Positives = 346/555 (62%), Gaps = 7/555 (1%) gb AAC31980.1 (L39897) HecB [Pectobacterium chrysanthemi] Length = 558
SEQ ID n°3410	Prot n°PL-589.1	Contig38	359037	360506	24%	Identities = 56/257 (21%), Positives = 120/257 (45%), Gaps = 9/257 (3%) pir B70367 hypothetical protein aq_765 - Aquifex aeolicus gb AAC06926.1 (AE000708) putative protein [Aquifex aeolicus] Length = 480
SEQ ID n°3411	Prot n°PL-68.1	Contig41	101633	103486	22%	Identities = 98/297 (32%), Positives = 138/297 (45%), Gaps = 25/297 (8%) pir D42463 hypothetical protein Bcv' (pinB 5' region) - Shigella boydii (fragment) Length = 536
SEQ ID n°3412	Prot n°PL-590.1	Contig38	357460	358284	No Hits found	
SEQ ID n°3413	Prot n°PL-591.1	Contig38	356773	358146	86%	Identities = 355/457 (77%), Positives = 406/457 (88%) sp P37129 HEMN_SALTY OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) gb AAA19690.1 (U06779) putative oxygen-independent coproporphyrinogen III oxidase
SEQ ID n°3414	Prot n°PL-592.1	Contig38	352010	355255	5%	Identities = 38/125 (30%), Positives = 61/125 (48%), Gaps = 25/125 (20%) pir D75833 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb AAAF12566.1 AE001828_35 (AE001828) conserved hypothetical protein [Deinococcus radiodurans] Length = 609
SEQ ID n°3415	Prot n°PL-593.1	Contig38	350697	351986	48%	Identities = 164/396 (41%), Positives = 232/396 (58%), Gaps = 8/396 (2%) gb AAC82523.1 (AF027768) TnpA [Serratia marcescens] Length = 404

TABLEAU I

SEQ ID n°3416	Prot n°PL-594.1	Contig38	349159	350631	83%	Identities = 364/490 (74%), Positives = 411/490 (83%), Gaps = 21/490 (4%) sp P41789 NTRC_SALTY NITROGEN REGULATION PROTEIN NR(I) pir J553024 nitrogen regulation protein I ntrC - Salmonella typhimurium emb CAA59425.1 (X85104) nitrogen regulatory protein C [Salmonella typhimurium] Length = 469
SEQ ID n°3417	Prot n°PL-595.1	Contig38	348100	349149	83%	Identities = 275/349 (78%), Positives = 307/349 (87%) sp P06218 NTRB_KLEPN NITROGEN REGULATION PROTEIN NTRB pir J24114 nitrogen regulation protein II (EC 2.7.3.-) ntrB - Klebsiella pneumoniae emb CAA26923.1 (X03146) ntrB protein (aa 1-349) [Klebsiella pneumoniae] Length = 349
SEQ ID n°3418	Prot n°PL-596.1	Contig38	346537	347946	86%	Identities = 401/468 (85%), Positives = 436/468 (92%) sp P28786 GLNA_PROVU GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE) pir J523899 glutamate-ammonia ligase (EC 6.3.1.2) - Proteus vulgaris emb CAA48234.1 (X68129) glutamate-ammonia ligase [Proteus vulgaris] Length = 469
SEQ ID n°3419	Prot n°PL-597.1	Contig38	345469	346101	No Hits found	
SEQ ID n°3420	Prot n°PL-598.1	Contig38	344257	346077	91%	Identities = 525/591 (88%), Positives = 558/591 (93%) sp P32132 TYPA_ECOLI GTP-BINDING PROTEIN TYPABIPA (TYROSINE PHOSPHORYLATED PROTEIN A) pir J540816 65.4K GTP-binding protein (gluA-fdhE intergenic region) - Escherichia coli gb AAB03005.1 (L19201) matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar to elongation factor G, TetM/TetO tetracycline-resistance proteins [Escherichia coli] gb AAC7868.1 (AE000462) putative GTP-binding proteins [Escherichia coli] gb AAC7868.1 (AE000462) putative GTP-binding proteins [Escherichia coli] Length = 505
SEQ ID n°3421	Prot n°PL-599.1	Contig38	343589	344194	41%	Identities = 50/185 (27%), Positives = 84/185 (45%), Gaps = 19/185 (10%) emb CAB56502.1 (AJ249744) putative membrane protein CjaE [Campylobacter jejuni] Length = 505
SEQ ID n°3422	Prot n°PL-6.1	Contig41	6776	15698	35%	Identities = 717/2287 (31%), Positives = 1087/2287 (47%), Gaps = 251/2287 (11%) gb AAAF42109.1 (AE002526) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58] Length = 2514
SEQ ID n°3423	Prot n°PL-60.1	Contig41	103555	104940	85%	Identities = 374/461 (81%), Positives = 413/461 (89%) sp P21888 SYG_ECOLI CYSTEINYL-TRNA SYNTHETASE (CYSTEINE-TRNA LIGASE) (CYSRS) pir YYEC cysteine-IRNA ligase (EC 6.1.1.16) - Escherichia coli emb CAA41983.1 (X59293) cysteinyl-IRNA synthetase [Escherichia coli] gb AAA23658.1 (M59381) transfer RNA-Cys synthetase [Escherichia coli] gb AAB40279.1 (U82664) cysteinyl-IRNA synthetase [Escherichia coli] gb AAC73628.1 (AE000158) cysteine tRNA synthetase [Escherichia coli] prf 1714234A Cys-tRNA synthetase [Escherichia coli] Length = 461
SEQ ID n°3424	Prot n°PL-600.1	Contig38	341116	342570	74%	Identities = 295/473 (62%), Positives = 363/473 (76%), Gaps = 6/473 (1%) gb AAAF93852.1 (AE004154) carbon starvation protein A, putative [Vibrio cholerae] Length = 494

Unknown, similar to toxins

TABLEAU I

SEQ ID n°3425	Prot n°PL-601.1	Contig38	340333	340959	88%	Identities = 120/197 (60%), Positives = 151/197 (75%) sp P32145 YIH_X_ECOLI_HYPOTHETICAL 22.7 KD PROTEIN IN GLNA-RBN INTERGENIC REGION Length = 199
SEQ ID n°3426	Prot n°PL-602.1	Contig38	338862	339779	80%	Identities = 229/305 (75%), Positives = 269/305 (87%) sp P32148 YID_ECOLI_HYPOTHETICAL 37.1 KD PROTEIN IN RBN-FDHE INTERGENIC REGION (O329) pir S40832 hypothetical 37.1K protein (glaA-fdhe intergenic region) - Escherichia coli gb AAB03021.1 (L19201) ORF o329 [Escherichia coli] gb AAD13450.1 (AE000464) putative acetyltransferase (EC 2.3.1.18) [Escherichia coli] Length = 329
SEQ ID n°3427	Prot n°PL-603.1	Contig38	336525	338231	55%	Identities = 196/559 (35%), Positives = 318/559 (56%), Gaps = 2/559 (0%) sp P31433 YICH_ECOLI_HYPOTHETICAL 62.3 KD PROTEIN IN GLTS-SELC INTERGENIC REGION pir A65167 hypothetical 82.3 KD protein in gltS-seic intergenic region - Escherichia coli (strain K-12) gb AAC76679.1 (AE000443) of, hypothetical protein [Escherichia coli] Length = 589
SEQ ID n°3428	Prot n°PL-604.1	Contig38	334500	336041	70%	Identities = 294/508 (57%), Positives = 379/508 (73%), Gaps = 10/508 (1%) gb AAC38324.1 (AF031325) phenol hydroxylase [Bacillus thermoleovorans] Length = 524
SEQ ID n°3429	Prot n°PL-605.1	Contig38	332906	334291	86%	Identities = 364/444 (81%), Positives = 409/444 (91%) sp P27432 YICE_ECOLI_PUTATIVE PURINE PERMEASE YICE pir JH65166 hypothetical 48.9 KD protein in gltS 3'region - Escherichia coli (strain K-12) gb AAA62007.1 (L10328) o463 [Escherichia coli] gb AAC76678.1 (AE000443) putative transport protein [Escherichia coli] Length = 463
SEQ ID n°3430	Prot n°PL-606.1	Contig38	331455	332663	89%	Identities = 316/399 (79%), Positives = 359/399 (89%) sp P19833 GLTS_ECOLI_SODIUM/GLUTAMATE SYMPORT CARRIER PROTEIN (GLUTAMATE PERMEASE) pir S14031 gltS protein - Escherichia coli pir JOECNQ sodium-glutamate symport carrier protein - Escherichia coli emb CAA35540.1 (X17489) gltS protein [Escherichia coli] gb AAA62006.1 (L10328) glutamate permease [Escherichia coli] gb AAC76677.1 (AE000442) glutamate transport [Escherichia coli] emb CAA06472.1 (AJ005325) glutamate permease [synthetic construct] emb CAA06475.1 (AJ005328) glutamate permease [synthetic construct] emb CAA06485.1 (AJ005339) glutamate permease [synthetic construct] Length = 401
SEQ ID n°3431	Prot n°PL-607.1	Contig38	329600	330343	60%	Identities = 131/246 (53%), Positives = 172/246 (69%), Gaps = 3/246 (1%) db BAA92862.1 (AB040403) TRP-1 [Burkholderia glumae] Length = 246
SEQ ID n°3432	Prot n°PL-608.1	Contig38	326962	327744	39%	Identities = 57/217 (26%), Positives = 104/217 (47%), Gaps = 11/217 (5%) gb AAF4231.1 (AE002547) hypothetical protein [Neisseria meningitidis MC58] emb CAB83756.1 (AL162753) hypothetical protein [Neisseria meningitidis] Length = 223

TABLEAU I

SEQ ID n°3433	Prot n°PL-609.1	Contig38	321663	323744	85%	<p>Identities = 535/693 (77%), Positives = 607/693 (87%)</p> <p>sp P24230 RECG_ECOLI ATP-DEPENDENT DNA HELICASE REGC pir JH0265 DNA recombinase (EC 3.6.1.-) - Escherichia coli emb CAA42123.1 (X59560) recG [Escherichia coli] gb AAA24513.1 (M64367) DNA recombinase [Escherichia coli] gb AAC76676.1 (AE000442) DNA helicase, resolution of Holliday junctions, branch migration</p>
SEQ ID n°3434	Prot n°PL-61.1	Contig41	105707	106435	67%	<p>Identities = 159/240 (66%), Positives = 182/240 (79%)</p> <p>sp P43341 YBBF_ECOLI HYPOTHETICAL 26.9 KD PROTEIN IN PURE-PPIB INTERGENIC REGION pir IC64784 ybbF protein - Escherichia coli gb AAB40277.1 (U82664) similar to H. influenzae HI0735 [Escherichia coli] gb AAC73626.1 (AE000158) of, hypothetical protein [Escherichia coli] Identities = 111/187 (59%), Positives = 144/187 (76%), Gaps = 1/187 (0%)</p>
SEQ ID n°3435	Prot n°PL-610.1	Contig38	320655	321221	70%	<p>sp P04742 FIMB_ECOLI TYPE 1 FIMBRIAE REGULATORY PROTEIN FIMB pir S56537 recombinase fimB (involved in phase variation) - Escherichia coli pir JRGECFF type 1 fimbriae regulatory protein fimB - Escherichia coli gb AAA97208.1 (U14003) recombinase involved in phase variation [Escherichia coli] gb AAC77268.1 (AE000502) recombinase involved in phase variation; regulator for fimA [Escherichia coli] Length = 200</p>
SEQ ID n°3436	Prot n°PL-611.1	Contig38	319624	320244	36%	<p>Identities = 46/178 (25%), Positives = 76/178 (41%), Gaps = 29/178 (16%)</p> <p>gb AAB41914.1 (U31413) FcA precursor [Escherichia coli] Length =</p>
SEQ ID n°3437	Prot n°PL-612.1	Contig38	318757	319551	46%	<p>Identities = 78/228 (34%), Positives = 122/228 (53%), Gaps = 15/228 (6%)</p> <p>sp P75856 YCBR_ECOLI HYPOTHETICAL 25.4 KDA FIMBRIAL CHAPERONE IN PEPP-PYRD INTERGENIC REGION PRECURSOR pir B64834 probable fimbrial chaperone ycbR precursor - Escherichia coli gb AAC74025.1 (AE000196) putative chaperone [Escherichia coli] db BAA35694.1 (D90732) Periplasmic chaperone fccC protein [Escherichia</p>
SEQ ID n°3438	Prot n°PL-614.1	Contig38	317357	318094	No Hits found	
SEQ ID n°3439	Prot n°PL-615.1	Contig38	316611	317306	No Hits found	
SEQ ID n°3440	Prot n°PL-616.1	Contig38	315811	316548	51%	<p>Identities = 83/240 (34%), Positives = 130/240 (53%), Gaps = 19/240 (7%)</p> <p>emb CAA35987.1 (X51655) fimC [Escherichia coli] Length = 241</p>
SEQ ID n°3441	Prot n°PL-617.1	Contig38	314980	315810	46%	<p>sp P75856 YCBR_ECOLI HYPOTHETICAL 25.4 KDA FIMBRIAL CHAPERONE IN PEPP-PYRD INTERGENIC REGION PRECURSOR pir B64834 probable fimbrial chaperone ycbR precursor - Escherichia coli gb AAC74025.1 (AE000196) putative chaperone [Escherichia coli] db BAA35694.1 (D90732) Periplasmic chaperone fccC protein [Escherichia</p>

TABLEAU I

SEQ ID n°3442	Prot n°PL-618.1	Contig38	312166	314910	54%	Identities = 334/908 (36%), Positives = 502/908 (54%), Gaps = 70/908 (7%) sp P30130 FIMD_ECOLI OUTER MEMBRANE USHER PROTEIN FIMD PRECURSOR pir S56642 outer membrane usher protein fimD precursor - Escherichia coli gb AAAG7213.1 (U14003) CG Site No. 18349 [Escherichia coli] gb AAC77273.1 (AE000502) outer membrane protein; export and assembly of type 1 fimbriae, interrupted [Escherichia coli] Length
SEQ ID n°3443	Prot n°PL-619.1	Contig38	310872	312075	No Hits found	Identities = 259/363 (71%), Positives = 287/363 (78%), Gaps = 10/363 (2%) sp P09029 PURK_ECOLI PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE ATPASE SUBUNIT (AIR CARBOXYLASE) (AIRC) pir DCECPK phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) carbon dioxide-fixation chain - Escherichia coli gb AA244450.1 (M19657) 5'- phosphoribosyl-5-amino-4-imidazole carboxylase II [purK, EC 4.1.1.21] [Escherichia coli] gb AAB40275.1 (U82664) 5'-phosphoribosyl-5-amino-4- imidazole carboxylase II [Escherichia coli] gb AAC73624.1 (AE000168) phosphoribosylaminoimidazole carboxylase = AIR carboxylase, CO(2)- fixing subunit [Escherichia coli] Length = 355
SEQ ID n°3444	Prot n°PL-62.1	Contig41	107110	108207	76%	Identities = 606/709 (85%), Positives = 649/709 (91%), Gaps = 11/709 (1%) sp P17580 SPOT_ECOLI GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'- PYROPHOSPHOHYDROLASE ((PPGPP)ASE) (PENTA-PHOSPHATE GUANOSINE-3'-PYROPHOSPHOHYDROLASE) pir SHECGD guanosine 3',5'- bis(diphosphate) 3'-pyrophosphatase (EC 3.1.7.2) - Escherichia coli gb AAA62003.1 (L10328) (p)ppGpp 3'-pyrophosphohydrolase [Escherichia coli] gb AAB00160.1 (M24503) (p)ppGpp 3'-pyrophosphohydrolase [Escherichia coli] gb AAC76874.1 (AE000442) (p)ppGpp synthetase II; also guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase Identities = 166/207 (80%), Positives = 179/207 (86%)
SEQ ID n°3445	Prot n°PL-620.1	Contig38	307485	309602	88%	sp P24234 KGUA_ECOLI GUANYLATE KINASE (GMP KINASE) pir KIECGU guanylate kinase (EC 2.7.4.8) - Escherichia coli gb AAB88711.1 (M84400) GMP kinase [Escherichia coli] gb AA62001.1 (L10328) 5'guanylate kinase [Escherichia coli] gb AAC76872.1 (AE000442) guanylate kinase [Escherichia coli] Length = 60/227 (26%), Positives = 96/227 (41%), Gaps = 48/227 (21%) Identities = 60/227 (26%), Positives = 96/227 (41%), Gaps = 48/227 (21%) gb AAF50913.1 (AE000357) CG11734 gene product [Drosophila melanogaster] Length = 4689
SEQ ID n°3446	Prot n°PL-621.1	Contig38	306514	307137	79%	Identities = 68/283 (23%), Positives = 118/283 (40%), Gaps = 59/283 (20%) gb AAF50913.1 (AE000357) CG11734 gene product [Drosophila melanogaster] Length = 4689
SEQ ID n°3447	Prot n°PL-622.1	Contig38	304518	305813	21%	
SEQ ID n°3448	Prot n°PL-623.1	Contig38	303016	304281	27%	
SEQ ID n°3449	Prot n°PL-624.1	Contig38	302979	303836	No Hits found	
SEQ ID n°3450	Prot n°PL-625.1	Contig38	301602	302291	No Hits found	
SEQ ID n°3451	Prot n°PL-626.1	Contig38	300180	301064	No Hits found	
SEQ ID n°3452	Prot n°PL-627.1	Contig38	298232	298972	No Hits found	

TABLEAU I

SEQ ID n°3453	Prot n°PL-628.1	Contig38	283576	295543	50%	<p>Identities = 218/544 (40%), Positives = 329/544 (60%), Gaps = 14/544 (2%) sp P25772 YICF_ECOLI_HYPOTHETICAL_63.2_KD_PROTEIN_IN_RPH-GMK INTERGENIC REGION Length = 560</p> <p>Identities = 145/206 (70%), Positives = 175/206 (84%) hypothetical 22.0 kD protein in rph-gmk intergenic region - Escherichia coli (strain K-12) gb AA61999.1 (L10328) o223 [Escherichia coli] gb AAC76670.1 (AE000442) orf, hypothetical protein [Escherichia coli]</p> <p>Identities = 162/321 (50%), Positives = 231/321 (71%), Gaps = 12/321 (3%) gb AAF81206.1 (AF247502) Yid2 [Salmonella dublin] Length = 316</p>
SEQ ID n°3454	Prot n°PL-629.1	Contig38	292965	293582	74%	<p>Identities = 251/407 (61%), Positives = 306/407 (74%), Gaps = 16/407 (3%) sp P31455 YIDR_ECOLI_HYPOTHETICAL_46.4_KD_PROTEIN_IN_IPA-GYRB INTERGENIC REGION pir B65171 hypothetical protein yidR - Escherichia coli (strain K-12) gb AAC76712.1 (AE000446) orf, hypothetical protein [Escherichia coli] Length = 416</p>
SEQ ID n°3455	Prot n°PL-63.1	Contig41	109474	110436	70%	<p>Identities = 320/412 (77%), Positives = 358/412 (86%) sp P09053 AVTA_ECOLI_VALINE-PYRUVATE_AMINOTRANSFERASE (TRANSAMINASE C) (ALANINE-VALINE TRANSAMINASE) pir S47793 valine-pyruvate transaminase (EC 2.6.1.66) - Escherichia coli gb AAB18549.1 (U00039) o417 [Escherichia coli] gb AAC76596.1 (AE000434) alanine-alpha-ketoglutarate (or valine-pyruvate) Length = 284/303 (93%), Positives = 298/303 (98%)</p>
SEQ ID n°3456	Prot n°PL-630.1	Contig38	291542	292846	70%	<p>Identities = 284/303 (93%), Positives = 298/303 (98%) sp P00960 SYGA_ECOLI_GLYCYL-TRNA_SYNTHETASE_ALPHA_CHAIN (GLYCINE-TRNA LIGASE ALPHA CHAIN) (GLYRS) pir SYECGA glycine-tRNA ligase (EC 6.1.1.14) alpha chain - Escherichia coli gb AAB18537.1 (U00039) glycine-tRNA synthetase, alpha subunit [Escherichia coli] gb AAC76584.1 (AE000433) glycine tRNA synthetase, Length = 558/689 (80%), Positives = 617/689 (88%)</p>
SEQ ID n°3457	Prot n°PL-631.1	Contig38	289018	290271	81%	<p>Identities = 185/397 (46%), Positives = 267/397 (66%), Gaps = 6/397 (1%) sp O34928 CYPX_BACSU_PUTATIVE_CYTOCHROME_P450_CYPX pir F69811 cytochrome P450 cypX - Bacillus subtilis gb AAC67280.1 (AF017113) CypB [Bacillus subtilis] emb CAB1551.1 (Z99121) cytochrome P450-like enzyme [Bacillus subtilis] emb CAB15523.1 (Z99122) cytochrome P450-like enzyme [Bacillus subtilis] Length = 405</p>
SEQ ID n°3458	Prot n°PL-632.1	Contig38	287129	288043	85%	<p>Identities = 287/397 (71%), Positives = 358/412 (86%) sp P00961 SYGB_ECOLI_GLYCYL-TRNA_SYNTHETASE_BETA_CHAIN (GLYCINE-TRNA LIGASE BETA CHAIN) (GLYRS) pir SYECGB glycine-tRNA ligase (EC 6.1.1.14) beta chain - Escherichia coli gb AAB18536.1 (U00039) glycine-tRNA synthetase, beta subunit [Escherichia coli] gb AAC76583.1 (AE000433) glycine tRNA synthetase, beta subunit Length = 185/397 (46%), Positives = 267/397 (66%), Gaps = 6/397 (1%)</p>
SEQ ID n°3459	Prot n°PL-633.1	Contig38	285050	287119	89%	<p>Identities = 185/397 (46%), Positives = 267/397 (66%), Gaps = 6/397 (1%) sp O34928 CYPX_BACSU_PUTATIVE_CYTOCHROME_P450_CYPX pir F69811 cytochrome P450 cypX - Bacillus subtilis gb AAC67280.1 (AF017113) CypB [Bacillus subtilis] emb CAB1551.1 (Z99121) cytochrome P450-like enzyme [Bacillus subtilis] emb CAB15523.1 (Z99122) cytochrome P450-like enzyme [Bacillus subtilis] Length = 405</p>
SEQ ID n°3460	Prot n°PL-634.1	Contig38	283209	284432	64%	<p>Identities = 185/397 (46%), Positives = 267/397 (66%), Gaps = 6/397 (1%) sp O34928 CYPX_BACSU_PUTATIVE_CYTOCHROME_P450_CYPX pir F69811 cytochrome P450 cypX - Bacillus subtilis gb AAC67280.1 (AF017113) CypB [Bacillus subtilis] emb CAB1551.1 (Z99121) cytochrome P450-like enzyme [Bacillus subtilis] emb CAB15523.1 (Z99122) cytochrome P450-like enzyme [Bacillus subtilis] Length = 405</p>

TABLEAU I

SEQ ID n°3461	Prot n°PL-635.1	Contig38	282368	283123	51%	<p>Identities = 86/229 (37%), Positives = 129/229 (55%), Gaps = 3/229 (1%) pir J70044 conserved hypothetical protein ymc - Bacillus subtilis gb AAC67279.1 (AF017113) Ymc [Bacillus subtilis] emb CAB15512.1 (Z99121) similar to hypothetical proteins [Bacillus subtilis] emb CAB15524.1 (Z99122) similar to hypothetical proteins [Bacillus subtilis] Length = 248</p> <p>Identities = 75/308 (24%), Positives = 143/308 (46%), Gaps = 42/308 (13%) sp P1360 YHBE_HAEIN HYPOTHETICAL PROTEIN H10878 gb AAC22534.1 (U32769) conserved hypothetical protein [Haemophilus influenzae Rd] Length = 306</p>
SEQ ID n°3462	Prot n°PL-638.1	Contig38	280748	281671	46%	<p>Identities = 426/530 (80%), Positives = 482/530 (90%) sp P23847 DPPA_EC01 PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN PRECURSOR (DIPEPTIDE-BINDING PROTEIN) (DBP) pir J39194 periplasmic dipeptide transport protein precursor dppA - Escherichia coli emb CAA41080.1 (X58051) dipeptide binding protein (DBP) [Escherichia coli] gb AAA23707.1 (M35045) dipeptide transporter protein [Escherichia coli] gb AAA23702.1 (L08399) dipeptide-binding protein [Escherichia coli] gb AAB18522.1 (U00039) dppA [Escherichia coli] gb AAC76569.1 (AE000431) dipeptide transport protein [Escherichia coli] Length = 535</p> <p>Identities = 298/339 (87%), Positives = 321/339 (93%) sp P37316 DPPB_EC01 DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPB pir J47765 dipeptide transport system permease protein dppb - Escherichia coli gb AAA23703.1 (L08399) transmembrane protein [Escherichia coli] gb AAB18521.1 (U00039) dppB [Escherichia coli] gb AAC76568.1 (AE000431) dipeptide transport system permease protein 1 [Escherichia coli] Length = 339</p>
SEQ ID n°3463	Prot n°PL-637.1	Contig38	278538	280145	84%	
SEQ ID n°3464	Prot n°PL-638.1	Contig38	277400	278419	92%	
SEQ ID n°3465	Prot n°PL-639.1	Contig38	276490	277389	87%	<p>Identities = 255/300 (85%), Positives = 280/300 (93%), Gaps = 1/300 (0%) sp P37315 DPPC_EC01 DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC pir J47764 dipeptide transport system permease protein dppC - Escherichia coli gb AAA23704.1 (L08399) transmembrane protein [Escherichia coli] gb AAB18520.1 (U00039) dppC [Escherichia coli] gb AAC76567.1 (AE000431) dipeptide transport system permease protein 2 [Escherichia coli] Length = 300</p>
SEQ ID n°3466	Prot n°PL-64.1	Contig41	111138	111803	53%	<p>Identities = 85/203 (41%), Positives = 120/203 (58%), Gaps = 3/203 (1%) sp P45273 RISA_HAEIN RIBOFLAVIN SYNTHASE ALPHA CHAIN pir J64132 riboflavin synthase (EC 2.5.1.9) alpha chain - Haemophilus influenzae gb AAC23257.1 (U32834) riboflavin synthase, alpha chain (ribE) [Haemophilus influenzae Rd] Length = 204</p>

TABLEAU I

SEQ ID n°3467	Prot n°PL-640.1	Contig38	275497	276477	90%	Identities = 282/327 (86%), Positives = 289/327 (91%), Gaps = 1/327 (0%) sp P37314 DPPD_ECOLI DIPEPTIDE TRANSPORT ATP-BINDING PROTEIN DPPD pir S61404 dipeptide transport protein dppD - Escherichia coli gb AA23705.1 (U08399) peripheral membrane protein [Escherichia coli] gb AAB18519.1 (U00039) dppD [Escherichia coli] gb AAC76566.1 (AE000431) putative ATP-binding component of dipeptide transport system [Escherichia coli] Length = 327
SEQ ID n°3468	Prot n°PL-641.1	Contig38	274481	275500	84%	Identities = 269/321 (83%), Positives = 292/321 (90%) sp P37313 DPPF_ECOLI DIPEPTIDE TRANSPORT ATP-BINDING PROTEIN DPPF pir S47762 dipeptide transport protein dppF - Escherichia coli gb AAB18518.1 (U00039) was dppE [Escherichia coli] gb AAC76565.1 (AE000431) putative ATP-binding component of dipeptide transport
SEQ ID n°3468	Prot n°PL-642.1	Contig38	273411	274124	61%	Identities = 95/215 (44%), Positives = 147/215 (68%), Gaps = 5/215 (2%) sp P37649 YHJ_K_ECOLI PROTEIN YHJ_K pir S47750 hypothetical protein (dctA-dppF intergenic region) - Escherichia coli gb AAB18506.1 (U00039) No definition line found [Escherichia coli] gb AAC76554.1 (AE000429) orf, hypothetical protein [Escherichia coli] Length = 651
SEQ ID n°3470	Prot n°PL-643.1	Contig38	271742	273232	67%	Identities = 253/473 (53%), Positives = 341/473 (71%), Gaps = 2/473 (0%) sp P37848 YHJ_ECOLI PROTEIN YHJ PRECURSOR pir S47748 53.1K protein precursor (kdgK-dctA intergenic region) - Escherichia coli gb AAB18504.1 (U00039) No definition line found [Escherichia coli] gb AAC76552.1 (AE000429) orf, hypothetical protein [Escherichia coli] Length = 498
SEQ ID n°3471	Prot n°PL-644.1	Contig38	270387	271436	70%	Identities = 198/314 (63%), Positives = 246/314 (78%), Gaps = 6/314 (1%) sp P37642 YHJ_ECOLI HYPOTHETICAL 37.9 KD PROTEIN IN TREF-KDGK INTERGENIC REGION (O337) pir S47742 hypothetical 37.9K protein (tref- kdgK intergenic region) - Escherichia coli gb AAB18498.1 (U00039) No definition line found [Escherichia coli] gb AAC76547.1 (AE000428) orf, hypothetical protein [Escherichia coli] Length = 337
SEQ ID n°3472	Prot n°PL-645.1	Contig38	268879	269838	No Hits found	Identities = 52/167 (31%), Positives = 82/167 (48%), Gaps = 6/167 (3%) dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°3473	Prot n°PL-646.1	Contig38	268843	269916	22%	Identities = 70/188 (37%), Positives = 106/188 (56%), Gaps = 13/188 (6%) gb AAF42109.1 (AE002528) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58] Length = 2514
SEQ ID n°3474	Prot n°PL-647.1	Contig38	267089	268502	22%	Identities = 69/184 (37%), Positives = 102/184 (54%), Gaps = 1/184 (0%) gb AAF68930.1 AF223162_1 (AF223162) putative IS10 transposase [Salmonella typhi] gb AAF69914.1 AF250878_75 (AF250878) putative IS10 transposase [Salmonella typhi] Length = 402
SEQ ID n°3475	Prot n°PL-648.2	Contig38	265887	266435		
SEQ ID n°3476	Prot n°PL-649.1	Contig38	265116	265724	50%	

TABLEAU I

SEQ ID n°3477	Prot n°PL-65.1	Contig41	112803	113736	33%	Identities = 64/217 (29%), Positives = 104/217 (47%), Gaps = 19/217 (8%) gb AAG03555.1 AE004454.7 (AE004454) hypothetical protein [Pseudomonas aeruginosa] Length = 278
SEQ ID n°3478	Prot n°PL-650.1	Contig38	259469	263911	56%	Identities = 616/1327 (46%), Positives = 840/1327 (62%), Gaps = 55/1327 (4%) sp P15320 HLYA_SERMA_HEMOLYSIN_PRECURSOR_pir J28182 hemolysin A - Serratia marcescens gb AAA50323.1 (M22618) hemolysin [Serratia marcescens] Length = 1608
SEQ ID n°3479	Prot n°PL-651.1	Contig38	257736	259403	76%	Identities = 342/560 (61%), Positives = 429/560 (76%), Gaps = 8/560 (1%) sp P15321 HLYB_SERMA_HEMOLYSIN_ACTIVATOR_PROTEIN_PRECURSOR_pir J28182 hemolysin B - Serratia marcescens gb AAA50322.1 (M22618) hemolysin determinant [Serratia marcescens]
SEQ ID n°3480	Prot n°PL-652.1	Contig38	254581	256227	29%	Identities = 87/394 (22%), Positives = 164/394 (41%), Gaps = 66/394 (16%) gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae] Length = 552
SEQ ID n°3481	Prot n°PL-653.1	Contig38	253461	254189	45%	Identities = 66/213 (30%), Positives = 110/213 (50%), Gaps = 17/213 (7%) sp P07026 SDIA_ECOLI_SDIA_REGULATORY_PROTEIN_pir JQECU1 probable transcription regulator sdIA - Escherichia coli db BAA15736.1 (D90832) SdIA regulatory protein. [Escherichia coli] gb AAC74983.1 (AE000284) transcriptional regulator of ftsQAZ gene cluster
SEQ ID n°3482	Prot n°PL-654.1	Contig38	249587	250654	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°3483	Prot n°PL-655.1	Contig38	247553	248437	59%	Identities = 126/284 (44%), Positives = 188/284 (65%), Gaps = 4/284 (1%) gb AAC28598.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300
SEQ ID n°3484	Prot n°PL-656.1	Contig38	245204	245914	No Hits found	
SEQ ID n°3485	Prot n°PL-657.1	Contig38	242207	243589	57%	Identities = 206/489 (42%), Positives = 269/489 (54%), Gaps = 47/489 (9%) pdb 1F31A Chain A, Crystal Structure Of Tn5 Transposase Complexed With Transposon End Dna Length = 481
SEQ ID n°3486	Prot n°PL-658.1	Contig38	241297	242196	21%	Identities = 39/131 (29%), Positives = 65/131 (48%), Gaps = 1/131 (0%) gb AAF96035.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 421
SEQ ID n°3487	Prot n°PL-659.1	Contig38	240182	241219	No Hits found	
SEQ ID n°3488	Prot n°PL-66.1	Contig41	113671	115068	38%	Identities = 97/403 (24%), Positives = 181/403 (44%), Gaps = 39/403 (9%) sp P37482 YYCB_BACSU_HYPOTHETICAL_43.2_KD_PROTEIN_IN_DNAC-RPL_INTERGENIC_REGION_pir J565973 transport protein homolog yycB - Bacillus subtilis db BAA05179.1 (D26185) unknown [Bacillus subtilis] emb CAB16085.1 (Z89124) similar to ABC transporter (permease) [Bacillus subtilis] Length = 402

TABLEAU I

SEQ ID n°3488	Prot n°PL-660.1	Contig38	237659	241207	56%	Identities = 452/1176 (38%), Positives = 671/1176 (56%), Gaps = 17/1176 (1%) gb AAAF96034.1 (AE004353) lcnF-related protein [Vibrio cholerae] Length = 1181	Unknown, similar to toxins
SEQ ID n°3490	Prot n°PL-662.1	Contig38	236913	237665	41%	Identities = 70/206 (33%), Positives = 103/206 (49%), Gaps = 6/206 (2%) gb AAAF96033.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 469	
SEQ ID n°3491	Prot n°PL-663.1	Contig38	235444	236880	81%	Identities = 345/467 (73%), Positives = 397/467 (84%) sp P05101 MET2_ECOLI MODIFICATION METHYLASE ECORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE ECORII) (M.ECORII) pi I XYECR2 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) EcoRII - Escherichia coli (strain HB101) emb CAA28725.1 (X05050) EcoRII cytosine methylase (AA 1-477) [Escherichia coli] Length = 477	
SEQ ID n°3492	Prot n°PL-664.1	Contig38	233446	234780	No Hits found		
SEQ ID n°3493	Prot n°PL-665.1	Contig38	229740	230807	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188	
SEQ ID n°3494	Prot n°PL-666.1	Contig38	228831	229541	No Hits found		
SEQ ID n°3495	Prot n°PL-667.1	Contig38	220985	225418	24%	Identities = 253/893 (28%), Positives = 358/893 (39%), Gaps = 121/893 (13%) emb CAB82067.1 (AL161803) putative Rhs protein [Streptomyces coelicolor A3(2)] Length = 927	
SEQ ID n°3496	Prot n°PL-668.1	Contig38	218608	219761	No Hits found		
SEQ ID n°3497	Prot n°PL-669.1	Contig38	218679	220514	60%	Identities = 286/580 (49%), Positives = 386/580 (66%), Gaps = 9/580 (1%) gb AAC62387.1 (AF044506) VgrG protein [Escherichia coli] Length = 580 Identities = 125/368 (33%), Positives = 198/368 (52%), Gaps = 14/368 (3%) pi B64843 hypothetical protein b1012 - Escherichia coli gb AAC74097.1 (AE000202) orf, hypothetical protein [Escherichia coli] db BAA35789.1 (D80738) Hypothetical 49.3 kd protein in ldt-deoR intergenic region. [Escherichia coli] Length = 382	
SEQ ID n°3498	Prot n°PL-67.1	Contig41	115081	116193	52%		
SEQ ID n°3499	Prot n°PL-670.1	Contig38	217920	218597	No Hits found		
SEQ ID n°3500	Prot n°PL-671.1	Contig38	216448	217830	57%	Identities = 206/489 (42%), Positives = 269/489 (54%), Gaps = 47/489 (9%) pdb 1F31A Chain A, Crystal Structure Of Tns Transposase Complexed With Transposon End Dna Length = 481 Identities = 39/131 (29%), Positives = 65/131 (48%), Gaps = 1/131 (0%) gb AAAF96035.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 421	
SEQ ID n°3501	Prot n°PL-672.1	Contig38	215751	216473	26%		
SEQ ID n°3502	Prot n°PL-673.1	Contig38	214639	215676	No Hits found		
SEQ ID n°3503	Prot n°PL-674.1	Contig38	212116	215664	56%	Identities = 452/1176 (38%), Positives = 672/1176 (56%), Gaps = 17/1176 (1%) gb AAAF96034.1 (AE004353) lcnF-related protein [Vibrio cholerae] Length = 1181	Unknown, similar to toxins
SEQ ID n°3504	Prot n°PL-675.1	Contig38	211984	212835	No Hits found		

TABLEAU I

SEQ ID n°3505	Prot n°PL-677.1	Contig38	210557	212122	43%	Identities = 135/436 (30%), Positives = 225/436 (50%), Gaps = 13/436 (2%) gb AAAF96033.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 469
SEQ ID n°3506	Prot n°PL-678.1	Contig38	210033	210683	48%	Identities = 62/223 (27%), Positives = 105/223 (46%), Gaps = 13/223 (5%) gb AAAF96032.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 227
SEQ ID n°3507	Prot n°PL-679.1	Contig38	209230	210039	No Hits found	Identities = 490/810 (60%), Positives = 844/810 (79%), Gaps = 6/810 (0%) sp P77504 YBBP_ECOLI_HYPOTHETICAL_89.3_KD_PROTEIN_IN_TESA-RHSD INTERGENIC REGION pir G64780 probable membrane protein ybbP - Escherichia coli gb AAB40250.1 (U82664) hypothetical protein [Escherichia coli] gb AAC73598.1 (AE000155) putative oxidoreductase [Escherichia coli] Length = 804
SEQ ID n°3508	Prot n°PL-68.1	Contig41	116413	118845	78%	Identities = 523/876 (59%), Positives = 675/876 (76%), Gaps = 15/876 (1%) gb AAAF96030.1 (AE004353) clpB protein [Vibrio cholerae] Length = 869
SEQ ID n°3510	Prot n°PL-681.1	Contig38	205801	206586	54%	Identities = 92/231 (39%), Positives = 143/231 (61%) gb AAAF96029.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 257
SEQ ID n°3511	Prot n°PL-682.1	Contig38	204464	205816	64%	Identities = 196/447 (43%), Positives = 294/447 (64%), Gaps = 3/447 (0%) gb AAAF96028.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 444
SEQ ID n°3512	Prot n°PL-683.1	Contig38	202609	203895	53%	Identities = 152/488 (31%), Positives = 243/488 (49%), Gaps = 75/488 (15%) gb AAAF96026.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 495
SEQ ID n°3513	Prot n°PL-684.1	Contig38	201551	202603	57%	Identities = 141/351 (40%), Positives = 206/351 (58%), Gaps = 18/351 (5%) gb AAAF96025.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 338
SEQ ID n°3514	Prot n°PL-685.1	Contig38	199740	201587	62%	Identities = 285/615 (46%), Positives = 386/615 (62%), Gaps = 26/615 (4%) gb AAAF96024.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 589
SEQ ID n°3515	Prot n°PL-686.1	Contig38	197813	199291	84%	Identities = 360/474 (75%), Positives = 423/474 (88%) gb AAAF96022.1 (AE004353) conserved hypothetical protein [Vibrio cholerae] Length = Identities = 222/280 (79%), Positives = 249/280 (88%)
SEQ ID n°3516	Prot n°PL-687.1	Contig38	194392	195234	79%	sp P37634 YHIR_ECOLI_HYPOTHETICAL_31.9_KD_PROTEIN_IN_PRLC-GOR INTERGENIC REGION (O280A) pir S47719 hypothetical 31.9K protein (prlC- gor intergenic region) - Escherichia coli gb AAB18475.1 (U00039) No definition line found [Escherichia coli] gb AAC76524.1 (AE000426)orf, hypothetical protein [Escherichia coli] Length = 280

TABLEAU I

SEQ ID n°3517	Prot n°PL-688.1	Contig38	192926	194296	90%	<p>Identities = 378/450 (84%), Positives = 414/450 (92%)</p> <p>sp P06715 GSHR_ECOLI GLUTATHIONE REDUCTASE (GR) (GRASE) pir JRDCEU glutathione reductase (NADPH) (EC 1.6.4.2) - Escherichia coli pdb 1GER B Chain B, Glutathione Reductase (EC 1.6.4.2) Complexed With Fad pdb 1GET B Chain B, Glutathione Reductase (EC 1.6.4.2) Wild-Type Complexed With NADp And Fad pdb 1GER A Chain A, Glutathione Reductase (EC 1.6.4.2) Complexed With Fad pdb 1GET A Chain A, Glutathione Reductase (EC 1.6.4.2) Wild-Type Complexed With NADp And Fad gb AAA23926.1 (M13141) glutathione reductase (EC 1.6.4.2) [Escherichia coli] gb AAB18476.1 (U00039) glutathione oxidoreductase [Escherichia coli] gb AAC76525.1 (AE000426) glutathione oxidoreductase [Escherichia coli] Length = 450</p>
SEQ ID n°3518	Prot n°PL-689.1	Contig38	191572	192696	No Hits found	<p>Identities = 172/227 (75%), Positives = 195/227 (85%)</p> <p>sp P31219 YBBA_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP- BINDING PROTEIN YBBA pir JF64780 probable ABC-type transport protein ybaA - Escherichia coli gb AAB40249.1 (U82684) hypothetical abc transporter [Escherichia coli] gb AAC73597.1 (AE000155) putative ATP-binding component of a transport system [Escherichia coli] Length = 228</p> <p>Identities = 75/320 (23%), Positives = 141/320 (43%), Gaps = 31/320 (9%)</p> <p>sp Q02171 MYSP_ONCVO PARAMYOSIN gb AAA29431.1 (M95813) paramyosin [Onchocerca volvulus] Length = 879</p>
SEQ ID n°3519	Prot n°PL-69.1	Contig41	118842	119528	85%	<p>Identities = 84/192 (43%), Positives = 128/192 (65%), Gaps = 1/192 (0%)</p> <p>sp P32173 MOBA_ECOLI MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN A (PROTEIN FA) pir J540803 molybdopterin-guanine dinucleotide biosynthesis protein A - Escherichia coli gb AAB02992.1 (L19201) CG Site No. 921 [Escherichia coli] gb AAC76855.1 (AE000461) molybdopterin -> molybdopterin-guanine dinucleotide, protein Ar [Escherichia coli] Length = 194</p> <p>Identities = 223/327 (68%), Positives = 256/327 (78%)</p> <p>gb AAD47614.1 AF146615_2 (AF146615) YihE [Pectobacterium carotovorum subsp. carotovorum] Length = 328</p>
SEQ ID n°3520	Prot n°PL-690.1	Contig38	189923	191578	25%	<p>Identities = 150/207 (72%), Positives = 183/207 (87%)</p> <p>gb AAD38401.1 AF155130_1 (AF155130) DsbA [Yersinia pestis] = 207</p>
SEQ ID n°3521	Prot n°PL-691.1	Contig38	188728	189327	58%	<p>Identities = 94/399 (23%), Positives = 177/399 (43%), Gaps = 37/399 (9%)</p> <p>pir JG75064 hypothetical protein PAB1002 - Pyrococcus abyssi (strain Orsay) emb CAB50412.1 (AJ248287) hypothetical protein [Pyrococcus abyssi] Length = 428</p>
SEQ ID n°3522	Prot n°PL-692.1	Contig38	187527	188519	77%	<p>Identities = 495/869 (56%), Positives = 619/869 (70%) db JBAAB4909.1 (AB024946) orfT4 [Escherichia coli] Length = 873</p>
SEQ ID n°3523	Prot n°PL-693.1	Contig38	186883	187506	83%	
SEQ ID n°3524	Prot n°PL-694.1	Contig38	185561	186727	45%	
SEQ ID n°3525	Prot n°PL-695.1	Contig38	182958	185585	69%	

TABLEAU I

SEQ ID n°3526	Prot n°PL-696.1	Contig38	181552	182565	72%	<p>Identities = 198/329 (60%), Positives = 245/329 (74%) dbj BAA01531.1 (D10689) M5 protein (Salmonella choleraesuis) Length = 345</p> <p>Identities = 707/930 (76%), Positives = 787/930 (84%), Gaps = 3930 (0%) sp P00582 DPO1_ECOLI DNA POLYMERASE I (POL I) pir DJEIC DNA-directed DNA polymerase (EC 2.7.7.7) I - Escherichia coli emb CAA23807.1 (V00317) DNA polymerase I [Escherichia coli] gb AA24402.1 (J01663) DNA polymerase I [Escherichia coli] gb AAB02998.1 (L19201) DNA polymerase I [Escherichia coli] gb AAC76861.1 (AE000461) DNA polymerase I, 3' -> 5' polymerase, 5' -> 3' and 3' -> 5' exonuclease [Escherichia coli]</p> <p>Identities = 65/258 (25%), Positives = 111/258 (42%), Gaps = 18/258 (6%) gb AAC35427.1 (U97057) beta-lactamase inhibitory protein II precursor [Streptomyces extoliatu] Length = 311</p>
SEQ ID n°3527	Prot n°PL-697.1	Contig38	178288	181077	84%	<p>Identities = 158/197 (80%), Positives = 172/197 (87%) sp P24253 YIHA_ECOLI HYPOTHETICAL GTP-BINDING PROTEIN IN POLA-HEMN INTERGENIC REGION Length = 210</p> <p>Identities = 138/220 (62%), Positives = 170/220 (76%), Gaps = 4/220 (1%) gb AAB40248.1 (U82664) acyl-coA thioesterase I precursor [Escherichia coli] Length = 218</p>
SEQ ID n°3528	Prot n°PL-698.1	Contig38	175858	177349	23%	<p>Identities = 282/401 (70%), Positives = 335/401 (83%) sp P18335 ARGD_ECOLI ACETYLORNITHINE AMINOTRANSFERASE (ACOAT) pir B65130 acetylornithine transaminase (EC 2.6.1.11) - Escherichia coli gb AA58156.1 (U18997) acetylornithine delta-amino transferase [Escherichia coli] gb AAC76384.1 (AE000412) acetylornithine delta-amino transferase [Escherichia coli] Length = 401</p> <p>Identities = 206/210 (98%), Positives = 208/210 (98%) sp P03020 CRP_ECOLI CATABOLITE GENE ACTIVATOR (CAMP RECEPTOR PROTEIN) (CAMP-REGULATORY PROTEIN) pir QRECC cAMP receptor protein - Escherichia coli pdb 2CGP A Chain A, Catabolite Gene Activator Protein DNA COMPLEX, ADENOSINE-3', 5'-Cyclic-Monophosphate gb AAA23601.1 (J01598) cAMP receptor protein (crp) [Escherichia coli] gb AAA26515.1 (M13772) catabolite gene activator protein [Shigella flexneri] gb AAA58154.1 (U18997) cyclic AMP receptor protein [Escherichia coli] gb AAC76382.1 (AE000411) cyclic AMP receptor protein [Escherichia coli] Length = 210</p>
SEQ ID n°3529	Prot n°PL-699.1	Contig38	174952	175584	64%	<p>Identities = 240/288 (83%), Positives = 271/288 (93%) sp P37307 KPPR_ECOLI PROBABLE PHOSPHORIBULOKINASE (PHOSPHOPENTOKINASE) (PRK) pir F55129 phosphoribulokinase (EC 2.7.1.19) - Escherichia coli (strain K-12) gb AAC76380.1 (AE000411) probable phosphoribulokinase [Escherichia coli] Length = 289</p>
SEQ ID n°3530	Prot n°PL-70.1	Contig41	119466	120131	65%	
SEQ ID n°3531	Prot n°PL-700.1	Contig38	171468	172677	81%	
SEQ ID n°3532	Prot n°PL-701.1	Contig38	170784	171416	95%	
SEQ ID n°3533	Prot n°PL-702.1	Contig38	169061	169930	93%	

TABLEAU I

SEQ ID n°3534	Prot n°PL-703.1	Contig38	167847	168824	78%	<p>Identities = 214/319 (67%), Positives = 258/319 (80%)</p> <p>sp P45524 YHET_ECOLI_HYPOTHETICAL 38.5 KD PROTEIN IN KIFB-PRKB INTERGENIC REGION pir D65129 hypothetical 38.5 KD protein in kifb-prkb intergenic region - Escherichia coli (strain K-12) gb AA58150.1 (U18997) ORF_o340 [Escherichia coli] gb AAC76378.1 (AE000411) orf, hypothetical protein [Escherichia coli] Length = 340</p>
SEQ ID n°3535	Prot n°PL-704.1	Contig38	168842	167726	59%	<p>Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%)</p> <p>gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300</p>
SEQ ID n°3536	Prot n°PL-705.1	Contig38	168138	168746	58%	<p>Identities = 70/200 (35%), Positives = 120/200 (60%), Gaps = 4/200 (2%)</p> <p>gb AAG05694.1 (AE004657) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 205</p>
SEQ ID n°3537	Prot n°PL-706.1	Contig38	164619	168097	81%	<p>Identities = 333/482 (69%), Positives = 409/482 (84%), Gaps = 2/482 (0%)</p> <p>gb AAF93383.1 (AE004110) PTS system, sucrose-specific IIBC component, putative [Vibrio cholerae] Length = 482</p>
SEQ ID n°3538	Prot n°PL-707.1	Contig38	163683	164588	81%	<p>Identities = 211/298 (70%), Positives = 250/298 (83%)</p> <p>(AE004110) GckR family protein [Vibrio cholerae] gb AAF83382.1 Length = 305</p>
SEQ ID n°3539	Prot n°PL-708.1	Contig38	161460	162431	14%	<p>Identities = 28/85 (32%), Positives = 47/85 (54%), Gaps = 1/85 (1%)</p> <p>sp P77354 YAFU_ECOLI_HYPOTHETICAL 12.1 KD PROTEIN IN DNAQ-GMHA INTERGENIC REGION pir C64746 yafU protein - Escherichia coli gb AAB08840.1 (U70214) hypothetical protein [Escherichia coli] gb AAC73322.1 (AE000130) orf, hypothetical protein [Escherichia coli] Length = 112</p>
SEQ ID n°3540	Prot n°PL-709.1	Contig38	158881	159795	30%	<p>Identities = 49/174 (28%), Positives = 94/174 (53%), Gaps = 6/174 (3%)</p> <p>emb CAB61937.1 (AL133278) putative lysR-family transcriptional regulator [Streptomyces coelicolor A3(2)] Length = 303</p>
SEQ ID n°3541	Prot n°PL-71.1	Contig41	120182	120987	78%	<p>Identities = 179/257 (69%), Positives = 209/257 (80%)</p> <p>sp P7388 YBBO_ECOLI_HYPOTHETICAL OXIDOREDUCTASE IN USHA-TESA INTERGENIC REGION pir D64780 probable retinol dehydrogenase (EC 1.1.1.-) - Escherichia coli gb AAB40247.1 (U82864) similar to human protein that oxidizes 11-cis retinol into 11-cis retinaldehyde [Escherichia coli] gb AAC73595.1 (AE000155) putative oxidoreductase [Escherichia coli]</p>

TABLEAU I

SEQ ID n°3542	Prot n°PL-710.1	Contig38	157401	158678	29%	Identities = 58/264 (21%), Positives = 124/264 (46%), Gaps = 28/264 (9%) pir T20770 hypothetical protein F11C3.3 - Caenorhabditis elegans emb CAB04089.1 (Z81496) similar to myosin heavy chain-cDNA EST EMBL:T02297 comes from this gene; cDNA EST EMBL:T00788 comes from this gene; cDNA EST yk202c10.3 comes from this gene; cDNA EST yk202c10.5 comes from this gene; cDNA EST yk205b2.3 comes from this gene-cDN> emb CAB05605.1 (Z83107) similar to myosin heavy chain-cDNA EST EMBL:T02297 comes from this gene; cDNA EST EMBL:T00788 comes from this gene; cDNA EST yk202c10.3 comes from this gene; cDNA EST yk202c10.6 comes from this gene; cDNA EST yk205b2.3 comes from this gene-cDN> Length = 1963.
SEQ ID n°3543	Prot n°PL-711.1	Contig38	156008	156847	48%	Identities = 83/272 (30%), Positives = 131/272 (47%), Gaps = 17/272 (6%) emb CAB61439.1 (Z32686) mrpH [Proteus mirabilis] Length = 275
SEQ ID n°3544	Prot n°PL-712.1	Contig38	155447	156007	43%	Identities = 68/143 (47%), Positives = 91/143 (63%), Gaps = 2/143 (1%) emb CAA83639.2 (Z32686) mrpG [Proteus mirabilis] Length = 182
SEQ ID n°3545	Prot n°PL-713.1	Contig38	154613	155371	71%	Identities = 141/250 (56%), Positives = 188/250 (74%) emb CAA83636.1 (Z32686) mrpD [Proteus mirabilis] Length = 252
SEQ ID n°3546	Prot n°PL-714.1	Contig38	151476	154283	65%	Identities = 463/800 (57%), Positives = 611/800 (75%), Gaps = 4/800 (0%) emb CAA83635.1 (Z32686) mrpC [Proteus mirabilis] Length = 871
SEQ ID n°3547	Prot n°PL-715.1	Contig38	150964	151680	39%	Identities = 63/163 (34%), Positives = 94/163 (50%), Gaps = 5/163 (2%) emb CAA83634.1 (Z32686) mrpB [Proteus mirabilis] Length = 186
SEQ ID n°3548	Prot n°PL-716.1	Contig38	149122	149694	77%	Identities = 138/183 (75%), Positives = 161/183 (87%) emb CAB61438.1 (Z32686) MrpI [Proteus mirabilis] Length = 188
SEQ ID n°3549	Prot n°PL-717.1	Contig38	148862	148787	82%	Identities = 502/638 (78%), Positives = 584/638 (87%), Gaps = 5/638 (0%) sp P45535 YHES_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP- BINDING PROTEIN YHES pir C65129 hypothetical ABC transporter in klf- prkb intergenic region - Escherichia coli (strain K-12) gb AAA58149.1 (U18997) ORF_0637 [Escherichia coli] gb AAC76377.1 (AE000411) putative ATP-binding component of a transport system [Escherichia coli]
SEQ ID n°3550	Prot n°PL-718.1	Contig38	145705	146277	84%	Identities = 159/185 (81%), Positives = 170/185 (86%), Gaps = 8/185 (4%) sp P30856 SLYD_ECOLI FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SLYD (PPIASE) (ROTAMASE) (HISTIDINE RICH PROTEIN) (WHP) pir A49987 probable fkbP-type peptidyl-prolyl cis-trans isomerase slyd - Escherichia coli emb CAA79705.1 (Z21496) histidine rich protein [Escherichia coli] gb AAA58146.1 (L13261) sensitivity to lysis gene [Escherichia coli] gb AAA58146.1 (U18997) histidine rich protein [Escherichia coli] gb AAC41458.1 (L28082) slyD gene product [Escherichia coli] gb AAC76374.1 (AE000411) FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli] Length = 196

TABLEAU I

SEQ ID n°3551	Prot n°PL-719.1	Contig38	144366	145130	81%	Identities = 179/254 (70%), Positives = 216/254 (84%), Gaps = 1/254 (0%) sp P45523 FKBA_ECOLI_FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKPA PRECURSOR (PPIASE) (ROTAMASE) pir 65035 fkbp-type peptidyl-prolyl cis-trans isomerase fkpA (EC 5.2.1.-) - Escherichia coli gb AA58144.1 (U18997) ORF_1270 [Escherichia coli] gb AAC41459.1 (L28082) fkpA gene product [Escherichia coli] gb AAC76372.1 (AE000410) FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli] Length = 270
SEQ ID n°3552	Prot n°PL-72.1	Contig41	121036	121893	77%	Identities = 182/278 (65%), Positives = 224/278 (80%) sp P77395 YBBN_ECOLI_HYPOTHETICAL_33.1_KD PROTEIN IN USHA-TESA INTERGENIC REGION pir C64780.ybbN protein - Escherichia coli gb AAB40246.1 (U82664) similar to H. influenzae HI1159 [Escherichia coli] gb AAC73594.1 (AE000155) putative thioredoxin-like protein [Escherichia coli] Identities = 189/244 (77%), Positives = 216/244 (88%) pir E65128_hypothetical protein b3346 - Escherichia coli (strain K-12) gb AAA58143.1 (U18997) ORF_1244: glg start [Escherichia coli] gb AAC76371.1 (AE000410) of, hypothetical protein [Escherichia coli] Length = 244
SEQ ID n°3553	Prot n°PL-720.1	Contig38	143350	144084	87%	Identities = 588/702 (83%), Positives = 636/702 (89%), Gaps = 3/702 (0%) sp P26229 EFG_SALTY_ELONGATION_FACTOR_G (EF-G) pir JC1424 translation elongation factor EF-G - Salmonella typhimurium emb CAA45880.1 (X64591) elongation factor G [Salmonella typhimurium] Identities = 370/393 (94%), Positives = 383/393 (97%) pir S13560 translation elongation factor EF-Tu.A - Salmonella typhimurium Length = 384
SEQ ID n°3554	Prot n°PL-721.1	Contig38	139010	141118	90%	Identities = 215/232 (92%), Positives = 227/232 (97%) sp P02384 RL1_ECOLI_50S_RIBOSOMAL_PROTEIN_L1 pir RSEC1 ribosomal protein L1 - Escherichia coli emb CAA23622.1 (V00339) rplA (L1) [Escherichia coli] gb AAC43082.1 (U00006) 50S ribosomal subunit protein L1 [Escherichia coli] gb AAC76958.1 (AE000472) 50S ribosomal subunit protein L1, regulates synthesis of L1 and L11 [Escherichia coli] Length = 234
SEQ ID n°3555	Prot n°PL-722.1	Contig38	137753	138937	92%	Identities = 1282/1342 (95%), Positives = 1319/1342 (97%) sp P00575 RPOB_ECOLI_DNA-DIRECTED_RNA_POLYMERASE_BETA_CHAIN (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT) pir RNEOB DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Escherichia coli gb AAB18647.1 (U76222) RNA polymerase beta subunit [Escherichia coli] gb AAC76961.1 (AE000472) RNA polymerase, beta subunit [Escherichia coli] Length = 1342

TABLEAU I

SEQ ID n°3558	Prot n°PL-725.1	Contig38	125276	129496	94%	<p>Identities = 1294/1407 (91%), Positives = 1357/1407 (95%)</p> <p>sp P00577 RPOC_ECOLI DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT) pir JRNECC DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Escherichia coli emb CAA23626.1 (V00339) rpoC [Escherichia coli] gb AAC76862.1 (AE000472) RNA polymerase, beta prime subunit [Escherichia coli] Length = 1407</p>
SEQ ID n°3559	Prot n°PL-727.1	Contig38	122605	123495	No Hits found	<p>Identities = 55/222 (24%), Positives = 101/222 (44%), Gaps = 39/222 (17%)</p> <p>db BAB14754.1 (AK023984) unnamed protein product [Homo sapiens] Length = 242</p>
SEQ ID n°3560	Prot n°PL-728.1	Contig38	121936	122592	45%	<p>Identities = 119/384 (30%), Positives = 196/384 (50%), Gaps = 12/384 (3%)</p> <p>db BAB07775.1 (AP001620) aminotransferase required for NAD biosynthesis (Nfs protein) [Bacillus halodurans] Length = 383</p>
SEQ ID n°3561	Prot n°PL-729.1	Contig38	120776	121936	49%	<p>Identities = 249/294 (84%), Positives = 274/294 (92%)</p> <p>sp P77367 YBBK_ECOLI HYPOTHETICAL 33.7 KD PROTEIN IN USHA-TESA INTERGENIC REGION pir H64779 probable membrane protein ybbk - Escherichia coli gb AAB40243.1 (U82664) similar to M. tuberculosis MTCY277.09 [Escherichia coli] gb AAC73581.1 (AE000155) putative protease [Escherichia coli] Length = 305</p>
SEQ ID n°3562	Prot n°PL-73.1	Contig41	121918	122838	88%	<p>Identities = 66/172 (38%), Positives = 103/172 (59%), Gaps = 5/172 (2%)</p> <p>db BAB02686.1 (AB018114) gb AAD14522.1-gene_id:MFG10.2-similar to unknown protein [Arabidopsis thaliana] Length = 390</p>
SEQ ID n°3563	Prot n°PL-730.1	Contig38	119688	120294	49%	<p>Identities = 64/254 (25%), Positives = 104/254 (40%), Gaps = 25/254 (9%)</p> <p>emb CAA11778.1 (AJ223998) PCZA361.23 [Amycolatopsis orientalis] Length = 274</p>
SEQ ID n°3564	Prot n°PL-731.1	Contig38	118911	119678	No Hits found	<p>Identities = 124/348 (35%), Positives = 193/348 (54%), Gaps = 13/348 (3%)</p> <p>sp P27127 RFAB_ECOLI LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--(GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE) pir B42982 UDP-D-galactose--(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase (EC 2.4.1.-) - Escherichia coli gb AAA24085.1 (M80599) lipopolysaccharide core biosynthesis protein [Escherichia coli] gb AAB16605.1 (U00039) UDP-D-galactose:(glucosyl)lipopolysaccharide -alpha-1,3-D-galactosyltransferase [Escherichia coli] gb AAC76852.1 (AE000440) UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase [Escherichia coli] Length = 369</p>
SEQ ID n°3565	Prot n°PL-732.1	Contig38	118130	118939	38%	
SEQ ID n°3566	Prot n°PL-733.1	Contig38	117040	118119	52%	
SEQ ID n°3567	Prot n°PL-734.1	Contig38	115799	116731	No Hits found	

TABLEAU I

SEQ ID n°3568	Prot n°PL-736.1	Contig38	114203	115135	70%	<p>Identities = 162/316 (51%), Positives = 221/316 (69%), Gaps = 16/316 (5%) sp P03841 MALM_ECOLI_MALTOSE_OPERON_PERIPLASMIC_PROTEIN_PRECURSOR_pir BVECM maltose operon periplasmic protein - Escherichia coli emb CAA28166.1 (X04477) periplasmic protein (AA 1-306) [Escherichia coli] gb AAC77007.1 (AE000477) periplasmic protein of maltose regulon [Escherichia coli] Length = 306</p>
SEQ ID n°3569	Prot n°PL-737.1	Contig38	112665	113954	85%	<p>Identities = 305/434 (70%), Positives = 367/434 (84%), Gaps = 10/434 (2%) sp P31242 LAMB_KLEPN_MALTOPORIN_PRECURSOR (MALTOSE-INDUCIBLE PORIN) pir IS23581 lamB protein precursor - Klebsiella pneumoniae emb CAA47377.1 (X66952) maltoporin [Klebsiella pneumoniae] Length = 429</p>
SEQ ID n°3570	Prot n°PL-738.1	Contig38	111522	112631	81%	<p>Identities = 311/371 (83%), Positives = 342/371 (91%), Gaps = 2/371 (0%) pir JMECMK inner membrane protein malk - Escherichia coli gb AAC43129.1 (U00006) cytoplasmic membrane protein for maltose uptake [Escherichia coli] gb AAC77005.1 (AE000476) ATP-binding component of transport system for maltose [Escherichia coli] Length = 371</p>
SEQ ID n°3571	Prot n°PL-739.1	Contig38	109944	111143	87%	<p>Identities = 316/394 (80%), Positives = 358/394 (90%) sp P02928 MALE_ECOLI_MALTOSE-BINDING_PERIPLASMIC_PROTEIN_PRECURSOR (MALTODEXTRIN-BINDING PROTEIN) (MMBP) pir JGECM periplasmic maltose-binding protein precursor - Escherichia coli gb AAC43128.1 (U00006) periplasmic maltose-binding protein [Escherichia coli] gb AAB59056.1 (J01648) periplasmic maltose-binding protein [Escherichia coli] gb AAC77004.1 (AE000476) periplasmic maltose-binding protein; substrate recognition for transport and chemotaxis [Escherichia coli] Length = 834</p>
SEQ ID n°3572	Prot n°PL-74.1	Contig41	123824	126568	76%	<p>Identities = 603/840 (71%), Positives = 704/840 (83%), Gaps = 11/840 (1%) sp Q59385 ATCU_ECOLI_PROBABLE_COPPER-TRANSPORTING_ATPASE_pir C64779 probable copper-transporting ATPase (EC 3.6.1.-) - Escherichia coli gb AAB40238.1 (U82864) probable copper-transporting atpase [Escherichia coli] gb AAC73586.1 (AE000154) putative ATPase [Escherichia coli] Length = 834</p>
SEQ ID n°3573	Prot n°PL-740.1	Contig38	108266	109822	80%	<p>Identities = 385/514 (74%), Positives = 433/514 (83%), Gaps = 3/514 (0%) sp P18812 MALF_ENTAE_MALTOSE_TRANSPORT_SYSTEM_PERMEASE_PROTEIN_MALF_pir S05332 inner membrane protein malf - Enterobacter aerogenes Length = 514</p>
SEQ ID n°3574	Prot n°PL-741.1	Contig38	107363	108253	92%	<p>Identities = 261/296 (88%), Positives = 277/296 (93%) sp P07622 MALG_ECOLI_MALTOSE_TRANSPORT_SYSTEM_PERMEASE_PROTEIN_MALG_pir JMECMG maltose transport inner membrane protein malG - Escherichia coli emb CAA26628.1 (X02871) put. mal G protein (aa 1-286) [Escherichia coli] gb AAC43126.1 (U00006) maltose transport inner membrane protein [Escherichia coli] gb AAC77002.1 (AE000476) part of maltose permease, inner membrane [Escherichia coli] Length</p>

TABLEAU I

SEQ ID n°3575	Prot n°PL-742.1	Contig38	105273	107297	46%	Identities = 197/624 (31%), Positives = 312/624 (49%), Gaps = 38/624 (6%) emb CAB73311.1 (AL139077) putative integral membrane protein
SEQ ID n°3576	Prot n°PL-743.1	Contig38	102448	104562	41%	Identities = 201/576 (34%), Positives = 313/576 (53%), Gaps = 13/576 (2%) gb AAC32475.1 (AF044503) VgrG protein [Escherichia coli] Length = 657
SEQ ID n°3577	Prot n°PL-744.1	Contig38	101087	102487	No Hits found	
SEQ ID n°3578	Prot n°PL-745.1	Contig38	99925	101082	32%	Identities = 69/289 (23%), Positives = 124/289 (42%), Gaps = 15/289 (5%) gb AAG04210.1 (AE004517_5) (AE004517) hypothetical protein [Pseudomonas aeruginosa] Length = 362
SEQ ID n°3579	Prot n°PL-746.1	Contig38	98742	100088	27%	Identities = 68/289 (23%), Positives = 123/289 (42%), Gaps = 15/289 (5%) gb AAG04210.1 (AE004517_5) (AE004517) hypothetical protein [Pseudomonas aeruginosa] Length = 362
SEQ ID n°3580	Prot n°PL-747.1	Contig38	97559	98821	28%	Identities = 68/289 (23%), Positives = 120/289 (40%), Gaps = 15/289 (5%) gb AAG04210.1 (AE004517_5) (AE004517) hypothetical protein [Pseudomonas aeruginosa] Length = 362
SEQ ID n°3581	Prot n°PL-748.1	Contig38	95325	96338	72%	Identities = 198/329 (60%), Positives = 245/329 (74%) db BAA01531.1 (D10889) M5 protein [Salmonella choleraesuis] Length = 345
SEQ ID n°3582	Prot n°PL-749.1	Contig38	91923	94010	75%	Identities = 429/692 (61%), Positives = 530/692 (75%), Gaps = 4/692 (0%) sp P15977 MALQ_EC01_4-ALPHA-GLUCANOTRANSFERASE (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME) pir J05137_4-alpha-glucanotransferase (EC 2.4.1.25) - Escherichia coli gb AA58214.1 (U18997) amyloamylase [Escherichia coli] gb AAC76441.1 (AE000417) 4-alpha-glucanotransferase (amyloamylase) [Escherichia coli] Length = 694
SEQ ID n°3583	Prot n°PL-75.1	Contig41	127282	128106	63%	Identities = 132/248 (53%), Positives = 174/248 (69%), Gaps = 1/248 (0%) sp P77301 YBAP_EC01_HYPOTHETICAL_29.9_KD_PROTEIN_IN_USHA-TESA INTERGENIC REGION pir J64779 ybaP protein - Escherichia coli gb AAB40236.1 (U82684) hypothetical protein [Escherichia coli] gb AAC73584.1 (AE000154) putative ligase [Escherichia coli] Length = 264
SEQ ID n°3584	Prot n°PL-750.1	Contig38	89511	91913	82%	Identities = 580/801 (72%), Positives = 668/801 (82%), Gaps = 5/801 (0%) gb AAA58215.1 (U18997) maltodextrin phosphorylase [Escherichia coli] Length = 797
SEQ ID n°3585	Prot n°PL-751.1	Contig38	86255	88969	79%	Identities = 652/804 (72%), Positives = 771/804 (85%), Gaps = 3/804 (0%) pir RGECMT regulatory protein malt - Escherichia coli gb AAC76443.1 (AE000418) positive regulator of mal regulon [Escherichia coli] Length = 901
SEQ ID n°3586	Prot n°PL-752.1	Contig38	85035	86246	53%	Identities = 141/381 (37%), Positives = 215/381 (56%), Gaps = 13/381 (3%) gb AAF93247.1 (AE004098) multidrug resistance protein, putative [Vibrio cholerae] Length = 400

TABLEAU I

SEQ ID n°3587	Prot n°PL-753.1	Contig38	83121	84392	51%	Identities = 130/420 (30%), Positives = 220/420 (51%), Gaps = 27/420 (6%) pir G75036 4-aminobutyrate transaminase (EC 2.6.1.19) PAB2386 - Pyrococcus abyssi (strain Orsay) emb CAB50188.1 (AJ248287) 4- AMINOBUTYRATE qui se dilate AMINOTRANSFERASE (EC 2.6.1.19) [Pyrococcus abyssi] Length = 457
SEQ ID n°3588	Prot n°PL-754.1	Contig38	82060	83160	44%	Identities = 100/338 (29%), Positives = 163/338 (47%), Gaps = 19/338 (5%) pir T36916 probable zinc-binding dehydrogenase - Streptomyces coelicolor emb CAB48402.1 (AL096743) putative zinc-binding dehydrogenase [Streptomyces coelicolor A3(2)] Length = 329
SEQ ID n°3589	Prot n°PL-755.1	Contig38	81414	82064	43%	Identities = 49/186 (26%), Positives = 94/186 (50%), Gaps = 8/186 (4%) pir H72277-hypothetical protein TM1254 - Thermotoga maritima (strain MSB8) gb AAD36329.1 (AE001780_13 (AE001780) beta-phosphoglucuronidase, putative [Thermotoga maritima] Length = 216
SEQ ID n°3590	Prot n°PL-756.1	Contig38	80191	81354	48%	Identities = 116/356 (32%), Positives = 187/356 (51%), Gaps = 8/356 (2%) gb AAG06920.1 (AE004773_9 (AE004773) hypothetical protein [Pseudomonas aeruginosa] Length = 383
SEQ ID n°3591	Prot n°PL-757.1	Contig38	79595	80176	64%	Identities = 100/199 (50%), Positives = 131/199 (65%), Gaps = 1/199 (0%) ref NP_012318.1 YJ1217wp spiP40893YJ17_YEAST HYPOTHETICAL 22.0 KD PROTEIN IN HXT11-HXT8 INTERGENIC REGION pir S50710 hypothetical protein YJ1217w - yeast [Saccharomyces cerevisiae] emb CAA83993.1 (Z34098) ORF [Saccharomyces cerevisiae] emb CAA89514.1 (Z49492) ORF YJ1217w [Saccharomyces cerevisiae] Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°3592	Prot n°PL-758.1	Contig38	78342	79408	21%	Identities = 277/370 (74%), Positives = 315/370 (84%), Gaps = 1/370 (0%) gb AAD48428.1 (AF154064_1 (AF154064) ThiH [Salmonella typhimurium] gb AAF33524.1 (AF170176) 89% identity over 377 amino acids with E. coli ThiH (SW:P30140) [Salmonella typhimurium LT2] Length = 377
SEQ ID n°3594	Prot n°PL-76.1	Contig41	128845	130503	80%	Identities = 397/544 (72%), Positives = 484/544 (84%), Gaps = 2/544 (0%) gb AAF12718.1 (AF068226_1 (AF068226) UDP-sugar hydrolase precursor [Enterobacter aerogenes] Length = 550
SEQ ID n°3595	Prot n°PL-760.1	Contig38	74724	75491	76%	Identities = 208/286 (72%), Positives = 231/286 (80%) (beta-hydroxyethyl)thiazole monophosphate synthesis protein ThiG - Escherichia coli Length = 324
SEQ ID n°3596	Prot n°PL-761.1	Contig38	73776	74525	74%	Identities = 151/245 (61%), Positives = 190/245 (76%), Gaps = 1/245 (0%) spiP30138 THIF_ECOLI THIF PROTEIN Length = 251

TABLEAU I

SEQ ID n°3597	Prot n°PL-762.1	Contig38	73115	73765	71%	<p>Identities = 138/198 (69%), Positives = 157/198 (78%)</p> <p>sp P30137 THIE_ECOLI_THIAMINE-PHOSPHATE PYROPHOSPHORYLASE (TMP PYROPHOSPHORYLASE) (TMP-PPASE) (THIAMINE-PHOSPHATE SYNTHASE) pir S35118 thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) thIE - Escherichia coli gb AAC43091.1 (U00006) thIE [Escherichia coli] gb AAB95617.1 (M88701) thIE [Escherichia coli] gb AAC76967.1 (AE000473) thiamin biosynthesis, thiazole moiety</p>
SEQ ID n°3598	Prot n°PL-764.1	Contig38	71185	73131	87%	<p>Identities = 533/623 (85%), Positives = 565/623 (90%), Gaps = 6/623 (0%)</p> <p>sp P30136 THIC_ECOLI_THIAMINE BIOSYNTHESIS PROTEIN THIC pir E65206 thiamin biosynthesis protein thIC - Escherichia coli gb AAC43092.1 (U00006) CG Site No. 115 [Escherichia coli] gb AAC76968.1 (AE000473) thiamin biosynthesis, pyrimidine moiety [Escherichia coli] Length = 631</p>
SEQ ID n°3599	Prot n°PL-765.1	Contig38	70232	70894	67%	<p>Identities = 111/220 (50%), Positives = 154/220 (69%) gb AAF95088.1 (AE004269) conserved hypothetical protein [Vibrio cholerae] Length =</p> <p>Identities = 173/253 (68%), Positives = 208/253 (81%)</p>
SEQ ID n°3600	Prot n°PL-766.1	Contig38	69174	69947	79%	<p>sp P32684 YJAD_ECOLI_HYPOTHETICAL 29.8 KD PROTEIN IN THIC-HEME INTERGENIC REGION pir G65206 hypothetical 29.8 kD protein in thic-heme intergenic region - Escherichia coli (strain K-12) gb AAC43094.1 (U00006) No definition line found [Escherichia coli] gb AAC76970.1 (AE000473) orf, hypothetical protein [Escherichia coli] pir J2105267A NADH pyrophosphatase [Escherichia coli] Length = 257</p>
SEQ ID n°3601	Prot n°PL-767.1	Contig38	67997	69061	91%	<p>Identities = 300/354 (84%), Positives = 327/354 (91%)</p> <p>sp P29680 DCUP_ECOLI_UROPORPHYRINOGEN DECARBOXYLASE (URO-D) (UPD) pir H65206 uroporphyrinogen decarboxylase (EC 4.1.1.37) - Escherichia coli gb AAC76971.1 (AE000473) uroporphyrinogen decarboxylase [Escherichia coli] Length = 354</p>
SEQ ID n°3602	Prot n°PL-768.1	Contig38	67324	68325	53%	<p>Identities = 149/224 (66%), Positives = 180/224 (79%), Gaps = 2/224 (0%)</p> <p>pir A65207 hypothetical 24.9 kD protein in heme-hupa intergenic region - Escherichia coli (strain K-12) gb AAC43096.1 (U00006) similar to O. berteriana mitochondrion. protein involved in cytochrome c biogenesis [Escherichia coli] gb AAC76972.1 (AE000473) endonuclease V (deoxyinosine 3' endonuclease) [Escherichia coli] Length = 225</p>
SEQ ID n°3603	Prot n°PL-769.1	Contig38	65488	66192	57%	<p>Identities = 83/225 (36%), Positives = 137/225 (60%), Gaps = 5/225 (2%)</p> <p>sp P32681 YJAH_ECOLI_HYPOTHETICAL 26.3 KD PROTEIN IN HUPA-HYDH INTERGENIC REGION (O231) pir D65207 hypothetical 26.3K protein (hupA-hydH intergenic region) - Escherichia coli (strain K-12) gb AAC43099.1 (U00006) No definition line found [Escherichia coli] gb AAC76975.1 (AE000473) orf, hypothetical protein [Escherichia coli] Length = 231</p>

TABLEAU I

SEQ ID n°3604	Prot n°PL-77.1	Contig41	130882	132111	82%	<p>Identities = 292/405 (72%), Positives = 341/405 (84%), Gaps = 1/405 (0%) sp P52067 FSR_ECOLI_FOSMIDOMYCIN_RESISTANCE_PROTEIN pir JC5041 fosmidomycin resistance protein - Escherichia coli db BAA11120.1 (D73370) fosmidomycin resistance protein [Escherichia coli] gb AAB40233.1 (U82684) fosmidomycin resistance protein [Escherichia coli] gb AAC73581.1 (AE000154) fosmidomycin resistance protein [Escherichia coli] Identities = 312/426 (73%), Positives = 361/426 (84%), Gaps = 1/426 (0%) sp P15640 PUR2_ECOLI_PHOSPHORIBOSYLAMINE--GLYCINE_LIGASE (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) phosphoribosylamine--glycine ligase (EC 6.3.4.13) - Escherichia coli emb CAA36213.1 (X51950) purD gene product [Escherichia coli] gb AAC43103.1 (U00006) phosphoribosylglycineamide synthetase [Escherichia coli] gb AAC76979.1 (AE000473) phosphoribosylglycineamide synthetase = GAR synthetase [Escherichia coli] Length = 429</p>
SEQ ID n°3605	Prot n°PL-770.1	Contig38	64183	65469	82%	
SEQ ID n°3606	Prot n°PL-771.2	Contig38	62575	64164		
SEQ ID n°3607	Prot n°PL-772.1	Contig38	1	1008	23%	<p>Identities = 62/130 (47%), Positives = 79/130 (60%), Gaps = 9/130 (6%) db BAB07424.1 (AP001519) transposase (12) [Bacillus halodurans] Length = 561</p>
SEQ ID n°3608	Prot n°PL-773.1	Contig38	1468	3303	22%	<p>Identities = 85/316 (26%), Positives = 136/316 (42%), Gaps = 33/316 (10%) gb AAF42109.1 (AE002526) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58] Length = 2514</p>
SEQ ID n°3609	Prot n°PL-774.1	Contig38	3661	6687	40%	<p>Identities = 271/879 (30%), Positives = 404/879 (45%), Gaps = 83/879 (9%) gb AAF42109.1 (AE002526) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58] Length = 2514</p>
SEQ ID n°3610	Prot n°PL-775.1	Contig38	10326	11042	No Hits found	
SEQ ID n°3611	Prot n°PL-776.1	Contig38	11943	13100	No Hits found	
SEQ ID n°3612	Prot n°PL-777.1	Contig38	13101	13883	No Hits found	
SEQ ID n°3613	Prot n°PL-778.1	Contig38	14303	15562	No Hits found	
SEQ ID n°3614	Prot n°PL-779.1	Contig38	16395	17762	70%	<p>Identities = 260/449 (57%), Positives = 328/449 (72%) gb AAG03788.1 AE004477_5 (AE004477) cystathionine beta-synthase [Pseudomonas aeruginosa] Length = 457</p>
SEQ ID n°3615	Prot n°PL-78.1	Contig41	132353	134059	83%	<p>Identities = 409/561 (72%), Positives = 482/561 (85%), Gaps = 9/561 (1%) sp P39830 YBAL_ECOLI_HYPOTHETICAL_58.4_KD_PROTEIN_IN_GSK-FSR INTERGENIC_REGION pir IE64778 probable membrane protein ybaL - Escherichia coli gb AAB40232.1 (U82684) similar to Y. enterocolitica RosB [Escherichia coli] gb AAC73580.1 (AE000154) putative transport protein [Escherichia coli] Length = 558</p>

Unknown, similar to
toxins

TABLEAU I

SEQ ID n°3616	Prot n°PL-780.1	Contig38	17780	18934	83%	Identities = 280/374 (74%), Positives = 329/374 (87%) pir S52983 probable cystathionine gamma-lyase (EC 4.4.1.1) - <i>Erwinia herbicola</i> (fragment) gb AAA64984.1 (M87280) transcription must start in the vector; putative ORF12 [<i>Erwinia herbicola</i>] Length = 611 "	
SEQ ID n°3617	Prot n°PL-781.1	Contig38	19025	19741	89%	Identities = 205/239 (85%), Positives = 223/239 (92%) sp P09743 DEOD_ECOLI PURINE NUCLEOSIDE PHOSPHORYLASE (INOSINE PHOSPHORYLASE) (PNP) pir A27854 purine-nucleoside phosphorylase (EC 2.4.2.1) - <i>Escherichia coli</i> gb AA24401.1 (M60917) purine nucleoside phosphorylase [Escherichia coli] gb AAA97280.1 (U14003) purine-nucleoside phosphorylase [Escherichia coli] gb AAC77337.1 (AE000508) purine-nucleoside phosphorylase [Escherichia coli] Length	
SEQ ID n°3618	Prot n°PL-782.1	Contig38	19824	21047	91%	Identities = 342/406 (84%), Positives = 382/406 (93%) sp P07851 DEOB_ECOLI PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE) pir S56607 phosphopentomutase (EC 5.4.2.7) deoB - <i>Escherichia coli</i> gb AAA97279.1 (U14003) phosphopentomutase [Escherichia coli] gb AAC77338.1 (AE000508)	
SEQ ID n°3619	Prot n°PL-783.1	Contig38	21247	22026	83%	Identities = 204/259 (78%), Positives = 227/259 (88%) sp P00882 DEOC_ECOLI DEOXYRIBOSE-PHOSPHATE ALDOLASE (PHOSPHODEOXYRIBOALDOLASE) (DEOXYRIBOALDOLASE) pir ADECD deoxyribose-phosphate aldolase (EC 4.1.2.4) - <i>Escherichia coli</i> gb AAA97277.1 (U14003) deoxyribose-phosphate aldolase [Escherichia coli] gb AAC77334.1 (AE000508) 2-deoxyribose-5-phosphate aldolase [Escherichia coli] Length = 259	
SEQ ID n°3620	Prot n°PL-784.1	Contig38	22353	23630	83%	Identities = 301/424 (70%), Positives = 361/424 (84%), Gaps = 7/424 (1%) gb AAF96495.1 (AE004305) NupC family protein [Vibrio cholerae] Length = 418	
SEQ ID n°3621	Prot n°PL-785.1	Contig38	23943	24638	56%	Identities = 111/222 (50%), Positives = 154/222 (69%), Gaps = 1/222 (0%) sp P46144 YEDJ_ECOLI HYPOTHETICAL 25.9 KD PROTEIN IN DCM-SERU INTERGENIC REGION pir F64980 membrane protein yedJ - <i>Escherichia coli</i> db BAA15790.1 (D90835) ORF_ID:344#10; similar to [SwissProt Accession Number P46144] [Escherichia coli] gb AAC75028.1 (AE000288) orf, hypothetical protein [Escherichia coli] Length = 231 "	
SEQ ID n°3622	Prot n°PL-786.1	Contig38	24872	25519	76%	Identities = 161/254 (63%), Positives = 201/254 (78%) sp P39408 YJUV_ECOLI HYPOTHETICAL 28.9 KD PROTEIN IN OSMY-DEOC INTERGENIC REGION Length = 259	
SEQ ID n°3623	Prot n°PL-787.1	Contig38	26556	31013	95%	Identities = 1406/1485 (94%), Positives = 1440/1485 (96%) gb AAC38625.1 (AF046867) insecticidal toxin complex protein TcaC [Photobacterium luminescens] Length = 1485	Unknown, similar to insecticidal toxins
SEQ ID n°3624	Prot n°PL-788.1	Contig38	31307	32899	95%	Identities = 502/531 (94%), Positives = 513/531 (96%) gb AAC38626.1 (AF046867) insecticidal toxin complex protein TcaZ [Photobacterium luminescens] Length = 532	Unknown, similar to insecticidal toxins

TABLEAU I

SEQ ID n°3625	Prot n°PL-789.1	Contig38	33966	34634	82%	Identities = 158/210 (75%), Positives = 183/210 (86%), Gaps = 1/210 (0%) gb AA85072.1 AE004039_7 (AE004039) conserved hypothetical protein [Xylella fastidiosa] Length = 236
SEQ ID n°3626	Prot n°PL-79.1	Contig41	134472	135113	42%	Identities = 52/190 (27%), Positives = 91/190 (47%), Gaps = 22/190 (11%) pir C55543 cnaU protein - Pseudomonas syringae pv. syringae gb AAC46034.1 U14657 CnaU [Pseudomonas syringae] Length = Identities = 230/397 (57%), Positives = 297/397 (73%), Gaps = 8/397 (2%) pir D64895 probable membrane protein b1433 - Escherichia coli gb AAC74515.1 AE000240 putative membrane transport protein [Escherichia coli] Length = 478
SEQ ID n°3627	Prot n°PL-790.1	Contig38	34908	36111	73%	Identities = 98/271 (36%), Positives = 146/271 (53%), Gaps = 22/271 (8%) gb AAF94898.1 AE004252 hypothetical protein [Vibrio cholerae] Length = 274
SEQ ID n°3628	Prot n°PL-791.1	Contig38	36123	37265	39%	Identities = 139/357 (38%), Positives = 205/357 (56%), Gaps = 4/357 (1%) gb AAF94899.1 AE004252 hypothetical protein [Vibrio cholerae] Length = 408
SEQ ID n°3629	Prot n°PL-792.1	Contig38	37235	38410	52%	Identities = 144/338 (42%), Positives = 199/338 (58%), Gaps = 13/338 (3%) gb AAF94900.1 AE004252 hypothetical protein [Vibrio cholerae] Length = 373
SEQ ID n°3630	Prot n°PL-793.1	Contig38	38368	39528	51%	Identities = 45/182 (24%), Positives = 82/182 (44%), Gaps = 19/182 (10%) sp P12903 FM12_KLEPN FIMBRIAL SUBUNIT TYPE 1 PRECURSOR pir YQKBT1 type 1 fimbrial protein precursor - Klebsiella pneumoniae (strain IA565) gb AA25091.1 (M20917) major fimbrial subunit precursor [Klebsiella pneumoniae] Length = 182
SEQ ID n°3631	Prot n°PL-794.1	Contig38	40325	40942	39%	Identities = 100/228 (43%), Positives = 146/228 (63%), Gaps = 4/228 (1%) sp P33342 YEHG_ECOLI HYPOTHETICAL 26.6 KD FIMBRIAL CHAPERONE IN GATY-MRP INTERGENIC REGION PRECURSOR pir E64978 hypothetical 26.6 kD fimbrial chaperone in mrp 5' region - Escherichia coli (strain K-12) gb AA60474.1 (U00007) yehC [Escherichia coli] gb AAC75171.1 (AE000300) putative chaperone [Escherichia coli] pir 2014253C yehC gene [Escherichia coli] Length = 239
SEQ ID n°3632	Prot n°PL-795.1	Contig38	41010	41708	61%	Identities = 334/846 (39%), Positives = 519/846 (60%), Gaps = 48/846 (5%) sp P33341 YEHB_ECOLI HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GATY-MRP INTERGENIC REGION PRECURSOR pir D64978 probable outer membrane usher protein precursor (mrp 5' region) - Escherichia coli (strain K-12) gb AA60473.1 (U00007) yehB [Escherichia coli] gb AAC75170.1 (AE000300) putative outer membrane protein [Escherichia coli] pir 2014253B yehB gene [Escherichia coli] Length =
SEQ ID n°3633	Prot n°PL-796.1	Contig38	41734	44208	62%	

TABLEAU I

SEQ ID n°3634	Prot n°PL-797.1	Contig38	44178	45311	34%	Identities = 79/303 (26%), Positives = 131/303 (43%), Gaps = 42/303 (13%) sp P33340 YEHA_EC01 HYPOTHETICAL 36.9 KDA PROTEIN IN GATY-MRP INTERGENIC REGION PRECURSOR pir JC64978 hypothetical 36.9 kD protein in mrp 5' region precursor - Escherichia coli (strain K-12) gb JAA60472.1 (U00007) yehA [Escherichia coli] dbj BAA15974.1 (D90848) ORF ID: o359#20 - similar to [SwissProt Accession Number P33340] [Escherichia coli] gb AAC75169.1 (AE000300) putative type-1 fimbrial protein [Escherichia coli] pir J2014253A yehA gene [Escherichia coli] Length = 123/263 (46%), Positives = 157/263 (58%), Gaps = 19/263 (7%)
SEQ ID n°3635	Prot n°PL-798.1	Contig38	48579	47370	54%	Identities = 123/263 (46%), Positives = 157/263 (58%), Gaps = 19/263 (7%) sp P27297 BAX_EC01 BAX PROTEIN pir J547791 hypothetical protein f274b - Escherichia coli gb AAB18547.1 (U00039) No definition line found - [Escherichia coli] gb AAC76594.1 (AE000434) putative ATP-binding protein [Escherichia coli] Length = 274
SEQ ID n°3636	Prot n°PL-799.1	Contig38	47576	48997	60%	Identities = 183/480 (38%), Positives = 282/480 (58%), Gaps = 29/480 (5%) gb AAF41650.1 (AE002475) alginate O-acetylation protein AlgI, putative [Neisseria meningitidis MC58] Length = 478
SEQ ID n°3637	Prot n°PL-8.1	Contig41	15908	17572	56%	Identities = 236/546 (43%), Positives = 323/546 (58%), Gaps = 26/546 (4%) gb AAF85347.1 (AE004062_2) (AE004062) outer membrane hemolysin - activator protein [Xylella fastidiosa] Length = 597
SEQ ID n°3638	Prot n°PL-80.1	Contig41	136233	137543	89%	Identities = 351/436 (80%), Positives = 366/436 (90%), Gaps = 2/436 (0%) sp P22937 INGK_EC01 INOSINE-GUANOSINE KINASE pir JQ0812 inosine kinase (EC 2.7.1.73) - Escherichia coli dbj BAA00690.1 (D00798) inosine-guanosine kinase [Escherichia coli] gb AAB40231.1 (U82864) inosine kinase [Escherichia coli] gb AAC73579.1 (AE000154) inosine-guanosine kinase [Escherichia coli] Length = 434
SEQ ID n°3639	Prot n°PL-800.1	Contig38	48954	50120	47%	Identities = 120/363 (33%), Positives = 186/363 (51%), Gaps = 50/363 (13%) emb CAB84712.1 (AL162756) putative periplasmic protein [Neisseria meningitidis] Length = 327
SEQ ID n°3640	Prot n°PL-801.1	Contig38	50077	51327	43%	Identities = 127/357 (35%), Positives = 182/357 (50%), Gaps = 21/357 (5%) emb CAB84713.1 (AL162756) putative periplasmic protein [Neisseria meningitidis] Length = 397
SEQ ID n°3641	Prot n°PL-802.1	Contig38	51535	52458	51%	Identities = 101/290 (34%), Positives = 158/290 (53%), Gaps = 8/290 (2%) gb AAB80743.1 (AF020810) putative transcription activator Mlg-14 [Salmonella typhimurium] Length = 298
SEQ ID n°3642	Prot n°PL-803.1	Contig38	52548	53885	89%	Identities = 349/445 (78%), Positives = 405/445 (90%) sp P46858 GNTU_EC01 LOW-AFFINITY GLUCONATE TRANSPORTER (GLUCONATE PERMEASE) (GNT-1 SYSTEM) pir JCA4989 gluconate permease component U - Escherichia coli dbj BAA12326.1 (D84362) low affinity gluconate permease [Escherichia coli] Length = 446

TABLEAU I

SEQ ID n°3643	Prot n°PL-804.1	Contig38	54593	55588	82%	<p>Identities = 233/331 (70%), Positives = 276/331 (82%)</p> <p>sp P48860 GNTR_ECOLI_GLUCONATE UTILIZATION SYSTEM GNT-1 TRANSCRIPTIONAL REPRESSOR [dbj BA112324.1] (D84362) repressor</p> <p>Identities = 335/459 (72%), Positives = 394/459 (84%)</p> <p>sp P31474 YIEO_ECOLI_HYPOTHETICAL 51.5 KD PROTEIN IN RBRS-RRSC INTERGENIC REGION [pir JC65179] hypothetical 51.5 kD protein in rBr-rsC intergenic region - Escherichia coli (strain K-12) gb AAA82107.1 (L10328) similar to drug resistance translocases [Escherichia coli] gb AAC76777.1 (AE000452) putative transport protein [Escherichia coli]</p> <p>Identities = 219/329 (66%), Positives = 268/329 (80%)</p>
SEQ ID n°3644	Prot n°PL-805.1	Contig38	540830	542021	84%	<p>sp P25551 RBRS_ECOLI_RIBOSE-OPERON REPRESSOR [pir B65179] ribose operon repressor - Escherichia coli [dbj BAA01259.1] (D10466) rbs repressor [Escherichia coli] gb AAC76776.1 (AE000452) regulator for rbs operon [Escherichia coli] Length = 330</p>
SEQ ID n°3645	Prot n°PL-806.1	Contig38	542018	543019	79%	<p>Identities = 219/309 (70%), Positives = 251/309 (80%), Gaps = 1/309 (0%)</p> <p>sp P05054 RBSK_ECOLI_RIBOKINASE [pir KIECRB] ribokinase (EC 2.7.1.15) - Escherichia coli [pdb 1RK2 B Chain B, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RKD] E. Coli Ribokinase Complexed With Ribose And Adp [pdb 1RK2 C Chain C, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 A Chain A, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 D Chain D, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 E Chain E, The Apo Form Of E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 F Chain F, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 G Chain G, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 H Chain H, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 I Chain I, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 J Chain J, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 K Chain K, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 L Chain L, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 M Chain M, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 N Chain N, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 O Chain O, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 P Chain P, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 Q Chain Q, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 R Chain R, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 S Chain S, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 T Chain T, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 U Chain U, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 V Chain V, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 W Chain W, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 X Chain X, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 Y Chain Y, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 Z Chain Z, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AA Chain AA, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AB Chain AB, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AC Chain AC, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AD Chain AD, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AE Chain AE, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AF Chain AF, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AG Chain AG, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AH Chain AH, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AI Chain AI, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AJ Chain AJ, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AK Chain AK, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AL Chain AL, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AM Chain AM, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AN Chain AN, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AO Chain AO, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AP Chain AP, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AQ Chain AQ, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AR Chain AR, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AS Chain AS, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AT Chain AT, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AU Chain AU, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AV Chain AV, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AW Chain AW, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AX Chain AX, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AY Chain AY, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 AZ Chain AZ, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BA Chain BA, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BB Chain BB, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BC Chain BC, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BD Chain BD, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BE Chain BE, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BF Chain BF, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BG Chain BG, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BH Chain BH, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BI Chain BI, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BJ Chain BJ, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BK Chain BK, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BL Chain BL, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BM Chain BM, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BN Chain BN, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BO Chain BO, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BP Chain BP, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BQ Chain BQ, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BR Chain BR, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BS Chain BS, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BT Chain BT, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BU Chain BU, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BV Chain BV, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BW Chain BW, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BX Chain BX, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BY Chain BY, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 BZ Chain BZ, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 CA Chain CA, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 CB Chain CB, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 CC Chain CC, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 CD Chain CD, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 CE Chain CE, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 CF Chain CF, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 [pdb 1RK2 CG Chain CG, E. Col</p>

TABLEAU I

SEQ ID n°3648	Prot n°PL-809.1	Contig38	544930	545901	89%	<p>Identities = 263/311 (84%), Positives = 293/311 (93%)</p> <p>sp P04984 RBSC_ECOLI RIBOSE TRANSPORT SYSTEM PERMEASE PROTEIN RBSC pir G65178 high affinity ribose transport protein rbsC - Escherichia coli gb AAA62103.1 (L10328) high affinity ribose transport protein [Escherichia coli] gb AAC76773.1 (AE000452) D-ribose high-affinity transport system [Escherichia coli] Length = 321</p>
SEQ ID n°3649	Prot n°PL-81.1	Contig41	137642	138745	65%	<p>Identities = 159/376 (42%), Positives = 241/376 (63%), Gaps = 10/376 (2%)</p> <p>emb CAB63286.1 (AJ251713) O-antigen chain length determinant-like protein [Yersinia pestis] Length = 383</p>
SEQ ID n°3650	Prot n°PL-810.1	Contig38	545908	547413	86%	<p>Identities = 396/501 (78%), Positives = 440/501 (87%)</p> <p>sp P04983 RBSC_ECOLI RIBOSE TRANSPORT ATP-BINDING PROTEIN RBSC pir B26304 ribose transport protein rbsA - Escherichia coli gb AAA51473.1 (M13169) high affinity ribose transport protein [Escherichia coli] gb AAC76772.1 (AE000452) ATP-binding component of D-ribose high-affinity transport system [Escherichia coli] Length = 501</p>
SEQ ID n°3651	Prot n°PL-811.1	Contig38	548093	549604	71%	<p>Identities = 291/500 (58%), Positives = 370/500 (73%), Gaps = 2/500 (0%)</p> <p>pir C65178 hypothetical 57.4 kD protein in asnA-kup intergenic region - Escherichia coli (strain K-12) gb AAC76769.1 (AE000451) putative 2-component regulator [Escherichia coli] Length = 506</p>
SEQ ID n°3652	Prot n°PL-812.1	Contig38	549609	551066	68%	<p>Identities = 252/428 (58%), Positives = 335/428 (77%), Gaps = 2/428 (0%)</p> <p>sp P03818 YIEM_ECOLI HYPOTHETICAL 49.6 KD PROTEIN IN ASNA-KUP INTERGENIC REGION pir JQEC03 hypothetical 49.8K protein (asnA 3' region) - Escherichia coli (strain K-12) gb AAC76768.1 (AE000451) orf, hypothetical protein [Escherichia coli] Length = 427</p>
SEQ ID n°3653	Prot n°PL-813.1	Contig38	551073	552065	78%	<p>Identities = 247/330 (74%), Positives = 283/330 (84%)</p> <p>sp P00963 ASNA_ECOLI ASPARTATE-AMMONIA LIGASE (ASPARAGINE SYNTHETASE A) pir JAJECNA aspartate-ammonia ligase (EC 6.3.1.1) - Escherichia coli gb AAA24248.1 (J01657) asparagine synthetase A [Escherichia coli] gb AAA24253.1 (K00826) asparagine synthetase A [Escherichia coli] gb AAA62098.1 (L10328) asparagine synthetase A [Escherichia coli] gb AAC76767.1 (AE000451) asparagine synthetase A</p>
SEQ ID n°3654	Prot n°PL-814.2	Contig38	553606	555495		<p>Identities = 155/207 (74%), Positives = 180/207 (86%), Gaps = 1/207 (0%)</p> <p>sp P17113 GIDB_ECOLI GLUCOSE INHIBITED DIVISION PROTEIN B pir JBVEQCB gidB protein - Escherichia coli gb AAA62092.1 (L10328) glucose inhibited division protein [Escherichia coli] emb CAA25774.1 (X01631) gidB protein [Escherichia coli] gb AAC76763.1 (AE000451) glucose-inhibited division; chromosome replication? [Escherichia coli]</p>
SEQ ID n°3655	Prot n°PL-815.1	Contig38	555509	556129	81%	

TABLEAU I

SEQ ID n°3656	Prot n°PL-816.1	Contig38	557148	557972	87%	<p>Identities = 228/271 (83%), Positives = 249/271 (91%), Gaps = 1/271 (0%)</p> <p>sp P00855 ATP6_ECOLI ATP SYNTHASE A CHAIN (PROTEIN 6) pir JLWEC6_H+-transporting ATP synthase (EC 3.6.1.34) protein 6 - Escherichia coli emb CAA23514.1 (V00284) reading frame gene 2 (A) [Escherichia coli] emb CAA25776.1 (X01631) uncB protein [Escherichia coli] gb AA24731.1 (J01594) ATP synthase a subunit (atp-2) [Escherichia coli] gb AAA62090.1 (L10328) ATP synthase F0 subunit a [Escherichia coli] emb CAA23520.1 (V00286) alternate apB CDS [Escherichia coli] gb AAC76761.1 (AE000450) membrane-bound ATP synthase, F0 sector, subunit a [Escherichia coli] Length = 271</p>
SEQ ID n°3657	Prot n°PL-817.1	Contig38	559355	560896	92%	<p>Identities = 468/513 (91%), Positives = 500/513 (97%)</p> <p>sp P00822 ATPA_ECOLI ATP SYNTHASE ALPHA CHAIN pir PWECB_H+- transporting ATP synthase (EC 3.6.1.34) alpha chain - Escherichia coli gb AAA62086.1 (L10328) ATP synthase F1 alpha subunit [Escherichia coli] gb AAC76757.1 (AE000450) membrane-bound ATP synthase, F1 sector, alpha-subunit [Escherichia coli] Length = 513</p>
SEQ ID n°3658	Prot n°PL-818.1	Contig38	560955	561818	93%	<p>Identities = 256/287 (89%), Positives = 272/287 (94%)</p> <p>gb AAF19361.1 AF188265.7 (AF188265) ATP synthase subunit gamma [Salmonella typhimurium] Length = 287</p>
SEQ ID n°3659	Prot n°PL-819.1	Contig38	561853	563235	95%	<p>Identities = 433/460 (94%), Positives = 450/460 (97%)</p> <p>sp P00824 ATPB_ECOLI ATP SYNTHASE BETA CHAIN pir PWECB_H+- transporting ATP synthase (EC 3.6.1.34) beta chain - Escherichia coli emb CAA23527.1 (V00267) reading frame beta [Escherichia coli] emb CAA23594.1 (V00311) reading frame papB [Escherichia coli] gb AAA83875.1 (M25464) H+ ATPase F1 beta subunit [Escherichia coli] gb AA24737.1 (J01594) ATP synthase beta subunit (atp-8) [Escherichia coli] gb AAA62084.1 (L10328) ATP synthase F1 beta subunit [Escherichia coli] emb CAA25782.1 (X01631) uncD protein [Escherichia coli] gb AAC76755.1 (AE000450) membrane-bound ATP synthase, F1 sector, beta-subunit Identities = 201/305 (65%), Positives = 253/305 (82%)</p>
SEQ ID n°3660	Prot n°PL-82.1	Contig41	138929	139906	76%	<p>sp P43413 HEMZ_YEREN FERROCHELATASE (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) pir S70735 ferrochelatase (EC 4.99.1.1) - Yersinia enterocolitica emb CAA87897.1 (Z47767) ferrochelatase [Yersinia enterocolitica] Length = 308</p>
SEQ ID n°3661	Prot n°PL-820.1	Contig38	563808	565181	86%	<p>Identities = 357/456 (78%), Positives = 402/456 (87%)</p> <p>sp P17114 GLMU_ECOLI UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (N-ACETYLGLUCOSAMINE-1-PHOSPHATE URIDYLTRANSFERASE) pir C65176 glmU protein - Escherichia coli (strain K12) gb AAC76753.1 (AE000450) N-acetyl glucosamine-1-phosphate uridylyltransferase [Escherichia coli] Length = 456</p>

TABLEAU I

SEQ ID n°3662	Prot n°PL-822.1	Contig38	565289	567118	85%	Identities = 503/609 (82%), Positives = 550/609 (89%) sp P17169 GLMS_ECOLI GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) p I XNECGM glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Escherichia coli gb AAC76752.1 (AE000450) L-glutamine:D-fructose-6-phosphate
SEQ ID n°3663	Prot n°PL-823.1	Contig38	568033	569151	22%	Identities = 64/152 (42%), Positives = 83/152 (54%), Gaps = 3/152 (1%) p I S18689 Sc/Svp protein - Escherichia coli plasmid p15B emb CAA44052.1 (X62121) DNA Inversion product [Escherichia coli] Length = 753
SEQ ID n°3664	Prot n°PL-824.1	Contig38	569199	569783	57%	Identities = 78/198 (39%), Positives = 125/198 (62%), Gaps = 2/198 (1%) sp Q47427 TFAB_ECOLI TAIL FIBER ASSEMBLY PROTEIN HOMOLOG p I S18684 gene T protein - Escherichia coli plasmid p15B emb CAA44047.1 (X62121) T [Escherichia coli] Length = 203
SEQ ID n°3665	Prot n°PL-825.1	Contig38	570553	571626	20%	Identities = 53/116 (45%), Positives = 75/116 (63%), Gaps = 4/116 (3%) db JBA76527.2 (AB017336) tail fiber [Pectobacterium carotovorum] Length = 667
SEQ ID n°3666	Prot n°PL-826.2	Contig38	572498	573112		Identities = 112/281 (39%), Positives = 141/281 (49%), Gaps = 71/281 (25%) ref NP_046771.1 gpV sp P31340 VPV_BPP2 BASEPLATE ASSEMBLY PROTEIN V (GPV) gb AAD03282.1 (AF063097) gpV [Bacteriophage P2] Length = 211
SEQ ID n°3668	Prot n°PL-828.1	Contig38	575847	576846	68%	Identities = 187/326 (80%), Positives = 230/326 (70%), Gaps = 43/326 (13%) ref NP_046773.1 gpJ sp P51767 VPJ_BPP2 BASEPLATE ASSEMBLY PROTEIN J (GPJ) gb AAD03284.1 (AF063097) gpJ [Bacteriophage P2] Length = 302
SEQ ID n°3669	Prot n°PL-829.1	Contig38	576835	577452	66%	Identities = 109/174 (62%), Positives = 139/174 (79%) ref NP_046774.1 gpl sp P2670 VPI_BPP2 TAIL PROTEIN I (GPI) gb AAD03285.1 (AF063097) gpl [Bacteriophage P2] Length = 176
SEQ ID n°3670	Prot n°PL-83.1	Contig41	140083	140727	88%	Identities = 178/218 (81%), Positives = 198/218 (90%) gb AAB40228.1 (U92864) adenylate kinase [Escherichia coli] Length = 233
SEQ ID n°3671	Prot n°PL-830.1	Contig38	577386	578576	43%	Identities = 138/270 (51%), Positives = 172/270 (63%), Gaps = 45/270 (16%) gi 9634074 similar to P2 tail fiber protein H, PIR Accession Number B42291 gb AAC34164.1 (U32222) similar to P2 tail fiber protein H, PIR Accession Number B42291 [Enterobacteria phage 186] Length = 462

TABLEAU I

SEQ ID n°3672	Prot n°PL-831.1	Contig38	579061	579660	60%	Identities = 87/199 (43%), Positives = 124/199 (61%), Gaps = 1/199 (0%) sp P09153 YCFA_EC01_HYPOTHETICAL_21.7_KD_PROTEIN_IN_INTE-PIN INTERGENIC REGION pir A64861 ycfA protein, phage protein-related - Escherichia coli gb AAC74240.1 (AE000214) orf, hypothetical protein [Escherichia coli] Length = 200
SEQ ID n°3673	Prot n°PL-832.1	Contig38	580436	581050	33%	Identities = 52/94 (55%), Positives = 69/94 (73%) pir A42463 hypothetical protein Bcv (pin8 5' region) - Shigella boydii (fragment) db BAA00552.1 (D00660) Bcv gene product [Shigella boydii] Length = Identities = 291/388 (75%), Positives = 335/388 (86%) gb AAD54236.1 (AF153829) unknown [Salmonella typhi] Length = 390
SEQ ID n°3674	Prot n°PL-833.1	Contig38	581405	582577	82%	Identities = 207/826 (25%), Positives = 364/826 (44%), Gaps = 73/826 (8%) db BAA36253.1 (AB008550) orf25, similar to T gene of P2 [Pseudomonas aeruginosa phage phi CTX] Length = 904
SEQ ID n°3675	Prot n°PL-834.1	Contig38	583505	586000	43%	Identities = 195/370 (52%), Positives = 246/370 (65%), Gaps = 26/370 (7%) ref NP_052275.1 D protein sp P21679 VPD_BP186_LATE_CONTROL_GENE D PROTEIN (GPD) gb AAC34172.1 (U32222) D protein [Enterobacteria phage 186] Length = 389
SEQ ID n°3676	Prot n°PL-835.1	Contig38	586446	587549	66%	Identities = 298/367 (81%), Positives = 327/367 (88%), Gaps = 1/367 (0%) sp P00353 DHAS_EC01_ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (ASA DEHYDROGENASE) (ASADH) pir IDEEDCA aspartate-semialdehyde dehydrogenase (EC 1.2.1.1) - Escherichia coli pdb 1BRM C Chain C, Aspartate Beta-Semialdehyde Dehydrogenase From Escherichia coli pdb 1BRM B Chain B, Aspartate Beta-Semialdehyde Dehydrogenase From Escherichia coli pdb 1BRM A Chain A, Aspartate Beta-Semialdehyde Dehydrogenase From Escherichia coli emb CAA23511.1 (V00262) dehydrogenase [Escherichia coli] gb AAC76458.1 (AE000420) aspartate- semialdehyde dehydrogenase [Escherichia coli] gb AAC72855.1 (AF101226) aspartate semialdehyde dehydrogenase [Shigella sonnei] Length = 367
SEQ ID n°3677	Prot n°PL-836.1	Contig38	588054	589163	85%	
SEQ ID n°3678	Prot n°PL-837.1	Contig38	589306	590085	No Hits found	Identities = 681/804 (84%), Positives = 740/804 (91%) sp P06982 GYRB_EC01_DNA_GYRASE_SUBUNIT_B emb CAA27871.1 (X04341) gyrase B (AA 1-804) [Escherichia coli] Length = 804
SEQ ID n°3679	Prot n°PL-838.1	Contig38	591824	594241	90%	Identities = 278/362 (76%), Positives = 311/362 (85%), Gaps = 1/362 (0%) sp P22839 REFC_PROMI_REC_F PROTEIN pir JQ0735 recF protein - Proteus mirabilis gb AA83960.1 (M58352) putative [Proteus mirabilis] Length = 362
SEQ ID n°3680	Prot n°PL-839.1	Contig38	594258	595349	83%	

TABLEAU I

SEQ ID n°3681	Prot n°PL-84.1	Contig41	140910	142808	91%	<p>Identities = 529/627 (84%), Positives = 577/627 (91%), Gaps = 3/627 (0%) spiP10413HTPG_ECOLI HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN) G (HEAT-SHOCK PROTEIN C82.5) pir JHHEC62 heat shock protein C62.5 - Escherichia coli gb AA23460.1 (M38777) htpG ORF [Escherichia coli] gb AAB40227.1 (U82664) heat shock protein HtpG [Escherichia coli] gb AAC73575.1 (AE000153) chaperone Hsp90, heat shock protein C 62.5 [Escherichia coli] Length = 824</p> <p>Identities = 315/366 (86%), Positives = 344/366 (93%) spiP00583DIP3B_ECOLI DNA POLYMERASE III, BETA CHAIN pir DJEC3B DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Escherichia coli pdb 2POLJA Chain A, Pol.III (Beta Subunit) [E.C.2.7.7.7] pdb 2POLJB Chain B, Pol.III (Beta Subunit) [E.C.2.7.7.7] gb AAB59150.1 (J01602) DNA polymerase III beta-subunit [Escherichia coli] gb AAA62052.1 (L10328) DNA polymerase III beta-subunit [Escherichia coli] gb AAC76724.1 (AE000447) DNA polymerase III, beta-subunit [Escherichia coli] Length = 366</p> <p>Identities = 430/464 (92%), Positives = 442/464 (94%), Gaps = 2/464 (0%) spiP28440IDNAA_SERMA CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA gb AAA02924.1 (M17353) DnaA [Serratia marcescens] Length = 464</p>
SEQ ID n°3682	Prot n°PL-840.1	Contig38	595371	596471	91%	
SEQ ID n°3683	Prot n°PL-841.1	Contig38	595476	597864	93%	
SEQ ID n°3684	Prot n°PL-842.1	Contig38	595296	600936	85%	<p>Identities = 410/546 (75%), Positives = 471/546 (86%), Gaps = 3/546 (0%) spiP25714I60IM_ECOLI 60 KDA INNER-MEMBRANE PROTEIN pir B65173 probable 60K inner membrane protein - Escherichia coli (strain K-12) gb AAA62056.1 (L10328) 60 KD protein [Escherichia coli] gb AAC76728.1 (AE000447) 60 KD inner-membrane protein [Escherichia coli] Length = 548</p>
SEQ ID n°3685	Prot n°PL-843.1	Contig38	601183	602547	90%	<p>Identities = 385/454 (84%), Positives = 423/454 (92%) spiP25522THDF_ECOLI THIOPHENE AND FURAN OXIDATION PROTEIN THDF pir J085173 thiophene and furan oxidation 50 kD protein thdF - Escherichia coli (strain K-12) gb AAC76729.1 (AE000447) GTP-binding protein in thiophene and furan oxidation [Escherichia coli]</p>
SEQ ID n°3686	Prot n°PL-844.1	Contig38	602781	604031	28%	<p>Identities = 79/202 (39%), Positives = 119/202 (58%), Gaps = 5/202 (2%) spiO50224RECG_THIFE ATP-DEPENDENT DNA HELICASE RECG gb AAC21662.1 (AF032884) RecG [Acidithiobacillus ferrooxidans] Length = 652</p>
SEQ ID n°3687	Prot n°PL-845.1	Contig38	604028	606718	43%	<p>Identities = 222/929 (23%), Positives = 394/929 (41%), Gaps = 140/929 (15%) db BAA84909.1 (AB024948) orf74 [Escherichia coli] Length = 873</p>
SEQ ID n°3688	Prot n°PL-846.1	Contig38	607657	608976	67%	<p>Identities = 226/423 (53%), Positives = 308/423 (71%), Gaps = 1/423 (0%) pir F64904 hipA protein - Escherichia coli gb AAC74580.1 (AE000248) persistence to inhibition of murein or DNA biosynthesis, DNA-binding regulator [Escherichia coli] Length = 440</p>

TABLEAU I

SEQ ID n°3689	Prot n°PL-847.1	Contig38	609173	610879	53%	Identities = 194/555 (34%), Positives = 303/555 (53%), Gaps = 19/555 (3%) emb CAB83707.1 (AL162753) putative integral membrane protein [Neisseria meningitidis] Length = 550
SEQ ID n°3690	Prot n°PL-848.1	Contig38	610930	612789	73%	Identities = 375/619 (60%), Positives = 461/619 (73%), Gaps = 8/619 (1%) sp P14081 SELB_ECOLI SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR (SELB TRANSLATION FACTOR) pir IEFECB translation elongation factor EF-selB - Escherichia coli emb CAA34637.1 (X16644) SEL B (AA 1-614) [Escherichia coli] gb AAC76614.1 (AE000436) selenocysteinyl-IRNA-specific translation factor [Escherichia coli] prf 1602238A translation factor [Escherichia coli] Length = 614
SEQ ID n°3691	Prot n°PL-849.1	Contig38	612823	614214	71%	Identities = 307/462 (66%), Positives = 354/462 (76%) sp P23328 SELA_ECOLI L-SERYL-TRNA(SEC) SELENIUM TRANSFERASE (CYSTEINYL-TRNA(SEC) SELENIUM TRANSFERASE) (SELENOCYSTEINE SYNTHASE) (SELENOCYSTEINYL-TRNA(SEC) SYNTHASE) pir JA38730 selA protein - Escherichia coli gb AA24624.1 (M84177) selenocysteine synthase [Escherichia coli] Length = 463
SEQ ID n°3692	Prot n°PL-85.1	Contig41	143300	145399	43%	Identities = 178/762 (23%), Positives = 304/762 (39%), Gaps = 115/762 (15%) sp P44523 HXC1_HAEIN HEME-HEMOPEXIN UTILIZATION PROTEIN C PRECURSOR pir B64049 outer membrane protein hxcC homolog - Haemophilus influenzae (strain Rd KW20) gb AAC21789.1 (U32696) hemin receptor (hemR) [Haemophilus influenzae Rd] Length = 744
SEQ ID n°3693	Prot n°PL-850.1	Contig38	614225	615154	80%	Identities = 206/309 (66%), Positives = 251/309 (80%), Gaps = 2/309 (0%) sp P13024 FDHE_ECOLI FDHE PROTEIN pir S40835 fdhE protein - Escherichia coli gb AAB03024.1 (L19201) fdhE gene product [Escherichia coli] gb AAD13453.1 (AE000464) affects formate dehydrogenase-N [Escherichia coli] Length = 309
SEQ ID n°3694	Prot n°PL-851.1	Contig38	615647	616621	33%	Identities = 87/197 (34%), Positives = 110/197 (55%), Gaps = 14/197 (7%) sp P16559 TCMN_STIRGA MULTIFUNCTIONAL CYCLASE-DEHYDRATASE-3 O-METHYL TRANSFERASE TCMN pir S27698 tmN protein - Streptomyces glaucoscens gb AAA67518.1 (M80674) possible internal translational start site at position 9950; SAM binding site at position 10617 to 10636 [Streptomyces glaucoscens] Length = 494
SEQ ID n°3695	Prot n°PL-852.2	Contig38	617334	618287		
SEQ ID n°3696	Prot n°PL-853.2	Contig40	317108	317975		
SEQ ID n°3697	Prot n°PL-854.1	Contig40	317923	319116	No Hits found	
SEQ ID n°3698	Prot n°PL-855.1	Contig40	319336	320106	No Hits found	
SEQ ID n°3699	Prot n°PL-856.1	Contig40	320840	322267	17%	Identities = 54/178 (30%), Positives = 65/178 (47%), Gaps = 2/178 (1%) sp P46377 FAS5_RHOFA HYPOTHETICAL 47.9 KD OXIDOREDUCTASE IN FASCINATION LOCUS (ORF-5) pir E55578 hypothetical protein (ipl 3' region) - Rhodococcus fascians plasmid pFID188 emb CAA82745.1 (Z29635) orfs [Rhodococcus fascians] Length = 438

TABLEAU I

SEQ ID n°3700	Prot n°PL-857.1	Contig40	322756	323865	No Hits found	
SEQ ID n°3701	Prot n°PL-858.1	Contig40	323887	324501	44%	Identities = 48/190 (25%), Positives = 92/190 (48%), Gaps = 17/190 (8%) pir J72359 conserved hypothetical protein - Thermotoga maritima (strain MSB8) gb AAD35668.1 AE001733.6 (AE001733) conserved hypothetical protein [Thermotoga maritima] Length = 235
SEQ ID n°3702	Prot n°PL-859.1	Contig40	324737	325984	50%	Identities = 119/405 (29%), Positives = 210/405 (51%), Gaps = 20/405 (4%) sp P71243 WCAL_ECOLI_PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAL_pir JC84970 hypothetical protein b2044 - Escherichia coli (strain K-12) db JBA15898.1 (D90842) ORF_ID:0352#3; similar to [PIR Accession Number S16296] [Escherichia coli] gb AAC75105.1 (AE000295) putative colanic acid biosynthesis glycosyl-transferase [Escherichia coli] Length = 406 "
SEQ ID n°3703	Prot n°PL-86.1	Contig41	145798	146401	90%	Identities = 177/201 (88%), Positives = 186/201 (92%) sp P12727 RECR_ECOLI_RECOMBINATION PROTEIN RECR_pir JBECCR recombination protein recR - Escherichia coli emb CAA33768.1 (X15761) recR product (AA 1-201) [Escherichia coli] gb AAB40226.1 (U82664) recR [Escherichia coli] gb AAC73574.1 (AE000153) recombination and repair [Escherichia coli] Length = 201
SEQ ID n°3704	Prot n°PL-860.1	Contig40	325985	326695	No Hits found	
SEQ ID n°3705	Prot n°PL-861.1	Contig40	326730	327623	40%	Identities = 73/253 (28%), Positives = 120/253 (46%), Gaps = 11/253 (4%) pir J39957 succinoglycan biosynthesis glycosyltransferase (EC 2.4.1.-) ExoM Rhizobium melliott emb CAA80346.1 (Z22636) ExoM [Sinorhizobium melliott] Length = 309
SEQ ID n°3706	Prot n°PL-862.1	Contig40	327999	329012	72%	Identities = 198/329 (60%), Positives = 245/329 (74%) db JBAAD1531.1 (D10689) M5 protein [Salmonella choleraesuis] Length = 345
SEQ ID n°3707	Prot n°PL-863.1	Contig40	329641	330441	No Hits found	
SEQ ID n°3708	Prot n°PL-864.1	Contig40	330516	331664	40%	Identities = 74/359 (20%), Positives = 154/359 (42%), Gaps = 22/359 (6%) gb AAC895142.1 (AF075600) ABC translocator [Brochothrix campestris] Length = 545
SEQ ID n°3709	Prot n°PL-865.1	Contig40	331672	332739	21%	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) db JBA806239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188
SEQ ID n°3710	Prot n°PL-866.1	Contig40	333317	334540	39%	Identities = 77/346 (22%), Positives = 161/346 (46%), Gaps = 51/346 (14%) gb AAC61717.1 (AF081284) chromosomal hemolysin D [Escherichia coli] Length = 439

TABLEAU I

SEQ ID n°3711	Prot n°PL-867.1	Contig40	335787	337358	74%	<p>Identities = 352/438 (80%), Positives = 390/438 (88%), Gaps = 1/438 (0%) sp P21507 SRMB_ECOLI ATP-DEPENDENT RNA HELICASE SRMB pir G65035 ATP-dependent RNA-helicase SrmB - Escherichia coli emb CAA32364.1 (X14152) SrmB protein [Escherichia coli] dbj BAA02447.1 (D13189) putative ATP dependent RNA helicase [Escherichia coli] dbj BAA10922.1 (D64044) putative ATP dependent RNA helicase [Escherichia coli] gb AAC75628.1 (AE000344) ATP-dependent RNA helicase [Escherichia coli] Length = 444</p>
SEQ ID n°3712	Prot n°PL-868.1	Contig40	337407	338141	63%	<p>Identities = 125/238 (52%), Positives = 159/238 (66%) pir F65035 hypothetical protein in nadB-srmB intergenic region - Escherichia coli (strain K-12) gb AAC75628.1 (AE000344) putative enzyme [Escherichia coli] Length = 285</p>
SEQ ID n°3713	Prot n°PL-869.1	Contig40	338209	339813	85%	<p>Identities = 418/528 (79%), Positives = 467/528 (88%) pir OXECLD L- aspartate oxidase (EC 1.4.3.16) - Escherichia coli gb AAC75627.1 (AE000344) quinolinate synthetase, B protein [Escherichia coli] Length = Identities = 430/659 (65%), Positives = 508/659 (78%), Gaps = 18/659 (2%)</p>
SEQ ID n°3714	Prot n°PL-87.1	Contig41	146787	148783	75%	<p>sp P74876 DP3X_SALTY DNA POLYMERASE III SUBUNIT TAU [CONTAINS: DNA POLYMERASE III SUBUNIT GAMMA] gb AAC87559.1 (U66040) DNA polymerase III tau subunit [Salmonella typhimurium] Length = 842 Identities = 131/217 (60%), Positives = 163/217 (74%), Gaps = 4/217 (1%)</p>
SEQ ID n°3715	Prot n°PL-871.1	Contig40	340626	341276	72%	<p>sp P38106 RSEA_ECOLI SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN pir B57255 sigma-E factor negative regulatory protein mclA - Escherichia coli dbj BAA10919.1 (D64044) MCL A protein [Escherichia coli] gb AAA83999.1 (U10148) MclA [Escherichia coli] gb AAC45315.1 (U37089) RseA [Escherichia coli] gb AAC75625.1 (AE000343) sigma-E factor, negative regulatory protein [Escherichia coli] Length = 216</p>
SEQ ID n°3716	Prot n°PL-872.1	Contig40	341282	342238	88%	<p>Identities = 168/316 (52%), Positives = 227/316 (71%), Gaps = 4/316 (1%) pir T02998 sigma-E factor regulatory protein rseB - Salmonella typhimurium gb AAC26064.1 (AF001386) sigma-E factor regulatory protein [Salmonella typhimurium] Length = 318</p>
SEQ ID n°3717	Prot n°PL-873.1	Contig40	342896	344692	91%	<p>Identities = 550/599 (91%), Positives = 574/599 (95%) sp P07682 LEPA_ECOLI GTP-BINDING PROTEIN LEPA pir BVECLA GTP- binding membrane protein lepA - Escherichia coli gb AAC75622.1 (AE000343) GTP-binding elongation factor, may be inner membrane protein [Escherichia coli] Length = 599</p>
SEQ ID n°3718	Prot n°PL-874.1	Contig40	344713	345693	73%	<p>Identities = 194/328 (59%), Positives = 240/328 (73%), Gaps = 6/328 (1%) sp P00803 LEP_ECOLI SIGNAL PEPTIDASE I (SPASE I) (LEADER PEPTIDASE I) pir ZPECS signal peptidase I (EC 3.4.99.36) - Escherichia coli gb AAC75621.1 (AE000343) leader peptidase (signal peptidase I) [Escherichia coli] Length = 324</p>

TABLEAU I

SEQ ID n°3718	Prot n°PL-875.1	Contig40	345868	346548	95%	<p>Identities = 202/226 (89%), Positives = 218/226 (96%) sp P05797 RNC_ECOLI RIBONUCLEASE III (RNASE III) pir JNREC3 ribonuclease III (EC 3.1.26.3) mnc - Escherichia coli emb CAA26692.1 (X02946) ribonuclease III (mnc) (aa 1-226) [Escherichia coli] db JBA10914.1 (D84044) ribonuclease III [Escherichia coli] gb AA79829.1 (U36841) RNase III [Escherichia coli] gb AAC75620.1 (AE000343) RNase III, ds RNA [Escherichia coli] Length = 226</p> <p>Identities = 249/301 (82%), Positives = 281/301 (92%) sp P06816 ERA_ECOLI GTP-BINDING PROTEIN ERA pir J544713 GTP-binding protein era - Escherichia coli pir JRGCGT GTP-binding protein era - Escherichia coli pdb 1EGA B Chain B, Crystal Structure Of A Widely Conserved Gtpase Era - pdb 1EGA A Chain A, Crystal Structure Of A Widely Conserved Gtpase Era gb AAA03242.1 (M14658) era [Escherichia coli] db JBA10913.1 (D84044) GTP binding protein [Escherichia coli] gb AAB34156.1 (U36841) GTP-binding protein [Escherichia coli] gb AAA79828.1 (U36841) GTP-binding protein [Escherichia coli] gb AAC75619.1 (AE000343) GTP-binding protein [Escherichia coli] Length = 301</p>
SEQ ID n°3720	Prot n°PL-876.1	Contig40	346545	347453	92%	<p>Identities = 170/242 (70%), Positives = 203/242 (83%) sp P15027 RECO_ECOLI DNA REPAIR PROTEIN RECO (RECOMBINATION PROTEIN O) pir JBVECO DNA repair protein reco - Escherichia coli gb AAA24515.1 (M27251) recombination protein [Escherichia coli] gb AAA21842.1 (M26416) reco [Escherichia coli] db JBA10912.1 (D84044) reco protein [Escherichia coli] gb AAC75618.1 (AE000343) protein interacts with RecR and possibly RecF proteins [Escherichia coli] Length = 242</p>
SEQ ID n°3722	Prot n°PL-878.1	Contig40	348385	349116	82%	<p>Identities = 184/242 (76%), Positives = 208/242 (85%) sp P24223 PDXJ_ECOLI PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN PDXJ pir J42283 pyridoxal phosphate biosynthetic protein pdxJ - Escherichia coli gb AAA24315.1 (M74526) pdxJ [Escherichia coli] gb AAA21845.1 (M76470) pdxJ [Escherichia coli] gb AAA79826.1 (U36841) CG Site No. 418 [Escherichia coli] gb AAC75617.1 (AE000343) pyridoxine biosynthesis [Escherichia coli] Length = 243</p>
SEQ ID n°3723	Prot n°PL-879.1	Contig40	350447	351208	20%	<p>Identities = 44/80 (55%), Positives = 51/80 (63%), Gaps = 3/80 (3%) sp P76508 YFDL_ECOLI HYPOTHETICAL 18.3 KD PROTEIN IN INTC-DSDC INTERGENIC REGION pir JH65008 hypothetical protein b2355 - Escherichia coli (strain K-12) gb AAC75414.1 (AE000324) putative RNA polymerase beta [Escherichia coli] Length = 172</p>
SEQ ID n°3724	Prot n°PL-88.1	Contig41	150984	151740	54%	<p>Identities = 91/261 (34%), Positives = 142/261 (53%), Gaps = 9/261 (3%) gb AAF17282.1 (AF204805) unknown [Nostoc sp. GSV224] Length =</p>

TABLEAU I

SEQ ID n°3725	Prot n°PL-880.1	Contig40	351091	352836	17%	Identities = 38/67 (58%), Positives = 48/67 (71%), Gaps = 1/67 (1%) ref NP_050653.1 S. sp Q9T1V0 VPS_BPMU TAIL FIBER PROTEIN (GPS) gb AAAF01127.1 AF083977.46 (AF083977) S [Bacteriophage Mu] Length = 504
SEQ ID n°3726	Prot n°PL-881.1	Contig40	353391	354392	19%	Identities = 51/123 (41%), Positives = 68/123 (53%), Gaps = 4/123 (3%) sp P76508 YFDL_EC01 HYPOTHETICAL 18.3 KD PROTEIN IN INTC-DSDC INTERGENIC REGION pir H65008 hypothetical protein b2355 - Escherichia coli (strain K-12) gb AAC75414.1 (AE000324) putative RNA polymerase beta [Escherichia coli] Length = 172
SEQ ID n°3727	Prot n°PL-882.1	Contig40	354665	355951	16%	Identities = 52/117 (44%), Positives = 71/117 (60%), Gaps = 3/117 (2%) pir G64887 probable tail fiber protein GP37 - Escherichia coli gb AAC74454.1 (AE000234) putative membrane protein [Escherichia coli]
SEQ ID n°3728	Prot n°PL-883.1	Contig40	356092	356856	25%	Identities = 49/129 (37%), Positives = 64/129 (48%), Gaps = 7/129 (5%) sp P76508 YFDL_EC01 HYPOTHETICAL 18.3 KD PROTEIN IN INTC-DSDC INTERGENIC REGION pir H65008 hypothetical protein b2355 - Escherichia coli (strain K-12) gb AAC75414.1 (AE000324) putative RNA polymerase beta [Escherichia coli] Length = 172
SEQ ID n°3729	Prot n°PL-884.1	Contig40	357651	358250	60%	Identities = 91/199 (45%), Positives = 125/199 (62%), Gaps = 1/199 (0%) sp P09153 YCFA_EC01 HYPOTHETICAL 21.7 KD PROTEIN IN INTE-PIN INTERGENIC REGION pir A64861 ycfA protein, phage protein-related - Escherichia coli gb AAC74240.1 (AE000214) orf, hypothetical protein [Escherichia coli] Length = 200
SEQ ID n°3730	Prot n°PL-885.1	Contig40	368498	369164	No Hits found	Identities = 1048/1713 (61%), Positives = 1304/1713 (75%), Gaps = 41/1713 (2%) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558
SEQ ID n°3731	Prot n°PL-886.1	Contig40	360665	371305	36%	
SEQ ID n°3732	Prot n°PL-887.1	Contig40	372600	373226	No Hits found	
SEQ ID n°3733	Prot n°PL-888.1	Contig40	373985	376291	67%	Identities = 372/758 (49%), Positives = 520/758 (68%), Gaps = 8/758 (0%) pir S56346 arginine decarboxylase (EC 4.1.1.19) adi, biodegradative - Escherichia coli gb AAA87017.1 (U14003) adi gene product [Escherichia coli] gb AAC77078.1 (AE000484) biodegradative arginine decarboxylase [Escherichia coli] Length = 756
SEQ ID n°3734	Prot n°PL-889.1	Contig40	376422	377882	66%	Identities = 268/383 (69%), Positives = 323/383 (83%) emb CAA84588.1 (Z35428) ORF404 [Proteus mirabilis] Length = 404
SEQ ID n°3735	Prot n°PL-89.1	Contig41	152448	153077	63%	Identities = 94/198 (47%), Positives = 137/198 (68%) pir A75270 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb AAF12011.1 (AE002076_3 (AE002076) conserved hypothetical protein [Deinococcus radiodurans] Length = 198

TABLEAU I

SEQ ID n°3736	Prot n°PL-890.1	Contig40	378041	381991	88%	Identities = 1042/1295 (80%), Positives = 1164/1295 (89%), Gaps = 1/1295 (0%) sp P15254 PURL_ECOLI PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) gb AAA24456.1 (M19501) formylglycineamide ribonucleotide synthetase (EC.6.3.5.3) [Escherichia coli] gb AAA79819.1 (U36841) phosphoribosylformylglycineamide synthetase
SEQ ID n°3737	Prot n°PL-891.1	Contig40	383433	384929	71%	Identities = 316/484 (65%), Positives = 388/484 (79%), Gaps = 1/484 (0%) sp P52101 YFHK_ECOLI PROBABLE SENSOR PROTEIN YFHK pir C665033 hypothetical protein b2556 - Escherichia coli (strain K-12) gb AAC75809.1 (AE000342) putative 2-component sensor-protein [Escherichia coli]
SEQ ID n°3738	Prot n°PL-892.1	Contig40	384930	385778	43%	Identities = 86/210 (40%), Positives = 122/210 (57%), Gaps = 7/210 (3%) gb AAA79817.1 (U36841) alternate name yfhG; orf1 of GenBank Accession Number S67014 [Escherichia coli] Length = 239
SEQ ID n°3738	Prot n°PL-893.1	Contig40	385775	387112	92%	Identities = 383/443 (86%), Positives = 414/443 (92%) sp P21712 YFHA_ECOLI HYPOTHETICAL 49.1 KD PROTEIN IN GLNB-PURL INTERGENIC REGION (ORFXB) (ORF-2) pir A65033 hypothetical protein XB (glnB 5' region) - Escherichia coli gb AAC75807.1 (AE000341) putative 2-component transcriptional regulator [Escherichia coli] db BAA16462.1 (D90885) nitrogen regulator I homolog [Escherichia coli]
SEQ ID n°3740	Prot n°PL-894.1	Contig40	387179	388801	62%	Identities = 288/543 (49%), Positives = 354/543 (64%), Gaps = 8/543 (1%) gb AAF84763.1 (AE004015_6 (AE004015) NH3-dependent NAD synthetase [Xylella fastidiosa] Length = 545
SEQ ID n°3741	Prot n°PL-895.1	Contig40	388516	390400	59%	Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300
SEQ ID n°3742	Prot n°PL-896.1	Contig40	390822	391895	58%	Identities = 143/347 (41%), Positives = 209/347 (60%), Gaps = 1/347 (0%) emb CAC04221.1 (AL391515) conserved hypothetical protein [Streptomyces coelicolor A3(2)] Length = 366
SEQ ID n°3743	Prot n°PL-897.1	Contig40	391856	393286	50%	Identities = 160/448 (35%), Positives = 243/448 (53%), Gaps = 13/448 (2%) emb CAC04220.1 (AL391515) conserved hypothetical protein [Streptomyces coelicolor A3(2)] Length = 463
SEQ ID n°3744	Prot n°PL-898.1	Contig40	393704	394831	51%	Identities = 134/349 (38%), Positives = 194/349 (55%), Gaps = 8/349 (2%) gb AAC32475.1 (AF044503) VgrG protein [Escherichia coli] Length =
SEQ ID n°3745	Prot n°PL-899.1	Contig40	395301	395903	No Hits found	Identities = 68/224 (30%), Positives = 109/224 (48%), Gaps = 10/224 (4%) gb AAF96971.1 (AE004433) transcriptional regulator, LuxR family [Vibrio cholerae] Length = 319
SEQ ID n°3746	Prot n°PL-9.1	Contig41	18381	19127	43%	

THIS PAGE BLANK (USPTO)

TABLEAU I

SEQ ID n°3747	Prot n°PL-90.1	Contig41	153074	153748	77%	Identities = 142/223 (63%), Positives = 176/223 (78%) pir B75270 ABC transporter, ATP-binding protein - <i>Deinococcus radiodurans</i> (strain R1) gb AAF12012.1 AE002076_4 (AE002076) ABC transporter, ATP-binding protein [<i>Deinococcus radiodurans</i>] Length = 226
SEQ ID n°3748	Prot n°PL-900.1	Contig40	398451	397551	39%	Identities = 85/355 (23%), Positives = 145/355 (39%), Gaps = 62/355 (17%) gb AAG04176.1 AE004513_8 (AE004513) hypothetical protein [Pseudomonas aeruginosa] Length = 387
SEQ ID n°3749	Prot n°PL-901.1	Contig40	397509	398198	No Hits found	Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) dbj BAB06239.1 (AP001515) transposase related protein (20) [<i>Bacillus halodurans</i>] Length = 188
SEQ ID n°3750	Prot n°PL-902.1	Contig40	398448	399515	21%	Identities = 168/190 (88%), Positives = 175/190 (91%) sp P05823 TNRO_ECOLI TRANSPOSON TN2501 RESOLVASE pir RP5CR5 resolvase - <i>Escherichia coli</i> transposon Tn2501 gb AA27426.1 (M15197) resolvase [Transposon Tn2501] Length = 194
SEQ ID n°3751	Prot n°PL-903.1	Contig40	400989	401570	85%	Identities = 240/396 (60%), Positives = 295/396 (73%) sp P26353 HMPA_SALTY FLAVOHEMOPROTEIN (HEMOGLOBIN-LIKE PROTEIN) (FLAVOHEMOGLOBIN) (DIHYDROPTERIDINE REDUCTASE (FERRISIDEROPHORE REDUCTASE B) (NITRIC OXIDE DIOXYGENASE) (NOD) gb AAC24484.1 (AF020388) flavohemoglobin
SEQ ID n°3752	Prot n°PL-904.1	Contig40	401588	403024	No Hits found	Identities = 376/417 (90%), Positives = 395/417 (94%) sp P06192 GLYA_SALTY SERINE HYDROXYMETHYLTRANSFERASE (SERINE METHYLASE) (SHMT) pir B48427 glycine hydroxymethyltransferase (EC 2.1.2.1) - <i>Salmonella typhimurium</i> emb CAA33808.1 (X15816) serine hydroxymethyltransferase (AA 1-417)
SEQ ID n°3753	Prot n°PL-905.1	Contig40	404099	405289	73%	Identities = 249/376 (66%), Positives = 306/376 (81%), Gaps = 1/376 (0%) sp Q47142 HCAT_ECOLI PROBABLE 3-PHENYLPROPIONIC ACID TRANSPORTER pir G65030 hypothetical protein b2536 - <i>Escherichia coli</i> (strain K-12) gb AAC75589.1 (AE000340) MFS (major facilitator superfamily) transporter [Escherichia coli] dbj BAA16431.1 (D90883) similar to [SwissProt Accession Number P44629] [Escherichia coli] dbj BAA16439.1 (D90884) similar to [SwissProt Accession Number P44629] [Escherichia coli] Length = 379
SEQ ID n°3754	Prot n°PL-906.1	Contig40	405661	408914	93%	Identities = 174/315 (55%), Positives = 234/315 (74%) sp P36874 TRER_SALTY TREHALOSE OPERON REPRESSOR pir A57147 regulatory protein treR - <i>Salmonella typhimurium</i> gb AAA68987.1 (U07843) Submitter comments: Cloned as part of mgfA locus. ORF expresses a 37 kda protein. Locus is not regulated by Mg2+. Is homolog of E. coli treR gene, personal communication from Dr. Winfried Boos and also Dr. Kenn Rudd. see GenBank Accession Num>
SEQ ID n°3755	Prot n°PL-907.1	Contig40	407234	408379	75%	Identities = 174/315 (55%), Positives = 234/315 (74%) sp P36874 TRER_SALTY TREHALOSE OPERON REPRESSOR pir A57147 regulatory protein treR - <i>Salmonella typhimurium</i> gb AAA68987.1 (U07843) Submitter comments: Cloned as part of mgfA locus. ORF expresses a 37 kda protein. Locus is not regulated by Mg2+. Is homolog of E. coli treR gene, personal communication from Dr. Winfried Boos and also Dr. Kenn Rudd. see GenBank Accession Num>
SEQ ID n°3756	Prot n°PL-908.1	Contig40	408452	409399	73%	Identities = 174/315 (55%), Positives = 234/315 (74%) sp P36874 TRER_SALTY TREHALOSE OPERON REPRESSOR pir A57147 regulatory protein treR - <i>Salmonella typhimurium</i> gb AAA68987.1 (U07843) Submitter comments: Cloned as part of mgfA locus. ORF expresses a 37 kda protein. Locus is not regulated by Mg2+. Is homolog of E. coli treR gene, personal communication from Dr. Winfried Boos and also Dr. Kenn Rudd. see GenBank Accession Num>

TABLEAU I

SEQ ID n°3757	Prot n°PL-909.1	Contig40	409539	410969	87%	<p>sp P36672 PTTB_ECOLI PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIBC-TRE) (TREHALOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-TRE) pir C65236 phosphotransferase system trehalose permease - Escherichia coli (strain K-12) gb AAC77197.1 (AE000495) PTS system enzyme II, trehalose specific [Escherichia coli]</p> <p>Identities = 348/472 (73%), Positives = 419/472 (88%)</p>
SEQ ID n°3758	Prot n°PL-91.1	Contig41	154162	154803	69%	<p>sp P34000 ACRR_ECOLI POTENTIAL ACRA B OPERON REPRESSOR pir G64776 transcription regulator acrR - Escherichia coli gb AAAG7133.1 (U00734) 25 kDa protein [Escherichia coli] gb AAB40218.1 (U82664) potential acrAB operon repressor [Escherichia coli] gb AAC73566.1 (AE000152) acrAB operon repressor [Escherichia coli]</p> <p>Identities = 117/201 (58%), Positives = 156/201 (77%)</p>
SEQ ID n°3759	Prot n°PL-910.1	Contig40	411060	412730	76%	<p>sp P28904 TREC_ECOLI TREHALOSE-6-PHOSPHATE HYDROLASE (ALPHA, ALPHA-PHOSPHOTREHALASE) pir S58465 alpha, alpha-phosphotrehalase (EC 3.2.1.93) - Escherichia coli gb AAA97136.1 (U14003) trehalose-6-phosphate hydrolase [Escherichia coli] gb AAC77196.1 (AE000495) trehalase 6-P hydrolase [Escherichia coli]</p> <p>Identities = 373/545 (68%), Positives = 431/545 (78%), Gaps = 2/545 (0%)</p>
SEQ ID n°3760	Prot n°PL-911.1	Contig40	412833	413636	90%	<p>sp P22783 SUHB_ECOLI EXTRAGENIC SUPPRESSOR PROTEIN SUHB pir D65030 suppressor protein suhB - Escherichia coli gb AAC75586.1 (AE000339) enhances synthesis of sigma32 in mutant; extragenic suppressor, may modulate RNase III lethal action [Escherichia coli] dbj BAA18427.1 (D90883) EXTRAGENIC SUPPRESSOR PROTEIN SUHB. [Escherichia coli] dbj BAA16435.1 (D90884) EXTRAGENIC SUPPRESSOR PROTEIN SUHB. [Escherichia coli]</p> <p>Identities = 230/267 (86%), Positives = 249/267 (93%)</p>
SEQ ID n°3761	Prot n°PL-912.1	Contig40	413770	414485	80%	<p>sp P22783 SUHB_ECOLI EXTRAGENIC SUPPRESSOR PROTEIN SUHB pir D65030 suppressor protein suhB - Escherichia coli gb AAC75586.1 (AE000339) enhances synthesis of sigma32 in mutant; extragenic suppressor, may modulate RNase III lethal action [Escherichia coli] dbj BAA18427.1 (D90883) EXTRAGENIC SUPPRESSOR PROTEIN SUHB. [Escherichia coli] dbj BAA16435.1 (D90884) EXTRAGENIC SUPPRESSOR PROTEIN SUHB. [Escherichia coli]</p> <p>Identities = 178/241 (73%), Positives = 210/241 (86%), Gaps = 1/241 (0%)</p>
SEQ ID n°3762	Prot n°PL-913.1	Contig40	415126	416340	96%	<p>sp P39171 NIFS_ECOLI NIFS PROTEIN HOMOLOG dbj BAA18424.1 (D90883) UNKNOWN PROTEIN FROM 2D-PAGE (SPOT M92) (FRAGMENT). [Escherichia coli] emb CAB77086.1 (AX000472) unnamed protein product [Escherichia coli] emb CAB77088.1 (AX000476) unnamed protein product [unidentified] emb CAB77090.1 (AX000480) unnamed protein product [unidentified] emb CAC07716.1 (AX018964) unnamed protein product [Escherichia coli]</p> <p>Identities = 365/404 (90%), Positives = 390/404 (96%)</p>

TABLEAU I

SEQ ID n°3763	Prot n°PL-914.1	Contig40	417755	419605	85%	<p>Identities = 488/616 (79%), Positives = 543/616 (87%) sp P36641 HSCA_ECOLI CHAPERONE PROTEIN HSCA (HSC66) pir E85029 heat shock cognate protein 66 - Escherichia coli: gb AAC75578.1 (AE000339) heat shock protein, chaperone, member of Hsp70 protein family [Escherichia coli] dbj BAA16420.1 (D90883) heat shock cognate protein 66 [Escherichia coli] Length = 616</p>
SEQ ID n°3764	Prot n°PL-915.1	Contig40	420471	421766	80%	<p>Identities = 306/425 (72%), Positives = 362/425 (85%) gb AAF19377.1 AF201078_1 (AF201078) peptidase B [Salmonella typhimurium] Length = 427</p>
SEQ ID n°3765	Prot n°PL-916.1	Contig40	422316	424121	71%	<p>Identities = 313/598 (52%), Positives = 430/598 (71%) gb AAF82974.1 AE003869_11 (AE003869) conserved hypothetical protein [Xylella fastidiosa] Length = 602</p>
SEQ ID n°3766	Prot n°PL-917.1	Contig40	424648	425250	40%	<p>Identities = 65/116 (56%), Positives = 87/116 (74%) gb AAF82972.1 AE003869_9 (AE003869) hypothetical protein [Xylella fastidiosa] Length = 116</p>
SEQ ID n°3767	Prot n°PL-918.1	Contig40	426369	427382	72%	<p>Identities = 198/329 (60%), Positives = 245/329 (74%) dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] Length = 345</p>
SEQ ID n°3768	Prot n°PL-919.1	Contig40	427720	429366	29%	<p>Identities = 87/394 (22%), Positives = 164/394 (41%), Gaps = 66/394 (16%) gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyponeumoniae] Length = 552</p>
SEQ ID n°3769	Prot n°PL-92.1	Contig41	154933	156128	82%	<p>Identities = 279/394 (70%), Positives = 331/394 (83%), Gaps = 3/394 (0%) sp P31223 ACRA_ECOLI ACRIFLAVIN RESISTANCE PROTEIN A PRECURSOR pir J36938 acriflavin resistance protein acrA precursor - Escherichia coli: gb AAA23410.1 (M94248) acriflavin resistance protein [Escherichia coli] gb AAAG7134.1 (U00734) 42 kDa protein [Escherichia coli] gb AAB40217.1 (U82664) lipoprotein AcrA precursor [Escherichia coli] gb AAC73565.1 (AE000152) acridine efflux pump [Escherichia coli] Identities = 48/153 (31%), Positives = 75/153 (48%), Gaps = 5/153 (3%) dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] Length = 188</p>
SEQ ID n°3770	Prot n°PL-920.1	Contig40	429967	431034	21%	<p>Identities = 186/306 (60%), Positives = 232/306 (75%), Gaps = 4/306 (1%) pdb 1AKL Alkaline Protease From Pseudomonas Aeruginosa ifo3080</p>
SEQ ID n°3771	Prot n°PL-921.1	Contig40	431007	432023	68%	
SEQ ID n°3772	Prot n°PL-923.2	Contig40	433188	448848	55%	<p>pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC00285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] Length = 9378</p>
SEQ ID n°3773	Prot n°PL-924.1	Contig40	450533	452059	58%	<p>Identities = 205/496 (41%), Positives = 314/496 (62%), Gaps = 22/496 (4%) gb AAG05047.1 AE004593_9 (AE004593) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 491</p>
						Unknown, similar to proteins involved in antibiotic biosynthesis

TABLEAU I

SEQ ID n°3774	Prot n°PL-925.1	Contig40	452066	453424	44%	Identities = 123/448 (27%), Positives = 203/448 (44%), Gaps = 17/448 (3%) gb AAF96028.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 444
SEQ ID n°3775	Prot n°PL-926.1	Contig40	453863	455368	53%	Identities = 201/511 (39%), Positives = 274/511 (53%), Gaps = 38/511 (7%) dbj BAA84886.1 (AB024946)orf5 [Escherichia coli] Length = 523
SEQ ID n°3776	Prot n°PL-927.1	Contig40	456229	458166	10%	Identities = 44/130 (33%), Positives = 67/130 (50%), Gaps = 1/130 (0%) gb AAD39496.1 (AF145799) 1 (AF145799) immunogenic 23 kDa lipoprotein PG3 [Porphyromonas gingivalis] Length = 223
SEQ ID n°3777	Prot n°PL-928.1	Contig40	458841	461381	42%	Identities = 221/789 (27%), Positives = 363/789 (44%), Gaps = 70/789 (8%) gb AAG03651.1 (AE004484_4 (AE004484) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 1019
SEQ ID n°3778	Prot n°PL-929.1	Contig40	461375	462994	48%	Identities = 157/582 (26%), Positives = 260/582 (43%), Gaps = 89/582 (15%) gb AAG04898.1 (AE004579_11 (AE004579) hypothetical protein [Pseudomonas aeruginosa] Length = 569
SEQ ID n°3779	Prot n°PL-93.1	Contig41	156154	159303	89%	Identities = 824/1044 (78%), Positives = 936/1044 (88%), Gaps = 4/1044 (0%) sp P31224 ACRB_ECOLI ACRIFLAVIN RESISTANCE PROTEIN B pir B36938 acriflavin resistance protein acrfB - Escherichia coli gb AAA2341.1 (M94248) acriflavin resistance protein [Escherichia coli] gb AAA67135.1 (U00734) 114 kDa protein [Escherichia coli] gb AAB40216.1 (U82664) probable transmembrane protein AcrE [Escherichia coli] gb AAC73664.1 (AE000152) acridine efflux pump [Escherichia coli] Identities = 49/186 (26%), Positives = 82/186 (43%), Gaps = 16/186 (8%) gb AAG04898.1 (AE004579_10 (AE004579) hypothetical protein [Pseudomonas aeruginosa] Length = 380
SEQ ID n°3780	Prot n°PL-930.1	Contig40	462960	464078	21%	
SEQ ID n°3781	Prot n°PL-931.1	Contig40	464197	465306	No Hits found	
SEQ ID n°3782	Prot n°PL-932.1	Contig40	465833	466966	No Hits found	
SEQ ID n°3783	Prot n°PL-933.1	Contig40	466951	470334	26%	Identities = 167/779 (21%), Positives = 295/779 (37%), Gaps = 93/779 (11%) gb AAG03467.1 (AE004446_15 (AE004446) hypothetical protein [Pseudomonas aeruginosa] Length = 1101
SEQ ID n°3784	Prot n°PL-934.1	Contig40	471040	473469	43%	Identities = 210/789 (26%), Positives = 355/789 (44%), Gaps = 71/789 (8%) gb AAG04900.1 (AE004579_12 (AE004579) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 842
SEQ ID n°3785	Prot n°PL-935.1	Contig40	473470	474255	41%	Identities = 65/252 (25%), Positives = 110/252 (42%), Gaps = 9/252 (3%) gb AAG06681.1 (AE004751_7 (AE004751) hypothetical protein [Pseudomonas aeruginosa] Length = 271
SEQ ID n°3786	Prot n°PL-936.1	Contig40	475848	478385	49%	Identities = 304/835 (36%), Positives = 422/835 (50%), Gaps = 122/835 (14%) gb AAG06678.1 (AE004751_4 (AE004751) hypothetical protein [Pseudomonas aeruginosa] Length = 882
SEQ ID n°3787	Prot n°PL-937.1	Contig40	478568	479787	No Hits found	
						Unknown, similar to toxins

TABLEAU II

SEQ ID n° 6382	PL-2898.1	Contig9 from 584576 to 585256	p	63%	sp Q05740 TONB_YEREN TONB PROTEIN pir S30290 tonB protein - Yersinia enterocolitica emb CAA47747.1 (X67332) tonB [Yersinia enterocolitica] prf 1912295A tonB gene [Yersinia enterocolitica] SEQ ID n-2116
SEQ ID n° 6383	PL-4037.1	Contig9 from 585319 to 585750	m	72%	sp P04379 YCIA_ECOLI PUTATIVE ACYL-COA THIOESTER HYDROLASE YCIA PRECURSOR (P14 PROTEIN) pir A05224 conserved hypothetical protein ycia precursor [imported] - Escherichia coli gb AAB59067.1 (K00431) P14 protein (P14 gene; putative); putative [Escherichia coli] gb AAB60068.1 (U24195) ycia gene product [Escherichia coli] gb AAB60076.1 (U24196) ycia gene product [Escherichia coli] gb AAB60084.1 (U24197) ycia gene product [Escherichia coli] gb AAB60092.1 (U24198) ycia gene product [Escherichia coli] gb AAB60100.1 (U24199) ycia gene product [Escherichia coli] gb AAB60108.1 (U24200) ycia gene product [Escherichia coli] gb AAB60116.1 (U24201) ycia gene product [Escherichia coli] gb AAB60124.1 (U24202) ycia gene product [Escherichia coli] gb AAB60132.1 (U24203) ycia gene product [Escherichia coli] gb AAB60140.1 (U24204) ycia gene product [Escherichia coli] gb AAB60148.1 (U24205) ycia gene product [Escherichia coli] gb AAB60156.1 (U24206) ycia gene product [Escherichia coli] pir T45503 hypothetical protein yciB [imported] - Escherichia coli gb AAB60131.1 (U24203) yciB gene product [Escherichia coli] pir B82498 sulfate permease family protein VCA0103 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96017.1 (AE004353) sulfate permease family protein [Vibrio cholerae] SEQ ID n-2115
SEQ ID n° 6384	PL-4036.1	Contig9 from 585828 to 586364	m	79%	sp Q05740 TONB_YEREN TONB PROTEIN pir S30290 tonB protein - Yersinia enterocolitica emb CAA47747.1 (X67332) tonB [Yersinia enterocolitica] prf 1912295A tonB gene [Yersinia enterocolitica] SEQ ID n-2116
SEQ ID n° 6385	PL-2897.1	Contig9 from 586578 to 588335	p	67%	sp Q05740 TONB_YEREN TONB PROTEIN pir S30290 tonB protein - Yersinia enterocolitica emb CAA47747.1 (X67332) tonB [Yersinia enterocolitica] prf 1912295A tonB gene [Yersinia enterocolitica] SEQ ID n-2116

TABLEAU II

SEQ ID n° 6376	PL-2902.1	Contig9 from 578976 to 579884	p	89%	sp P77664 OPPC_ECOLI OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC pir H64871 oligo peptide transport system permease protein oppC - Escherichia coli dbj BAAL4777.1 (D90763) Oligopeptide transport system permease protein OppC. [Escherichia coli] gb AAC74327.1 (AE000223) homolog of Salmonella oligopeptide transport permease protein [Escherichia coli K12] dbj BAAL6040.1 (D90852) Oligopeptide transport system permease protein OppC. [Escherichia coli] gb AAG56100.1 AE005342_2 (AE005342) homolog of Salmonella oligopeptide transport permease protein [Escherichia coli O157:H7] gb AAG56101.1 AE005342_3 (AE005342) homolog of Salmonella ATP-binding protein of oligo peptide ABC transport system [Escherichia coli O157:H7] gb AAG56102.1 AE005342_4 (AE005342) homolog of Salmonella ATP-binding protein of oligo peptide ABC transport system [Escherichia coli O157:H7] gb AAG56103.1 AE005342_5 (AE005342) Z2024 gene product [Escherichia coli O157:H7] gb AAB60088.1 (U24197) cardiolipin synthase [Escherichia coli]	SEQ ID n-2122 SEQ ID n-2121 SEQ ID n-2120 #N/A SEQ ID n-2117 #N/A
SEQ ID n° 6377	PL-2901.1	Contig9 from 579894 to 580892	p	87%		
SEQ ID n° 6378	PL-2900.1	Contig9 from 580889 to 581890	p	91%		
SEQ ID n° 6379	PL-4436.1	Contig9 from 582019 to 582348	m	81%		
SEQ ID n° 6380	PL-2899.1	Contig9 from 582460 to 583929	m	84%		
SEQ ID n° 6381	PL-4434.1	Contig9 from 584292 to 584474	p	No Hits found		

TABLEAU II

SEQ ID n° 6372 PL-2906.1	Contig9 from 573341 to 573985	p 81%	gb AAG56097.1 AE005341.6 (AE005341) putative channel protein [Escherichia coli O157:H7] sp P06202 OPPA_SALTY PERIPLASMIC OLIGOPEPTIDE- BINDING PROTEIN PRECURSOR pir QREBOA oligo peptide-binding protein precursor - Salmonella typhimurium emb CAA29039.1 (X05491) Opp A (AAL-542) [Salmonella typhimurium] emb CAA27785.1 (X04194) precursor polypeptide [Salmonella typhimurium]	SEQ ID n-2126
SEQ ID n° 6373 PL-2905.1	Contig9 from 574540 to 576177	p 74%	sp P06202 OPPA_SALTY PERIPLASMIC OLIGOPEPTIDE- BINDING PROTEIN PRECURSOR pir QREBOA oligo peptide-binding protein precursor - Salmonella typhimurium emb CAA29039.1 (X05491) Opp A (AAL-542) [Salmonella typhimurium] emb CAA27785.1 (X04194) precursor polypeptide [Salmonella typhimurium]	SEQ ID n-2125
SEQ ID n° 6374 PL-2904.1	Contig9 from 576316 to 577956	p 83%	sp P08005 OPPB_SALTY OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPB pir QREBOB oligo peptide transport system permease protein oppB - Salmonella typhimurium emb CAA29040.1 (X05491) Opp B (AAL-306) [Salmonella typhimurium]	SEQ ID n-2124
SEQ ID n° 6375 PL-2903.1	Contig9 from 578041 to 578961	p 93%	sp P08005 OPPB_SALTY OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPB pir QREBOB oligo peptide transport system permease protein oppB - Salmonella typhimurium emb CAA29040.1 (X05491) Opp B (AAL-306) [Salmonella typhimurium]	SEQ ID n-2123

TABLEAU II

SEQ ID n° 6367	PL-2910.1	Contig9 from 565734 to 567077	p	76%	pir B83202 probable nucleotide sugar dehydrogenase PA3559 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06947.1 AE004776_10 (AE004776) probable nucleotide sugar dehydrogenase [Pseudomonas aeruginosa]	SEQ ID n-2131
SEQ ID n° 6368	PL-2909.1	Contig9 from 567086 to 568099	p	79%	gb AAD50494.1 AF172324_12 (AF172324) WbnF [Escherichia coli]	SEQ ID n-2129
SEQ ID n° 6369	PL-4438.1	Contig9 from 568398 to 568802	m	82%	sp P18955 HNS_SERMA DNA-BINDING PROTEIN H-NS (HISTONE-LIKE PROTEIN HLP-II) pir S02775 DNA- binding protein H-NS - Serratia marcescens	#N/A
SEQ ID n° 6370	PL-2908.1	Contig9 from 569448 to 570053	p	77%	gb AAG56095.1 AE005341_4 (AE005341) thymidine kinase [Escherichia coli O157:H7] sp P17547 ADHE_ECOLI ALDEHYDE-ALCOHOL DEHYDROGENASE [INCLUDES: ALCOHOL DEHYDROGENASE (ADH); ACETALDEHYDE DEHYDROGENASE [ACETYLATING] (ACDH); PYRUVATE-FORMATE-LYASE DEACTIVASE (PFL DEACTIVASE)] pir DEEC acetaldehyde dehydrogenase (acetylating) (EC 1.2.1.10) / alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli emb CAA1955.1 (X59263) alcohol dehydrogenase [Escherichia coli] gb AA23420.1 (M33504) alcohol dehydrogenase (adhE) [Escherichia coli] dbj BAA36121.1 (D90759) Alcohol dehydrogenase (EC 1.1.1.1). [Escherichia coli] gb AAC74323.1 (AE000222) CoA-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase; pyruvate-formate-lyase deactivase [Escherichia coli K12] dbj BAA16034.1 (D90852) alcohol dehydrogenase (EC 1.1.1.1) [Escherichia coli] dbj BAA7747.1 (AB008676) alcohol dehydrogenase [Escherichia coli]	SEQ ID n-2128
SEQ ID n° 6371	PL-2907.1	Contig9 from 570296 to 572929	m	92%		SEQ ID n-2127

TABLEAU II

SEQ ID n° 6365	PL-2912.1	Contig9 from 563300 to 564325	p 69%	<p>sp P37055 HNR_ECOLI HNR PROTEIN pir A36871 37K regulator response protein homolog - Escherichia coli emb CAA46802.1 (X66003) hnr [Escherichia coli] dbj BAA36103.1 (D90758) 37k regulator response protein homolog [Escherichia coli] dbj BAA36115.1 (D90759) 37k regulator response protein homolog [Escherichia coli] gb AAC74317.1 (AE000222) Hnr protein [Escherichia coli K12] dbj BAA16029.1 (D90852) 37K regulator response protein homolog [Escherichia coli] gb AAG56092.1 AE005341_1 (AE005341) Hnr protein [Escherichia coli O157:H7]</p> <p>sp P25520 GALU_ECOLI UTP--GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1- PHOSPHATE URIDYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE) pir JC2265 UTP--glucose-1- phosphate uridylyltransferase (EC 2.7.7.9) galu [validated] - Escherichia coli emb CAA42564.1 (X59940) ORF 1 [Escherichia coli] gb AA20118.1 (M98830) glucosephosphate uridylyltransferase [Escherichia coli] gb AAD15244.1 (U32811) UDP-glucose pyrophosphorylase [Shigella flexneri] dbj BAA36104.1 (D90758) UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) [Escherichia coli] dbj BAA36116.1 (D90759) UTP- glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) [Escherichia coli] gb AAC74318.1 (AE000222) glucose-1-phosphate uridylyltransferase [Escherichia coli K12] dbj BAA16030.1 (D90852) UTP--glucose-1- phosphate uridylyltransferase (EC 2.7.7.9) [Escherichia coli] gb AAG56093.1 AE005341_2</p>	SEQ ID n°2133
SEQ ID n° 6366	PL-2911.1	Contig9 from 564718 to 565710	p 72%		

TABLEAU II

SEQ ID n° 6363 PL-2913.1	Contig9 from 561768 to 562616	m 86%	sp P37051 PURU_ECOLI FORMYLtetrahydrofolate DEFORMYLASE (FORMYL-FH(4) HYDROLASE) pir C36871 formyltetrahydrofolate deformylase (EC 3.5.1.10) [validated] - Escherichia coli gb AAC36846.1 (L20251) formyltetrahydrofolate hydrolase [Escherichia coli] dbj BAA36100.1 (D90758) Formyltetrahydrofolate deformylase (EC 3.5.1.10) (formyl-fh(4) hydrolase). [Escherichia coli] dbj BAA36112.1 (D90759) Formyltetrahydrofolate deformylase (EC 3.5.1.10) (formyl- fh(4) hydrolase). [Escherichia coli] gb AAC74314.1 (AE000221) formyltetrahydrofolate deformylase; for purt-dependent FGAR synthesis [Escherichia coli K12] dbj BAA16026.1 (D90852) FORMYLtetrahydrofolate DEFORMYLASE (EC 3.5.1.10) (FORMYL- FH(4) HYDROLASE). [Escherichia coli] sp P37052 YCHJ_ECOLI HYPOTHETICAL 17.0 KDA PROTEIN IN HNR-PURU INTERGENIC REGION pir D64870 ychJ protein - Escherichia coli gb AAC74315.1 (AE000221) orf, hypothetical protein [Escherichia coli K12] dbj BAA16027.1 (D90852) ORF_ID:0249#9-similar to [SwissProt Accession Number P37052] [Escherichia coli] dbj BAA36101.1 (D90758) hypothetical protein (purt region) [Escherichia coli] dbj BAA36113.1 (D90759) hypothetical protein (purt region) [Escherichia coli]	SEQ ID n-2134
			SEQ ID n-3187	

TABLEAU II

SEQ ID n° 6359	PL-2916.1	Contig9 from 557021 to 557680	m	61%	sp Q46890 YGBL_ECOLI_HYPOTHETICAL_23.2_KDA PROTEIN IN PPFB-RPOS INTERGENIC REGION pir F65054 L-fucose-phosphate aldolase (EC 4.1.2.17) - Escherichia coli (strain K-12) gb AAA69248.1 (U29579) ORF_0212 [Escherichia coli] gb AAC75780.1 (AE000357) putative epimerase/aldolase [Escherichia coli K12] gb AAG14969.1 AF242208_2 (AF242208) putative enzyme [Escherichia coli] gb AAG14982.1 AF242210_1 (AF242210) putative enzyme [Escherichia coli]	SEQ ID n-2137
SEQ ID n° 6360	PL-2915.1	Contig9 from 557655 to 558932	m	65%	gb AAK03449.1 (AE006174) unknown [Pasteurella multocida]	SEQ ID n-2136
SEQ ID n° 6361	PL-2914.1	Contig9 from 558932 to 559837	m	74%	gb AAK03450.1 (AE006174) unknown [Pasteurella multocida]	SEQ ID n-2135
SEQ ID n° 6362	PL-4441.1	Contig9 from 560924 to 561337	p	56%	ref NP_043483.1 orf14 [Bacteriophage HPI] sp P51716 Y014_BPHP1_HYPOTHETICAL_14.9_KD PROTEIN IN REP-HOL INTERGENIC REGION (ORF14) pir S69520 hypothetical protein 14 - phage HPI gb AAB09199.1 (U24159) orf14 [Bacteriophage HPI]	#N/A

TABLEAU II

SEQ ID n° 6348	PL-2927.2	Contig9 from 540888 to 543791	p	No Hits found	#N/A
SEQ ID n° 6349	PL-2926.2	Contig9 from 543919 to 545175	p	20%	pir JQ1866 hypothetical 87.1K protein - bovine adenovirus 3
SEQ ID n° 6350	PL-2925.1	Contig9 from 545234 to 547093	p	No Hits found	SEQ ID n-2147
SEQ ID n° 6351	PL-2924.1	Contig9 from 547103 to 549187	p	23%	emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)]
SEQ ID n° 6352	PL-2923.1	Contig9 from 549212 to 550108	p	25%	emb CAB77354.1 (AL160331) hypothetical protein SCD8A.33c (fragment) [Streptomyces coelicolor A3(2)]
SEQ ID n° 6353	PL-2922.1	Contig9 from 550237 to 551178	p	No Hits found	SEQ ID n-2144
SEQ ID n° 6354	PL-2921.1	Contig9 from 551617 to 552762	p	No Hits found	SEQ ID n-2143
SEQ ID n° 6355	PL-2920.1	Contig9 from 552917 to 554302	m	80%	gb AAK03443.1 (AE006173) Gntp [Pasteurella multocida]
SEQ ID n° 6356	PL-2919.1	Contig9 from 554305 to 555270	m	71%	sp P44094 YA14_HAEIN HYPOTHETICAL PROTEIN HI1014 pir D64018 hypothetical protein HI1014 - Haemophilus influenzae (strain Rd KW20) gb AAC22675.1 (U32782) conserved hypothetical protein [Haemophilus influenzae Rd] SEQ ID n-2140
SEQ ID n° 6357	PL-2918.1	Contig9 from 555443 to 556210	m	66%	sp P44978 YGBI_HAEIN HYPOTHETICAL TRANSCRIPTIONAL REGULATOR HI1009 gb AAC22670.1 (U32781) glycerol-3-phosphate regulon repressor (glpR) [Haemophilus influenzae Rd] SEQ ID n-2139
SEQ ID n° 6358	PL-2917.1	Contig9 from 556223 to 557002	m	66%	gb AAG14970.1 AF242208_3 (AF242208) unknown [Escherichia coli]
					SEQ ID n-2138

TABLEAU II

SEQ ID n° 6337	PL-2934.1	Contig9 from 528738 to 529331	m	No Hits found		SEQ ID n-2156
SEQ ID n° 6338	PL-4043.2	Contig9 from 530038 to 530487	p	No Hits found	#N/A	
SEQ ID n° 6339	PL-2933.2	Contig9 from 530540 to 531661	p	33%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	#N/A
SEQ ID n° 6340	PL-2932.1	Contig9 from 531673 to 533079	p	21%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-2154
SEQ ID n° 6341	PL-2931.1	Contig9 from 533128 to 534324	p	32%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-2153
SEQ ID n° 6342	PL-4041.1	Contig9 from 534338 to 534796	p	No Hits found		SEQ ID n-9190
SEQ ID n° 6343	PL-4451.1	Contig9 from 534793 to 534972	p	No Hits found		#N/A
SEQ ID n° 6344	PL-2929.1	Contig9 from 535639 to 537240	p	13%	pir [F82511 vgrG protein VCA0018 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95932.1 (AB004345) vgrG protein [Vibrio cholerae]	SEQ ID n-2151
SEQ ID n° 6345	PL-4449.1	Contig9 from 537254 to 537670	p	43%	emb CAB77339.1 (AL160331) hypothetical protein SCD8A.18c [Streptomyces coelicolor A3(2)]	#N/A
SEQ ID n° 6346	PL-4448.1	Contig9 from 537667 to 538083	p	No Hits found		#N/A
SEQ ID n° 6347	PL-2928.1	Contig9 from 538166 to 540895	p	No Hits found		SEQ ID n-2150

TABLEAU II

SEQ ID n° 6326	PL-4463.1	Contig9 from 522084 to 522335	p	No Hits found	#N/A
SEQ ID n° 6327	PL-2974.1	Contig9 from 522412 to 522996	p	No Hits found	SEQ ID n-2200
SEQ ID n° 6328	PL-4461.1	Contig9 from 523105 to 523362	p	No Hits found	#N/A
SEQ ID n° 6329	PL-4460.1	Contig9 from 523412 to 523858	p	75%	#N/A
SEQ ID n° 6330	PL-3804.1	Contig9 from 523855 to 524250	p	77%	SEQ ID n-2982
SEQ ID n° 6331	PL-2973.1	Contig9 from 524619 to 525389	p	No Hits found	SEQ ID n-2199
SEQ ID n° 6332	PL-4459.1	Contig9 from 525423 to 525704	p	No Hits found	#N/A
SEQ ID n° 6333	PL-4457.1	Contig9 from 525843 to 526154	p	61%	#N/A
SEQ ID n° 6334	PL-4456.1	Contig9 from 526157 to 526447	p	46%	#N/A
SEQ ID n° 6335	PL-2972.2	Contig9 from 526810 to 527403	m	No Hits found	#N/A
SEQ ID n° 6336	PL-4455.1	Contig9 from 527865 to 528209	m	No Hits found	#N/A

gb|AAG53985.1|AF327444_1 (AF327444) putative
transposase A [Erwinia herbicola]

gb|AAG53986.1|AF327444_2 (AF327444) putative
transposase B [Erwinia herbicola]

pir||D82455 hypothetical protein VCA0468
[imported] - Vibrio cholerae (group
O1 strain N16961) gb|AAF96372.1| (AE004379)
hypothetical protein [Vibrio cholerae]
pir||E82455 conserved hypothetical protein
VCA0469 [imported] - Vibrio
cholerae
(group O1 strain N16961) gb|AAF96373.1|
(AE004379) conserved hypothetical protein
[Vibrio cholerae]

TABLEAU II

SEQ ID n° 6320	PL-2977.1	Contig9 from 515935 to 517863	p	87%	sp P14294 TOP3_ECOLI DNA TOPOISOMERASE III pir JV0049 DNA topoisomerase (EC 5.99.1.2) III Escherichia coli pdb 1D6M A Chain A, Crystal Structure Of E. Coli Dna Topoisomerase Iii gb AAA83923.1 (J05076) topoisomerase III [Escherichia coli] dbj BAAL5551.1 (D90819) DNA topoisomerase III (EC 5.99.1.-) [Escherichia coli] dbj BAAL5554.1 (D90820) DNA topoisomerase III (EC 5.99.1.-) [Escherichia coli] gb AAC74833.1 (AE000271) DNA topoisomerase III [Escherichia coli K12] sp P09030 EX3_ECOLI EXODEOXYRIBONUCLEASE III (EXONUCLEASE III) (EXO III) (AP ENDONUCLEASE VI) pir NCECX3 exodeoxyribonuclease III (EC 3.1.11.2) - Escherichia coli pdb 1AKO Exonuclease Iii From Escherichia Coli emb CAA31424.1 (X13002) exonuclease III [Escherichia coli] dbj BAAL5540.1 (D90818) Exodeoxyribonuclease III (EC 3.1.11.2) [Escherichia coli] dbj BAAL5544.1 (D90819) Exodeoxyribonuclease III (EC 3.1.11.2) [Escherichia coli] gb AAC74819.1 (AE000270) exonuclease III [Escherichia coli K12]	SEQ ID n-2203
SEQ ID n° 6321	PL-2976.1	Contig9 from 517921 to 518727	m	88%	emb CAA10420.1 (AJ131559) rlsa protein [Erwinia amylovora]	SEQ ID n-2202
SEQ ID n° 6322	PL-2975.1	Contig9 from 519230 to 520093	p	32%		SEQ ID n-2201
SEQ ID n° 6323	PL-4467.1	Contig9 from 520362 to 520646	m	No Hits found		#N/A
SEQ ID n° 6324	PL-4466.1	Contig9 from 520697 to 520903	m	No Hits found		#N/A
SEQ ID n° 6325	PL-4465.1	Contig9 from 520965 to 521186	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6317	PL-2979.1	Contig9 from 512286 to 514151	m	72%	<p>pir PRECT4 protease IV (EC 3.4.-.-) - Escherichia coli dbj BAJ15557.1 (D90820) Proteinase IV (EC 3.4.-.-) [Escherichia coli] gb AAC74836.1 (AE000271) protease IV, a signal peptide peptidase [Escherichia coli K12]</p> <p>sp P24250 YDJA_ECOLI PROTEIN YDJA pir A40360 hypothetical protein, 20K (seld-sppA intergenic region) - Escherichia coli gb AA24245.1 (M68961) ORF183 [Escherichia coli] dbj BAA15556.1 (D90820) ORF_ID:0329#2; similar to [PIR Accession Number A40360] [Escherichia coli] gb AAC74835.1 (AE000271) orf, hypothetical protein [Escherichia coli K12] gb AAG56751.1 AE005399_5 (AE005399) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2983 sp P16456 SELD_ECOLI SELENIDE, WATER DIKINASE (SELENOPHOSPHATE SYNTHETASE) (SELENIUM DONOR PROTEIN) pir JW0033 selenophosphate synthase - Escherichia coli gb AAA74748.1 (M30184) selenium metabolism protein [Escherichia coli] dbj BAA15555.1 (D90820) Selenide, water dikinase (EC 2.7.9.3) (Selenophosphate synthetase) (selenium donor protein). [Escherichia coli] gb AAC74834.1 (AE000271) selenophosphate synthase, H(2)Se added to acrylyl-tRNA [Escherichia coli K12]</p>	SEQ ID n-2205
SEQ ID n° 6318	PL-3805.1	Contig9 from 514322 to 514873	p	71%		
SEQ ID n° 6319	PL-2978.1	Contig9 from 514886 to 515929	p	83%		SEQ ID n-2204

TABLEAU II

SEQ ID n° 6312	PL-2982.1	Contig9 from 508075 to 509070	m	81%	sp P06977 G3PI_ECOLI GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A (GAPDH-A) pir DEECG3 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) A - Escherichia coli emb CAA26498.1 (X02662) put. GAPDH (aa 1-332) [Escherichia coli] dbj BAAL5576.1 (D90821) Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) A [Escherichia coli] gb AAC74849.1 (AE000273) glyceraldehyde-3- phosphate dehydrogenase A [Escherichia coli K12] gb AAG56768.1 AE005401_3 (AE005401) glyceraldehyde-3-phosphate dehydrogenase A [Escherichia coli O157:H7] SEQ ID n-2209
SEQ ID n° 6313	PL-3806.1	Contig9 from 509540 to 509950	p	68%	sp P39903 YEA_ECOLI HYPOTHETICAL 15.5 KDA PROTEIN IN ANSA-GAPA INTERGENIC REGION pir B64938 hypothetical protein b1778 - Escherichia coli (strain K-12) gb AAC74848.1 (AE000272) orf, hypothetical protein [Escherichia coli K12] gb AAG56767.1 AE005401_2 (AE005401) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2984
SEQ ID n° 6314	PL-4469.1	Contig9 from 510033 to 510302	p	69%	gb AAG56766.1 AE005401_1 (AE005401) Z2816 gene product [Escherichia coli O157:H7] #N/A
SEQ ID n° 6315	PL-2981.1	Contig9 from 510366 to 511004	m	65%	gb AAG56755.1 AE005399_9 (AE005399) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2208
SEQ ID n° 6316	PL-2980.1	Contig9 from 511017 to 512036	m	82%	sp P18840 ASG1_ECOLI L-ASPARAGINASE I (L- ASPARAGINE AMIDOHYDROLASE I) (L-ASNASE I) pir XDEC1 asparaginase (EC 3.5.1.1) I - Escherichia coli dbj BAAL5558.1 (D90820) L- asparaginase I (EC 3.5.1.1) (L-asparagine amidohydrolase I) [Escherichia coli] gb AAC74837.1 (AE000271) cytoplasmic L- asparaginase I [Escherichia coli K12] SEQ ID n-2207

TABLEAU II

SEQ ID n° 6307 PL-2987.1	Contig9 from 501459 to 503006	m	81%	sp P27377 NHAB_ECOLI_NA(+)/H(+) ANTIPORTER 2 (SODIUM/PROTON ANTIPORTER 2) pir G64864 Na+/H+ exchanging protein nhAB - Escherichia coli dbj BAA36033.1 (D90752) Na+/H+ antiporter protein nhAB [Escherichia coli] dbj BAA36041.1 (D90753) Na+/H+ antiporter protein nhAB [Escherichia coli] gb AAC74270.1 (AE000217) Na+/H+ antiporter, pH independent [Escherichia coli K12]	SEQ ID n-2214
SEQ ID n° 6308 PL-2986.1	Contig9 from 503229 to 503948	p	82%	pdb 1E2X A Chain A, Fadr, Fatty Acid Responsive Transcription Factor From E. coli sp P29011 DADA_ECOLI_D-AMINO ACID DEHYDROGENASE SMALL SUBUNIT pir B53383 D-amino-acid dehydrogenase (EC 1.4.99.1) small chain - Escherichia coli gb AAC36880.1 (L02948) D-amino acid dehydrogenase [Escherichia coli] dbj BAA36044.1 (D90753) D-amino acid dehydrogenase small subunit (EC 1.4.99.1). [Escherichia coli] gb AAC74273.1 (AE000217) D- amino acid dehydrogenase subunit [Escherichia coli K12] gb AAG56040.1 AE005336_1 (AE005336) D-amino acid dehydrogenase subunit [Escherichia coli O157:H7]	SEQ ID n-2213
SEQ ID n° 6309 PL-2985.1	Contig9 from 504469 to 505782	p	76%	gb AAC61705.1 (AF081283) alanine racemase [Escherichia coli]	SEQ ID n-2212
SEQ ID n° 6310 PL-2984.1	Contig9 from 505789 to 506877	p	75%	sp P77486 MIPA_ECOLI_MITA-INTERACTING PROTEIN PRECURSOR pir F64938 hypothetical protein b1782 - Escherichia coli (strain K-12) dbj BAA15583.1 (D90822) Outer membrane protein precursor. [Escherichia coli] dbj BAA15579.1 (D90821) Outer membrane protein precursor. [Escherichia coli] gb AAC74852.1 (AE000273) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-2211
SEQ ID n° 6311 PL-2983.1	Contig9 from 507222 to 507974	p	62%		

TABLEAU II

SEQ ID n° 6299	PL-3812.1	Contig9 from 495338 to 495802	m	No Hits found	SEQ ID n-2989
SEQ ID n° 6300	PL-3811.1	Contig9 from 495953 to 496366	m	No Hits found	SEQ ID n-2988
SEQ ID n° 6301	PL-2988.1	Contig9 from 497075 to 498082	m	No Hits found	SEQ ID n-2215
SEQ ID n° 6302	PL-3809.1	Contig9 from 498483 to 498962	p	65%	gb AAG54517.1 AE005197_6 (AE005197) Z0248 gene product [Escherichia coli O157:H7]
SEQ ID n° 6303	PL-4474.1	Contig9 from 499298 to 499432	m	No Hits found	SEQ ID n-2986
SEQ ID n° 6304	PL-4473.1	Contig9 from 499813 to 500145	p	81%	ref NP_044260.1 QacE [Enterobacter aerogenes] sp Q57225 QACE_ECOLI QUATERNARY AMMONIUM COMPOUND-RESISTANCE PROTEIN QACE (QUATERNARY AMMONIUM DETERMINANT E) pir A48905 small multidrug export protein qacE [validated] - Klebsiella pneumoniae pir T08519 small multidrug export protein qacE - Enterobacter aerogenes plasmid R751 emb CAA48311.1 (X68232) multiresistance protein [Klebsiella aerogenes] emb CAA51179.1 (X72585) multidrug exporter [Klebsiella aerogenes] gb AAC64463.1 (U67194) QacE [Enterobacter aerogenes]
SEQ ID n° 6305	PL-4472.1	Contig9 from 500199 to 500516	p	29%	sp P52646 YDBJ_ECOLI HYPOTHETICAL 8.7 KDA PROTEIN IN ONPN-HSLJ INTERGENIC REGION PRECURSOR
SEQ ID n° 6306	PL-3808.1	Contig9 from 500768 to 501277	m	73%	gb AAG56036.1 AE005335_9 (AE005335) reoxidizes DsbA protein following formation of disulfide bond in P-ring of flagella. [Escherichia coli O157:H7]

#N/A

#N/A

#N/A

SEQ ID n-2985

TABLEAU II

SEQ ID n° 6293	PL-2992.1	Contig9 from 488931 to 489434	m	71%	sp P57901 TPX_ECOLI THIOL PEROXIDASE (SCAVENGASE P20) sp P57669 TPX_SHIDY THIOL PEROXIDASE pir JC5504 thioredoxin peroxidase (EC 1.1.1.1.-) - Escherichia coli gb AAC7406.1 (AE000230) thiol peroxidase [Escherichia coli K12] gb AAC45284.1 (U93212) scavengase p20 [Escherichia coli] gb AAF28134.1 AF153317_31 (AF153317) thiol peroxidase [Shigella dysenteriae] gb AAG56478.1 AE005374_1 (AE005374) thiol peroxidase [Escherichia coli O157:H7] SEQ ID n° 2220
SEQ ID n° 6294	PL-2991.1	Contig9 from 489608 to 491230	p	73%	pir D64882 periplasmic oligopeptide-binding protein precursor - Escherichia coli dbj BAAL4922.1 (D90771) Periplasmic oligopeptide-binding protein precursor. [Escherichia coli] dbj BAAL4932.1 (D90772) periplasmic oligopeptide-binding protein precursor. [Escherichia coli] gb AAC74411.1 (AE000231) putative transport periplasmic protein [Escherichia coli K12] SEQ ID n° 2219
SEQ ID n° 6295	PL-2990.1	Contig9 from 491247 to 492230	p	72%	gb AAG40855.1 AF308568_2 (AF308568) zinc transport protein [Salmonella typhimurium] SEQ ID n° 2218
SEQ ID n° 6296	PL-4477.1	Contig9 from 492309 to 492533	m	No Hits found	#N/A
SEQ ID n° 6297	PL-2989.1	Contig9 from 492742 to 493662	m	89%	sp P76055 YDAO_ECOLI HYPOTHETICAL 35.6 KD PROTEIN IN DBPA-INTR INTERGENIC REGION pir C64884 ydaO protein - Escherichia coli gb AAC74426.1 (AE000232) orf, hypothetical protein [Escherichia coli K12] SEQ ID n° 2216
SEQ ID n° 6298	PL-4476.1	Contig9 from 493802 to 493984	p	No Hits found	#N/A

TABLEAU II

SEQ ID n° 6286	PL-2997.1	Contig9 from 482060 to 483082	m	84%	gb AAG22112.1 (AY008264) phage shock protein F [Yersinia enterocolitica]	SEQ ID n-2225
SEQ ID n° 6287	PL-2996.1	Contig9 from 483246 to 483920	p	85%	gb AAG22113.1 (AY008264) phage shock protein A [Yersinia enterocolitica]	SEQ ID n-2224
SEQ ID n° 6288	PL-4481.1	Contig9 from 483957 to 484175	p	76%	sp P23854 PSPB_ECOLI PHAGE SHOCK PROTEIN B pir S17122 phage shock protein B - Escherichia coli emb CAA40790.1 (X57560) pspB protein [Escherichia coli] dbj BA14874.1 (D90768) Phage shock protein B [Escherichia coli] dbj BA14882.1 (D90769) phage shock protein B [Escherichia coli] gb AAC74387.1 (AE000228) phage shock protein [Escherichia coli K12] gb AAG56499.1 AE005376_4 (AE005376) phage shock protein, putative inner membrane protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6289	PL-4480.1	Contig9 from 484175 to 484528	p	78%	gb AAG22115.1 (AY008264) phage shock protein C [Yersinia enterocolitica]	#N/A
SEQ ID n° 6290	PL-2995.1	Contig9 from 484595 to 485992	p	87%	gb AAG22117.1 (AY008264) hypothetical protein YcjX [Yersinia enterocolitica]	SEQ ID n-2223
SEQ ID n° 6291	PL-2994.1	Contig9 from 485989 to 487053	p	82%	gb AAG22118.1 (AY008264) hypothetical protein YcjF [Yersinia enterocolitica]	SEQ ID n-2222
SEQ ID n° 6292	PL-2993.1	Contig9 from 487310 to 488893	p	77%	sp Q9ZIB7 TYRR_ERWHE TRANSCRIPTIONAL REGULATORY PROTEIN TYRR gb AAD02000.1 (AF035010) regulatory protein TyrR [Erwinia herbicola]	SEQ ID n-2221

TABLEAU II

SEQ ID n°	Contig9 from	m	No Hits found	SEQ ID n°
6279 PL-3004.1	474341 to 475099	m		n-2235
6280 PL-3003.1	475534 to 476322	m	88%	n-2234
6281 PL-3002.1	476497 to 477306	m	91%	n-2233
6282 PL-3001.1	477307 to 478299	m	87%	n-2232
6283 PL-3000.1	478299 to 479189	m	82%	n-2231
6284 PL-2999.1	479176 to 480141	m	91%	n-2227
6285 PL-2998.1	480138 to 481802	m	81%	n-2226

sp P16657 FABI_SALTY ENOYL-[ACYL-CARRIER- PROTEIN] REDUCTASE [NADH] (NADH-DEPENDENT ENOYL-ACP REDUCTASE) pir [B43729 enoyl-[acyl- carrier-protein] reductase (NADH) (EC 1.3.1.9) - Salmonella typhimurium gb AA27059.1 (M31806) envM protein [Salmonella typhimurium] sp P36638 SAPF_SALTY PEPTIDE TRANSPORT SYSTEM ATP-BINDING-PROTEIN SAPF pir [S39589 peptide transport system ATP-binding protein sapF - Salmonella typhimurium emb CAA52288.1 (X74212) sapF [Salmonella typhimurium]	emb CAA10912.1 (AJ222649) sapD [Erwinia chrysanthemi]	gb AAG56512.1 AE005377_5 (AE005377) homolog of Salmonella peptide transport permease protein [Escherichia coli O157:H7] sp P36668 SAPB_SALTY PEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN SAPB pir [S39586 peptide transport system permease protein sapB - Salmonella typhimurium emb CAA52285.1 (X74212) sapB [Salmonella typhimurium]	sp Q47622 SAPA_ECOLI PEPTIDE TRANSPORT PERIPLASMIC PROTEIN SAPA PRECURSOR pir [A64878 peptide transport periplasmic protein sapA precursor - Escherichia coli emb CAA65937.1 (X97282) SapA protein [Escherichia coli] gb AAC74376.1 (AB000227) homolog of Salmonella peptide transport periplasmic protein [Escherichia coli K12]
--	---	--	---

TABLEAU II

SEQ ID n° 6275 PL-3008.1	Contig9 from 469920 to 470573	p 82%	sp P128225 PDXH_ECOLI PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (FNP/PMP OXIDASE) (PNPOX) pir B43261 pyridoxamine-phosphate oxidase (EC 1.4.3.5) pdxh - Escherichia coli pdb 1G76 A Chain A, X-Ray Structure Of Escherichia Coli Pyridoxine 5'-Phosphate Oxidase Complexed With Pyridoxal 5'-Phosphate At 2.0 A Resolution pdb 1G79 A Chain A, X-Ray Structure Of Escherichia Coli Pyridoxine 5'-Phosphate Oxidase Complexed With Pyridoxal 5'-Phosphate At 2.0 A Resolution gb AAA24709.1 (M92351) pyridoxamine phosphate oxidase [Escherichia coli] gb AAC74710.1 (AE000259) pyridoxinephosphate oxidase [Escherichia coli K12]	SEQ ID n-2239
			gb AAG56626.1 AE005387_4 (AE005387) tyrosine tRNA synthetase [Escherichia coli O157:H7]	
			sp Q51892 PDXY_PROMI PYRIDOXAMINE KINASE (PM KINASE)	
SEQ ID n° 6276 PL-3007.1	Contig9 from 470694 to 471968	p 89%	sp P15214 GT_PROMI GLUTATHIONE S-TRANSFERASE GST. 6.0 (GST B1-1) pir S29772 glutathione transferase (EC 2.5.1.18) - Proteus mirabilis pir S71882 glutathione transferase (EC 2.5.1.18) B1-1 - Proteus mirabilis pdb 1PMT Glutathione Transferase From Proteus Mirabilis pdb 2PMT A Chain A, Glutathione Transferase From Proteus Mirabilis pdb 2PMT B Chain B, Glutathione Transferase From Proteus Mirabilis pdb 2PMT C Chain C, Glutathione Transferase From Proteus Mirabilis pdb 2PMT D Chain D, Glutathione Transferase From Proteus Mirabilis gb AAC44362.1 (U38482) glutathione transferase [Proteus mirabilis]	SEQ ID n-2237
SEQ ID n° 6277 PL-3006.1	Contig9 from 472282 to 473145	p 84%		SEQ ID n-2238
SEQ ID n° 6278 PL-3005.1	Contig9 from 473242 to 473847	m 72%		SEQ ID n-2236

TABLEAU II

SEQ ID n° 6270	PL-3814.1	Contig9 from 466038 to 466451	m	74%	p1 V59384 LGUL_ECOLI LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) pir E64922 lactoylglutathione lyase (EC 4.4.1.5) glOA - Escherichia coli pdb 1F9Z A Chain A, Crystal Structure Of The Ni(II)-Bound Glyoxalase I From Escherichia Coli pdb 1F9Z B Chain B, Crystal Structure Of The Ni(II)-Bound Glyoxalase I From Escherichia Coli pdb 1FA5 A Chain A, Crystal Structure Of The Zn(II)-Bound Glyoxalase I Of Escherichia Coli pdb 1FA5 B Chain B, Crystal Structure Of The Zn(II)-Bound Glyoxalase I Of Escherichia Coli pdb 1FA6 A Chain A, Crystal Structure Of The Co(II)-Bound Glyoxalase I Of Escherichia Coli pdb 1FA6 B Chain B, Crystal Structure Of The Co(II)-Bound Glyoxalase I Of Escherichia Coli pdb 1FA7 A Chain A, Crystal Structure Of Cd(II)-Bound Glyoxalase I Of Escherichia Coli pdb 1FA7 B Chain B, Crystal	SEQ ID n-2991
SEQ ID n° 6271	PL-4485.1	Contig9 from 466621 to 466863	p	70%	gb AAG56637.1 AE005388_2 (AE005388) ori, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6272	PL-4484.1	Contig9 from 467424 to 467855	p	88%	gb AAK01704.1 AF330139_1 (AF330139) transcriptional activator RovA [Yersinia pseudotuberculosis]	#N/A
SEQ ID n° 6273	PL-3813.1	Contig9 from 467940 to 468410	m	71%	gb AAD50821.1 AF168687_2 (AF168687) outer membrane lipoprotein Pcp [Pectobacterium carotovorum subsp. carotovorum]	SEQ ID n-2990
SEQ ID n° 6274	PL-3009.1	Contig9 from 468752 to 469870	p	80%	gb AAG56629.1 AE005387_7 (AE005387) ori, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2240

TABLEAU II

SEQ ID n° 6266	PL-1250.1	Contig9 from 463200 to 464225	m	88%	sp U08446 PURR SALTY PURINE NUCLEOTIDE SYNTHESIS REPRESSOR gb AAC05741.1 (AF040636) purine nucleotide synthesis repressor [Salmonella typhimurium]	SEQ ID n-819
SEQ ID n° 6267	PL-4486.1	Contig9 from 464411 to 464545	m	No Hits found	#N/A	
SEQ ID n° 6268	PL-3815.1	Contig9 from 464808 to 465158	p	66%	sp P37010 YDHD_ECOLI 12.9 KDA PROTEIN IN LHR- SODB INTERGENIC REGION pir H64922 probable glutaredoxin-like protein ydhD - Escherichia coli--dbj BAA15420.1 (D90809) ORF_ID:0317#10; similar to [SwissProt Accession Number P37010] [Escherichia coli] gb AAC74726.1 (AE000260) orf, hypothetical protein [Escherichia coli K12] gb AAG56643.1 AE005389_8 (AE005388) orf, hypothetical protein [Escherichia coli O157:H7] sp P30014 RNT_ECOLI RIBONUCLEASE T (EXORIBONUCLEASE T) (RNASE T) pir A45065 ribonuclease T (EC 3.1.13.-) rnt - Escherichia coli gb AAC37008.1 (L01622) RNaseT [Escherichia coli] gb AAC74724.1 (AE000260) RNase T, degrades tRNA [Escherichia coli K12]	SEQ ID n-2992 488
SEQ ID n° 6269	PL-1251.1	Contig9 from 465385 to 466038	m	81%		SEQ ID n-320

TABLEAU II

SEQ ID n° 6260	PL-1245.1	Contig9 from 456880 to 457557	P	77%	<p>sp P29015 RISA_ECOLI_RIBOFLAVIN SYNTHASE ALPHA CHAIN pir S28526 riboflavin synthase (EC 2.5.1.9) alpha chain - Escherichia coli emb CAA48861.1 (X69109) riboflavin synthase [Escherichia coli] gb AAB47940.1 (U68703) riboflavin synthase, alpha chain [Escherichia coli] dbj BAI15429.1 (D90809) Riboflavin synthase a chain (EC 2.5.1.9). [Escherichia coli] dbj BAI15438.1 (D90810) Riboflavin synthase a chain (EC 2.5.1.9). [Escherichia coli] gb AAC74734.1 (AB000261) riboflavin synthase, alpha chain [Escherichia coli K12]</p>	SEQ ID n-313
SEQ ID n° 6261	PL-4487.1	Contig9 from 457766 to 457879	P	No Hits found	#N/A	
SEQ ID n° 6262	PL-1246.1	Contig9 from 457964 to 458941	P	No Hits found		SEQ ID n-314
SEQ ID n° 6263	PL-1247.1	Contig9 from 459245 to 460396	m	78%	<p>gb AAG56650.1 AE005389_6 (AE005389) cyclopropane fatty acyl phospholipid synthase [Escherichia coli O157:H7]</p>	SEQ ID n-315
SEQ ID n° 6264	PL-1248.1	Contig9 from 460817 to 462115	m	61%	<p>gb AAG56649.1 AE005389_5 (AE005389) putative transport protein [Escherichia coli O157:H7]</p>	SEQ ID n-316
SEQ ID n° 6265	PL-1249.1	Contig9 from 462285 to 463193	P	79%	<p>sp P37598 YDHB_ECOLI_HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PURR-CFA INTERGENIC REGION pir E64923 probable transcription regulator ydbH - Escherichia coli gb AAC74731.1 (AE000261) putative transcriptional regulator LYSR-type [Escherichia coli K12] gb AAG56648.1 AE005389_4 (AE005389) putative transcriptional regulator LYSR-type [Escherichia coli O157:H7]</p>	SEQ ID n-317

TABLEAU II

SEQ ID n° 6250	PL-1238.1	Contig9 from 446820 to 448136	p	68%	emb CAC17127.1 (AJ301654) SufD protein [Pectobacterium chrysanthemi]	SEQ ID n-905
SEQ ID n° 6251	PL-1239.1	Contig9 from 448133 to 449371	p	79%	emb CAC17128.1 (AJ301654) cysteine desulfurase [Pectobacterium chrysanthemi]	SEQ ID n-906
SEQ ID n° 6252	PL-4491.1	Contig9 from 449409 to 449825	p	70%	emb CAC17129.1 (AJ301654) SufB protein [Pectobacterium chrysanthemi]	#N/A
SEQ ID n° 6253	PL-1240.1	Contig9 from 449947 to 451029	p	58%	gb AAG55859.1 AE005321_2 (AE005321) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-908
SEQ ID n° 6254	PL-4490.1	Contig9 from 451140 to 451376	m	75%	sp P02939 MULI_ERWAM MAJOR OUTER MEMBRANE LIPOPROTEIN PRECURSOR (MUREIN-LIPOPROTEIN) pir NFWCWY murein-lipoprotein precursor - Erwinia amylovora gb AA24824.1 (J01577) lipoprotein [Erwinia amylovora] pir G83418 probable enoyl-CoA hydratase/isomerase PA1821 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05210.1 AE004608_9 (AE004608) probable enoyl-CoA hydratase/isomerase [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 6255	PL-1241.1	Contig9 from 451818 to 452669	p	52%	sp P77983 KPY1_SALTY PYRUVATE KINASE I (PK-1) emb CAA68205.1 (X99945) pyruvate kinase like protein [Salmonella typhimurium]	SEQ ID n-909
SEQ ID n° 6257	PL-4488.1	Contig9 from 454338 to 454673	m	No Hits found		SEQ ID n-911
SEQ ID n° 6258	PL-7250.1	Contig9 from 454793 to 454903	p	No Hits found		#N/A
SEQ ID n° 6259	PL-1244.1	Contig9 from 455280 to 456653	m	83%	gb AAG56652.1 AE005389_8 (AE005389) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-912

TABLEAU II

SEQ ID n° 6242	PL-1231.1	Contig9 from 432131 to 434509	P	90%	sp P23538 PPSA_ECOLI PHOSPHOENOLPYRUVATE SYNTHASE (PYRUVATE, WATER DIKINASE) (PEP SYNTHASE) pir S20554 pyruvate, water dikinase (EC 2.7.9.2) ppsa [validated] - Escherichia coli emb CAA42024.1 (X59381) pyruvate, water dikinase [Escherichia coli] dbj BAAL5471.1 (D90813) pyruvate, water dikinase (EC 2.7.9.2) [Escherichia coli] gb AAC74772.1 (AE000265) phosphoenolpyruvate synthase [Escherichia coli K12]	SEQ ID n-299
SEQ ID n° 6243	PL-1232.1	Contig9 from 434954 to 436063	m	77%	gb AAG56675.1 AE005392_1 (AE005392) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-900
SEQ ID n° 6244	PL-1233.1	Contig9 from 436420 to 439479	P	85%	gb AAG56674.1 AE005391_11 (AE005391) putative oxidase [Escherichia coli O157:H7]	SEQ ID n-901
SEQ ID n° 6245	PL-4495.1	Contig9 from 439476 to 439892	P	76%	pir F64926 conserved hypothetical protein b1686 - Escherichia coli dbj BAAL5452.1 (D90811) comA operon protein 2. [Escherichia coli] gb AAC74756.1 (AE000263) orf, hypothetical protein [Escherichia coli K12] #N/A	
SEQ ID n° 6246	PL-1235.1	Contig9 from 440678 to 441760	P	26%	pir A82488 hypothetical protein VCA0199 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96112.1 (AE004360) hypothetical protein [Vibrio cholerae]	SEQ ID n-302
SEQ ID n° 6247	PL-3816.1	Contig9 from 444152 to 444532	P	62%	emb CAC17124.1 (AJ301654) sufa protein [Pectobacterium chrysanthemi]	SEQ ID n-2993
SEQ ID n° 6248	PL-1236.1	Contig9 from 444545 to 446041	P	91%	emb CAC17125.1 (AJ301654) sufB protein [Pectobacterium chrysanthemi]	SEQ ID n-303
SEQ ID n° 6249	PL-1237.1	Contig9 from 446099 to 446845	P	83%	gb AAG56669.1 AE005391_6 (AE005391) putative ATP- binding component of a transport system [Escherichia coli O157:H7]	SEQ ID n-304

TABLEAU II

SEQ ID n° 6234	PL-1224.1	Contig9 from 423657 to 424451	m 63%	<p>Y... S54440 hemin-specific ATP-binding protein [validated] - Yersinia enterocolitica emb CAA54864.1 (X77867) ATPase component [Yersinia enterocolitica]</p> <p>sp Q56992 HMU_YERPE HEMIN TRANSPORT SYSTEM PERMEASE PROTEIN HMU pir T12072 ABC-type permease - Yersinia pestis gb AAC64869.1 (U60647) ABC-type permease [Yersinia pestis]</p> <p>emb CAA54865.1 (X77867) hemin binding protein [Yersinia enterocolitica]</p>	SEQ ID n-291
SEQ ID n° 6235	PL-1225.1	Contig9 from 424451 to 425452	m 79%		SEQ ID n-292
SEQ ID n° 6236	PL-1226.1	Contig9 from 425449 to 426267	m 72%		SEQ ID n-293
SEQ ID n° 6237	PL-1227.1	Contig9 from 426264 to 427337	m 74%	<p>sp P31517 HEMS_YEREN HEMIN TRANSPORT PROTEIN HEMS pir S54436 hems protein [validated] - Yersinia enterocolitica emb CAA54865.1 (X77867) hems [Yersinia enterocolitica]</p> <p>sp Q56989 HMUR_YERPE HEMIN RECEPTOR PRECURSOR pir T12069 hemin receptor - Yersinia pestis gb AAC64866.1 (U60647) TonB-dependent outer membrane receptor [Yersinia pestis]</p>	SEQ ID n-294
SEQ ID n° 6238	PL-1228.1	Contig9 from 427368 to 429389	m 75%		SEQ ID n-295
SEQ ID n° 6239	PL-4497.1	Contig9 from 429479 to 429676	m 43%	<p>sp P31516 HEMP_YEREN HEMIN UPTAKE PROTEIN HEMP pir S28041 hemp protein - Yersinia enterocolitica emb CAA48249.1 (X68147) hemp [Yersinia enterocolitica]</p> <p>gb AAG56691.1 AE005393_8 (AE005393) 3-deoxy-D- arabinoheptulosonate-7-phosphate synthase (DAHPSynthetase, tryptophan repressible) [Escherichia coli O157:H7]</p>	#N/A
SEQ ID n° 6240	PL-1229.1	Contig9 from 429849 to 430895	m 80%	<p>sp P03822 YDIA_ECOLI HYPOTHETICAL 31.2 KDA PROTEIN IN PFSA-AROH INTERGENIC REGION pir Q0ECAD probable membrane protein ydia - Escherichia coli gb AAC74773.1 (AE000265) orf, hypothetical protein [Escherichia coli K12] gb AAG56690.1 AE005393_7 (AE005393) orf, hypothetical protein [Escherichia coli O157:H7]</p>	SEQ ID n-296
SEQ ID n° 6241	PL-1230.1	Contig9 from 431037 to 431918	m 79%		SEQ ID n-298

TABLEAU II

SEQ ID n° 6225	PL-1218.1	Contig9 from 411051 to 412328	p	61%	pir A83071 hypothetical protein PA4591 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AG07979.1 AE004873.1 (AE004873) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-284
SEQ ID n° 6226	PL-1219.1	Contig9 from 412413 to 414212	m	40%	emb CAC01603.1 (AJ269505) peptide synthetase [Anabaena sp. 90]	SEQ ID n-285
SEQ ID n° 6227	PL-1220.1	Contig9 from 414322 to 415521	m	70%	pir B83357 probable MFS transporter PA2314 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AG05702.1 AE004657.9 (AE004657) probable MFS transporter [Pseudomonas aeruginosa]	SEQ ID n-287
SEQ ID n° 6228	PL-1221.1	Contig9 from 415567 to 418317	m	32%	emb CAB87990.1 (AJ277403) indigoldine synthase [Erwinia chrysanthemi]	SEQ ID n-288
SEQ ID n° 6229	PL-1222.1	Contig9 from 418745 to 419632	p	66%	pir D83357 probable transcription regulator PA2316 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AG05704.1 AE004657.11 (AE004657) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-289
SEQ ID n° 6230	PL-3818.1	Contig9 from 419789 to 420244	p	No Hits found		SEQ ID n-2995
SEQ ID n° 6231	PL-4502.1	Contig9 from 421372 to 421554	p	68%	pir S00485 gene 11-1 protein precursor - malaria parasite (Plasmodium falciparum) (fragments)	#N/A
SEQ ID n° 6232	PL-4501.1	Contig9 from 422364 to 422729	m	80%	sp Q52620 PORA_PROVU REGULATORY PROTEIN PORA dbj BAA02757.1 (D13561) PQR A [Proteus vulgaris]	#N/A
SEQ ID n° 6233	PL-1223.1	Contig9 from 422993 to 423607	p	No Hits found		SEQ ID n-290

TABLEAU II

SEQ ID n° 6218	PL-1214.1	Contig9 from 404819 to 405748	p	No Hits found	pir G82452 conserved hypothetical protein VCA0482 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96227.1 (AE004370) conserved hypothetical protein [Vibrio cholerae] gb AAF96386.1 (AE004380) conserved hypothetical protein [Vibrio cholerae]	SEQ ID n-280
SEQ ID n° 6219	PL-4504.1	Contig9 from 405898 to 406224	p	41%		#N/A
SEQ ID n° 6220	PL-3821.1	Contig9 from 406340 to 406750	p	42%	emb CAC05783.1 (AL391753) ORF47,	SEQ ID n-2998
SEQ ID n° 6221	PL-3820.1	Contig9 from 406904 to 407326	m	No Hits found		SEQ ID n-2997
SEQ ID n° 6222	PL-1215.1	Contig9 from 407769 to 408380	p	67%	pir D83071 probable ATP-binding component of ABC transporter PA4594 [imported] Pseudomonas aeruginosa (strain PAO1) gb AAG07982.1 AE004873_4 (AE004873) probable ATP- binding component of ABC transporter [Pseudomonas aeruginosa]	SEQ ID n-281
SEQ ID n° 6223	PL-1216.1	Contig9 from 408382 to 409587	p	63%	pir C83071 probable permease of ABC transporter PA4593 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07981.1 AE004873_3 (AE004873) probable permease of ABC transporter [Pseudomonas aeruginosa]	SEQ ID n-282
SEQ ID n° 6224	PL-1217.1	Contig9 from 409580 to 411058	p	77%	pir B83071 hypothetical protein PA4592 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07980.1 AE004873_2 (AE004873) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-283

TABLEAU II

SEQ ID n° 6212	PL-1211.1	Contig9 from 397959 to 399941	81%	<p>sp P77398 YFBG_ECOLI_HYPOTHETICAL_74.3_KD PROTEIN IN AIS-PMRD INTERGENIC REGION pir E64996 hypothetical protein b2255 - Escherichia coli (strain K-12) gb AAC75315.1 (AE000315) putative transformylase [Escherichia coli K12] dbj BAAL6078.1 (D90856) METHIONYL- TRNA FORMYLTRANSFERASE (EC 2.1.2.9). [Escherichia coli] dbj BAAL6082.1 (D90857) METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9). [Escherichia coli]</p>	SEQ ID n-277
SEQ ID n° 6213	PL-1212.1	Contig9 from 399941 to 400834	68%	<p>pir F64996 hypothetical protein b2256 - Escherichia coli (strain K-12) gb AAC75316.1 (AE000315) orf, hypothetical protein [Escherichia coli K12]</p>	SEQ ID n-278
SEQ ID n° 6214	PL-1213.1	Contig9 from 400842 to 402503	65%	<p>gb AAG57388.1 AE005458_5 (AE005458) orf, hypothetical protein [Escherichia coli O157:H7]</p>	SEQ ID n-279
SEQ ID n° 6215	PL-4507.1	Contig9 from 402518 to 402841	58%	<p>gb AAG57389.1 AE005458_6 (AE005458) Z3516 gene product [Escherichia coli O157:H7]</p>	#N/A
SEQ ID n° 6216	PL-4506.1	Contig9 from 402874 to 403218	59%	<p>gb AAC04776.1 (AF036677) unknown [Salmonella typhimurium]</p>	#N/A
SEQ ID n° 6217	PL-3822.1	Contig9 from 403324 to 403809	69%	<p>sp P23898 NLPC_ECOLI_PROBABLE_LIPOPROTEIN_NLPC PRECURSOR (ORF-17) pir D64929 probable lipoprotein nlpc precursor - Escherichia coli gb AA23529.1 (M14031) (possible lipoprotein) [Escherichia coli] dbj BAAL5476.1 (D90813) Probable lipoprotein Nlpc precursor (ORF-17). [Escherichia coli] dbj BAAL5488.1 (D90814) Probable lipoprotein Nlpc precursor (ORF-17). [Escherichia coli] gb AAC74778.1 (AE000266) lipoprotein [Escherichia coli K12]</p>	SEQ ID n-2999

TABLEAU II

SEQ ID n° 6206	PL-1206.1	Contig9 from 391133 to 393520	p	87%	sp P07395 SYFB_ECOLI PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS) pir I41284 phenylalanine--trna ligase (EC 6.1.1.20) beta-subunit - Escherichia coli pir SYECFB phenylalanine--trna ligase (EC 6.1.1.20) beta chain - Escherichia coli gb AAA51470.1 (K02844) phenylalanyl-trna synthetase beta-subunit [Escherichia coli] dbj BAA15481.1 (D90813) Phenylalanine-- trna ligase (EC 6.1.1.20) b chain [Escherichia coli] dbj BAA15493.1 (D90814) Phenylalanine--trna ligase (EC 6.1.1.20) b chain [Escherichia coli] gb AAC74783.1 (AE000366) phenylalanine trna synthetase, beta-subunit [Escherichia coli K12] sp P23302 IHFA_SERVA INTEGRATION HOST FACTOR ALPHA-SUBUNIT (IHF-ALPHA) pir A38173 integration host factor alpha chain - Serratia marcescens	SEQ ID n-271
SEQ ID n° 6207	PL-4510.1	Contig9 from 393525 to 393821	p	94%	gb AAA23526.1 (M14031) cytoplasmic membrane protein [Escherichia coli] gb AAG56696.1 AE005394_5 (AE005394) ATP-binding component of vitamin B12 transport system [Escherichia coli O157:H7] gb AAG57384.1 AE005458_1 (AE005458) putative enzyme [Escherichia coli O157:H7] gb AAG57385.1 AE005458_2 (AE005458) putative sugar transferase [Escherichia coli O157:H7]	SEQ ID n-272 SEQ ID n-273 SEQ ID n-274 SEQ ID n-276
SEQ ID n° 6208	PL-1207.1	Contig9 from 393887 to 394894	p	74%		#N/A
SEQ ID n° 6209	PL-1208.1	Contig9 from 394898 to 395674	p	54%		
SEQ ID n° 6210	PL-1209.1	Contig9 from 395835 to 396980	p	77%		
SEQ ID n° 6211	PL-1210.1	Contig9 from 396981 to 397958	p	83%		

TABLEAU II

SEQ ID n° 6203 PL-4513.1	Contig9 from 389267 to 389464	p 75%	sp P07085 RL35_ECOLI 50S RIBOSOMAL PROTEIN L35 (RIBOSOMAL PROTEIN A) pir R5EC35 ribosomal protein L35 [validated] - Escherichia coli dbj BAAL5484.1 (D90813) Ribosomal protein L35 [Escherichia coli] dbj BAAL5496.1 (D90814) Ribosomal protein L35 [Escherichia coli] gb AAC74787.1 (AE000266) 50S ribosomal subunit protein A [Escherichia coli K12] gb AAG56704.1 AE005394_13 (AE005394) 50S ribosomal subunit protein A [Escherichia coli O157:H7].....	#N/A
			sp P02421 RL20_ECOLI 50S RIBOSOMAL PROTEIN L20 pir R5EC20 ribosomal protein L20 [validated] - Escherichia coli gb AAC74786.1 (AE000266) 50S ribosomal subunit protein L20, and regulator [Escherichia coli K12] gb AAG56703.1 AE005394_12 (AE005394) 50S ribosomal subunit protein L20, and regulator [Escherichia coli O157:H7] dbj BAAL5482.1 (D90813) Phenylalanine--trNA ligase (EC 6.1.1.20) a chain [Escherichia coli] dbj BAAL5494.1 (D90814) Phenylalanine--trNA ligase (EC 6.1.1.20) a chain [Escherichia coli]	
SEQ ID n° 6204 PL-4512.1	Contig9 from 389506 to 389862	p 95%		#N/A
SEQ ID n° 6205 PL-1205.1	Contig9 from 390134 to 391117	p 87%		SEQ ID n-270

TABLEAU II

SEQ ID n° 6199	PL-1202.1	Contig9 from 335590 to 336261	P 63%	sp P5009 MLTE_ECOLI MEMBRANE-BOUND LYTIC MUREIN TRANSGLYCOSYLASE E (MUREIN HYDROLASE E) pir P64865 murein hydrolase E (EC 3.2.1.-) - Escherichia coli gb AAC74277.1 (AE000217) murein transglycosylase E [Escherichia coli K12] dbj BAA36051.1 (D90754) Hypothetical protein HI0761 [Escherichia coli] SEQ ID n-267
SEQ ID n° 6200	PL-1203.1	Contig9 from 337217 to 386320	P 32%	pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] sp P00955 SYT_ECOLI THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRS) pir SYECTT threonine--trna ligase (EC 6.1.1.3) - Escherichia coli pdb 1QF6 A Chain A, Structure Of E. Coli Threonyl-Trna Synthetase Complexed With Its Cognate Trna dbj BAA15498.1 (D90814) Threonine--trna ligase (EC 6.1.1.3) [Escherichia coli] dbj BAA1504.1 (D90815) Threonine--trna ligase (EC 6.1.1.3) [Escherichia coli] gb AAC74789.1 (AE000267) threonine trna synthetase [Escherichia coli K12] sp P33321 IF3_SALTY TRANSLATION INITIATION FACTOR IF-3 gb AAC36814.1 (L11254) translation initiation factor IF3 [Salmonella typhimurium] SEQ ID n-268
SEQ ID n° 6201	PL-1204.1	Contig9 from 386698 to 388626	P 92%	
SEQ ID n° 6202	PL-3824.1	Contig9 from 388744 to 389169	P 92%	SEQ ID n-269

TABLEAU II

SEQ ID n° 6192 PL-1196.1	Contig9 from 329362 to 330027	m	73%	sp P77247 YNIC_ECOLI_HYPOTHETICAL_24.3_ID PROTEIN IN PFKB-CEDA INTERGENIC REGION pir [G64931 ynic protein - Escherichia coli dbj BAA1508.1 (D90815) Phosphoglycolate phosphatase (EC 3.1.3.18). [Escherichia coli] dbj BAA1511.1 (D90816) Phosphoglycolate phosphatase (EC 3.1.3.18). [Escherichia coli] gb AAC74797.1 (AE000267) putative phosphatase [Escherichia coli K12] sp Q56956 YFEE_YERPE PUTATIVE YFEABCD REGULATOR YFEE gb AAC46151.1 (U50903) yfeE [Yersinia pestis] SEQ ID n-259
SEQ ID n° 6193 PL-3828.1	Contig9 from 330214 to 330756	p	74%	pir [E64931 hypothetical protein b1725 - Escherichia coli dbj BAA15501.1 (D90814) ORF_ID:0324#5; similar to [SwissProt Accession Number P46381] [Escherichia coli] dbj BAA15507.1 (D90815) ORF_ID:0324#5; similar to [SwissProt Accession Number P46381] [Escherichia coli] dbj BAA15510.1 (D90816) ORF_ID:0324#5; similar to [SwissProt Accession Number P46381] [Escherichia coli] gb AAC74795.1 (AE000267) orf, hypothetical protein [Escherichia coli K12] sp Q56955 YFED_YERPE CHELATED IRON TRANSPORT SYSTEM MEMBRANE PROTEIN YFED gb AAC46150.1 (U50597) yfeD [Yersinia pestis] sp Q56954 YFEC_YERPE CHELATED IRON TRANSPORT SYSTEM MEMBRANE PROTEIN YFEC gb AAC46149.1 (U50597) yfeC [Yersinia pestis] gb AAC46148.1 (U50597) yfeB [Yersinia pestis] SEQ ID n-260
SEQ ID n° 6195 PL-1198.1	Contig9 from 331800 to 332687	m	72%	sp Q56955 YFED_YERPE CHELATED IRON TRANSPORT SYSTEM MEMBRANE PROTEIN YFED gb AAC46150.1 (U50597) yfeD [Yersinia pestis] sp Q56954 YFEC_YERPE CHELATED IRON TRANSPORT SYSTEM MEMBRANE PROTEIN YFEC gb AAC46149.1 (U50597) yfeC [Yersinia pestis] gb AAC46148.1 (U50597) yfeB [Yersinia pestis] SEQ ID n-261
SEQ ID n° 6196 PL-1199.1	Contig9 from 332684 to 333562	m	88%	sp Q56954 YFEC_YERPE CHELATED IRON TRANSPORT SYSTEM MEMBRANE PROTEIN YFEC gb AAC46149.1 (U50597) yfeC [Yersinia pestis] gb AAC46148.1 (U50597) yfeB [Yersinia pestis] SEQ ID n-262
SEQ ID n° 6197 PL-1200.1	Contig9 from 333559 to 334455	m	87%	gb AAC46148.1 (U50597) yfeB [Yersinia pestis] SEQ ID n-265
SEQ ID n° 6198 PL-1201.1	Contig9 from 334452 to 335372	m	82%	gb AAC46147.1 (U50597) yfeA [Yersinia pestis] SEQ ID n-266

TABLEAU II

SEQ ID n° 6186 PL-3830.1	Contig9 from 322229 to 322726	p 69%	sp F76270 YEBC_ECOLI PROTEIN YEBC_pir H64944 probable membrane protein b1832 - Escherichia coli dbj BAAL5640.1 (D90826) ORF_ID:0335#13; similar to [SwissProt Accession Number P36088] [Escherichia coli] dbj BAAL5645.1 (D90827) ORF_ID:0335#13; similar to [SwissProt Accession Number P36088] [Escherichia coli] gb AAC74902.1 (AE000277) orf, hypothetical protein [Escherichia coli K12] sp P45577 PROQ_ECOLI PROP EFFECTOR gb AAD41527.1 L48409_1 (L48409) ProQ [Escherichia coli] SEQ ID n-3005
SEQ ID n° 6187 PL-1192.1	Contig9 from 322822 to 323541	p 75%	gb AAG56820.1 AE005405_11 (AE005405) carboxy- terminal protease for penicillin-binding protein 3 [Escherichia coli O157:H7] SEQ ID n-255
SEQ ID n° 6188 PL-1193.1	Contig9 from 323561 to 325612	p 83%	gb AAG56819.1 AE005405_10 (AE005405) heat shock protein, integral membrane protein [Escherichia coli O157:H7] SEQ ID n-256
SEQ ID n° 6189 PL-1194.1	Contig9 from 325942 to 326829	p 86%	sp P77529 YDUN_ECOLI HYPOTHETICAL SYMPORTER YDUN pir A64932 hypothetical protein b1729 - Escherichia coli (strain K-12) dbj BAAL5509.1 (D90815) Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein). [Escherichia coli] dbj BAAL5512.1 (D90816) Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein). [Escherichia coli] gb AAC74799.1 (AE000268) part of a kinase [Escherichia coli K12] SEQ ID n-257
SEQ ID n° 6190 PL-1195.1	Contig9 from 326897 to 328288	m 88%	gb AAG56714.1 AE005396_1 (AE005396) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-258
SEQ ID n° 6191 PL-3829.1	Contig9 from 328476 to 329024	m 63%	

TABLEAU II

SEQ ID n° 6180	PL-4526.1	m	71%	Contig9 from 317892 to 318122	sp P28689 HOLE_ECOLI DNA POLYMERASE III, THETA SUBUNIT pir S34951 DNA-directed DNA polymerase (EC 2.7.7.7) III theta chain - Escherichia coli gb AA23697.1 (L04572) DNA polymerase III theta subunit [Escherichia coli] gb AA23982.1 (L05381) DNA polymerase III theta subunit [Escherichia coli] dbj BA15650.1 (D90827) DNA-directed DNA polymerase (EC 2.7.7.7) III q chain [Escherichia coli] gb AAC74912.1 (AE000278) DNA polymerase III, theta subunit [Escherichia coli] K12] gb AAG56832.1 AE005406_11 (AE005406) DNA polymerase III theta subunit [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6181	PL-3832.1	p	66%	Contig9 from 318436 to 318939	pir F82368 ferritin VC0078 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93256.1 (AE004098) ferritin [Vibrio cholerae]	SEQ ID n-3007
SEQ ID n° 6182	PL-4525.1	p	51%	Contig9 from 319134 to 319520	gb AAG56831.1 AE005406_10 (AE005406) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6183	PL-1191.1	p	57%	Contig9 from 319523 to 320416	gb AAG56830.1 AE005406_9 (AE005406) putative resistance protein [Escherichia coli O157:H7]	SEQ ID n-254
SEQ ID n° 6184	PL-3831.1	p	41%	Contig9 from 320616 to 320969	sp P76277 YEBY_ECOLI HYPOTHETICAL 12.4 KDA PROTEIN IN PHA-HOLE INTERGENIC REGION PRECURSOR pir G64945 hypothetical protein b1839 precursor - Escherichia coli gb AAC74909.1 (AE000278) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-3006
SEQ ID n° 6185	PL-4524.1	m	65%	Contig9 from 321321 to 321563	sp P76274 YEBV_ECOLI HYPOTHETICAL 8.8 KDA PROTEIN IN PRC-PPHA INTERGENIC REGION	#N/A

TABLEAU II

SEQ ID n° 6176 PL-1189.1	Contig9 from 314516 to 315886	m 74%	sp F12680 PABB_SALTY PARA-AMINO BENZOATE SYNTHASE COMPONENT I (ADC SYNTHASE) pir A31132 p- aminobenzoate synthase (EC 4.1.3.-) component I Salmonella typhimurium gb AAA88618.1 (M22079) p-aminobenzoate synthase component I [Salmonella typhimurium] SEQ ID n-251 sp P76260 YOA_H ECOLI HYPOTHETICAL 6.6 KD PROTEIN IN FADD-PABB INTERGENIC REGION pir C64942 hypothetical protein b1811 - Escherichia coli (strain K-12) gb AAC74881.1 (AE000275) orf, hypothetical protein [Escherichia coli K12] gb AAG56800.1 AE005404_3 (AE005404) orf, hypothetical protein [Escherichia coli O157:H7] sp P33219 YEBF_ECOLI HYPOTHETICAL LIPOPROTEIN YEBF PRECURSOR pir G64946 lipoprotein yebf precursor - Escherichia coli gb AAA23859.1 (L20897) putative [Escherichia coli] dbj BAA15653.1 (D90827) ORF_ID:0336#14; similar to [SwissProt Accession Number P33219] [Escherichia coli] gb AAC74917.1 (AE000278) orf, hypothetical protein [Escherichia coli K12] #N/A
SEQ ID n° 6178 PL-4528.1	Contig9 from 316364 to 316687	p 41%	sp O32449 PIP_SERVA PROLINE IMINOPEPTIDASE (PIP) (PROLYL AMINOPEPTIDASE) (PAP) pir JC5696 prolyl aminopeptidase (EC 3.4.11.5) - Serratia marcescens pdb 1QTR A Chain A, Crystal Structure Analysis Of The Prolyl Aminopeptidase From Serratia Marcescens dbj BAA23336.1 (D87897) prolyl aminopeptidase [Serratia marcescens] SEQ ID n-253
SEQ ID n° 6179 PL-1190.1	Contig9 from 316761 to 317714	p 83%	

TABLEAU II

SEQ ID n° 6173	PL-1187.1	Contig9 from 310811 to 311794	m	82%	sp P08186 PTNA_ECOLI PTS SYSTEM, MANNOSE-SPECIFIC IIAB COMPONENT (EIIAB-MAN) (MANNOSE-PERMEASE IIAB COMPONENT) (PHOSPHOTRANSFERASE COMPONENT) (EII-MAN) pir WQECW3 phosphotransferase system enzyme II (EC 2.7.1.69), mannose-specific, factor IIAB - Escherichia coli gb AA24443.1 (J02699) mannose permease subunit III-Man [Escherichia coli] dbj BAA15624.1 (D90825) Phosphotransferase system enzyme II (EC 2.7.1.69), Mannose-specific, factor III [Escherichia coli] dbj BAA15629.1 (D90826) Phosphotransferase system enzyme II (EC 2.7.1.69), Mannose-specific, factor III [Escherichia coli] gb AAC74887.1 (AE000276) PTS enzyme IIAB, mannose-specific [Escherichia coli K12]	SEQ ID n-249
SEQ ID n° 6174	PL-1188.1	Contig9 from 312417 to 313781	m	85%	sp P16095 SDHL_ECOLI L-SERINE DEHYDRATASE 1 (L-SERINE DEAMINASE 1) (SDH 1) (L-SD1) pir DWECL L-serine dehydratase (EC 4.2.1.13) 1 - Escherichia coli gb AA63580.1 (M28695) L-serine deaminase [Escherichia coli] dbj BAA15621.1 (D90825) L-serine dehydratase 1 (EC 4.2.1.13) (L-serine deaminase SDH 1) (L-SD1). [Escherichia coli] gb AAC74884.1 (AE000275) L-serine deaminase [Escherichia coli K12]	SEQ ID n-250
SEQ ID n° 6175	PL-3833.1	Contig9 from 313956 to 314519	m	67%	gb AAG56802.1 AE005404_5 (AE005404) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-3008

TABLEAU II

sp P08187 PTNC_ECOLI PTS SYSTEM, MANNOSE-SPECIFIC IIC COMPONENT (EII-P-MAN)				
(MANNOSE-PERMEASE IIC COMPONENT)				
(PHOSPHOTRANSFERASE COMPONENT) (EII-P-MAN) pir WOECMP				ENZYME II, C
phosphotransferase system enzyme II (EC 2.7.1.69),				mannose-specific, factor
IIC - Escherichia coli gb AAA2444.1 (J02699)				
mannose permease subunit II-P-Man [Escherichia coli] dbj BAAL5625.1 (D90825)				
Phosphotransferase system enzyme II (EC 2.7.1.69),				mannose-specific, factor
II-P [Escherichia coli] dbj BAAL5630.1 (D90826)				Phosphotransferase system enzyme II (EC 2.7.1.69),
mannose-specific, factor				
II-P [Escherichia coli] gb AAC74888.1 (AE000276)				PTS enzyme IIC, mannose-specific
[Escherichia coli K12]				
gb AAG56807.1 AE005404_10 (AE005404) PTS enzyme IIC, mannose-specific [Escherichia coli O157:H7]				
Contig9 from				
SEQ ID n° 6172 PL-1186.1	309952 to	m	89%	
	310752			

SEQ ID n-248

TABLEAU II

SEQ ID n° 6169 PL-1184.1	Contig9 from 307486 to 308067	m 65%	sp P76264 YEBN_ECOLI_HYPOTHETICAL_22.1 ID PROTEIN IN MANZ-CSPC INTERGENIC REGION pir E64943 probable membrane protein b1821 - Escherichia coli dbj BAAL5632.1 (D90826) ORF_ID:0335#4; similar to [SwissProt Accession Number P39154] [Escherichia coli] gb AAC74891.1 (AE000276) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-246
SEQ ID n° 6170 PL-3834.1	Contig9 from 308493 to 308951	m 70%	gb AAG56809.1 AE005404_12 (AE005404) orf, hypothetical protein. [Escherichia coli O157:H7] sp P08188 PTND_ECOLI_PTS_SYSTEM, MANNOSE- SPECIFIC IID COMPONENT (EIID-MAN) (MANNOSE-PERMEASE IID COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, D COMPONENT) (EII-M-MAN) pir WQECMM phosphotransferase system enzyme II (EC 2.7.1.69), mannose-specific, factor IID - Escherichia coli gb AAA24445.1 (J02699) mannose permease subunit Ii-M-Man [Escherichia coli] dbj BAAL5631.1 (D90826) PTS system, Mannose-specific IID component (EIID-MAN) (Mannose- permease IID component) (phosphotransferase enzyme II, D component) (EII-M-MAN). [Escherichia coli] gb AAC74889.1 (AE000276) PTS enzyme IID, mannose-specific [Escherichia coli K12] gb AAG56808.1 AE005404_11 (AE005404) PTS enzyme IID, mannose-specific [Escherichia coli O157:H7]	SEQ ID n-3009
SEQ ID n° 6171 PL-1185.1	Contig9 from 309072 to 309938	m 87%		SEQ ID n-247

TABLEAU II

SEQ ID n° 6162 PL-1181.1	Contig9 from 299831 to 300643	P	No Hits found	SEQ ID n-243
SEQ ID n° 6163 PL-7254.1	Contig9 from 300708 to 300878	P	No Hits found	#N/A
SEQ ID n° 6164 PL-4537.1	Contig9 from 301093 to 301353	M	No Hits found	#N/A
SEQ ID n° 6165 PL-4536.1	Contig9 from 301547 to 301840	P	72%	<p>pir G82648 conserved hypothetical protein XF1702 [imported] - Xylella fastidiosa (strain 9a5c)</p> <p>gb AAF84511.1 AE003994_10 (AE003994) conserved hypothetical protein [Xylella fastidiosa]</p> <p>sp P55383 Y4CA_RHISN HYPOTHETICAL 133.7 KD PROTEIN Y4CA pir T28628 Y4CA protein - Rhizobium sp. plasmid pNGR234a gb AAB91631.1 (AE000067) Y4CA [Rhizobium sp. NGR234]</p>
SEQ ID n° 6166 PL-1182.1	Contig9 from 302022 to 305900	M	11%	SEQ ID n-244
SEQ ID n° 6167 PL-4532.1	Contig9 from 306084 to 306266	M	No Hits found	#N/A
SEQ ID n° 6168 PL-1183.1	Contig9 from 306601 to 307419	P	70%	<p>sp P36999 RRNA_ECOLI RIBOSOMAL RNA LARGE SUBUNIT METHYLTRANSFERASE A (RRNA) -METHYLTRANSFERASE (23S RRNA MIG745 METHYLTRANSFERASE) pir S49049 probable S- adenosylmethionine-dependent methyltransferase yebH - Escherichia coli</p> <p>dbj BAA05855.1 (D28496) ORF30 [Escherichia coli] dbj BAA15633.1 (D90826) Mycinamicin- resistance protein MyrA. [Escherichia coli] gb AAC74892.1 (AE000276) putative enzyme [Escherichia coli K12]</p>

SEQ ID n-245

TABLEAU II

SEQ ID n° 6158 PL-1178.1	Contig9 from 295397 to 296974	p 89%	sp P04079 GUA_ECOLI GMP SYNTHASE [GLUTAMINE- HYDROLYZING] (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE) pir SYECGU GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) [validated] Escherichia coli pdb 1GPM A Chain A, Escherichia Coli Gmp Synthetase Complexed With Amp And Pyrophosphate pdb 1GPM C Chain C, Escherichia Coli Gmp Synthetase Complexed With Amp And Pyrophosphate pdb 1GPM B Chain B, Escherichia Coli Gmp Synthetase Complexed With Amp And Pyrophosphate pdb 1GPM D Chain D, Escherichia Coli Gmp Synthetase Complexed With Amp And Pyrophosphate gb AAB18619.1 (M10101) GMP synthetase [Escherichia coli] gb AAC75560.1 (AE000337) GMP synthetase (glutamine- hydrolyzing) [Escherichia coli K12] dbj BA16394.1 (D90880) GMP synthase (glutamine- hydrolyzing) (EC 6.3.5.2) [Escherichia coli]	SEQ ID n-239
SEQ ID n° 6159 PL-4543.1	Contig9 from 297004 to 297318	p 79%	gb AAB69349.1 (AF015307) DNA invertase [Acetobacter pasteurianus] gb AAC97179.1 (AF044847) putative DNA invertase [Acetobacter pasteurianus]	#N/A
SEQ ID n° 6160 PL-1179.1	Contig9 from 297427 to 299076	p 84%	sp P05103 MTP7_PSEAE MODIFICATION METHYLASE PAER7I (ADENINE-SPECIFIC METHYLTRANSFERASE PAER7I) (M.PAER7I)	SEQ ID n-240
SEQ ID n° 6161 PL-1180.1	Contig9 from 299077 to 299817	p 96%	sp P05104 T2P7_PSEAE TYPE II RESTRICTION ENZYME PAER7I (ENDONUCLEASE PAER7I) (R.PAER7I) pir NDPS7A type II site-specific deoxyribonuclease (EC 3.1.21.4) Paer7I - Pseudomonas aeruginosa plasmid pMG7 emb CAA27026.1 (X03274) put. endonuclease (aa 1- 246) [Pseudomonas aeruginosa]	SEQ ID n-242

TABLEAU II

SEQ ID n° 6152	PL-1172.1	Contig9 from 285784 to 286674	p	48%	pir E83058 hypothetical protein PA4705 [imported] - Pseudomonas aeruginosa (strain PA01) gb AA08091.1 AE004884.9 (AE004884) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-233
SEQ ID n° 6153	PL-1173.1	Contig9 from 286828 to 287628	p	43%	sp Q05613 TONB_PSEPU TONB PROTEIN pir S28444 tonB protein - Pseudomonas putida emb CAA49716.1 (X70139) inner-membrane protein TonB [Pseudomonas putida]	SEQ ID n-234
SEQ ID n° 6154	PL-1174.1	Contig9 from 287760 to 289817	p	66%	gb AAG56835.1 AE005407_3 (AE005407) protease II [Escherichia coli O157:H7]	SEQ ID n-235
SEQ ID n° 6155	PL-1175.1	Contig9 from 289980 to 292223	p	54%	pir A81436 probable outer membrane siderophore receptor Cj0178 [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB72661.1 (AL139074) putative outer membrane siderophore receptor [Campylobacter jejuni]	SEQ ID n-236
SEQ ID n° 6156	PL-1176.1	Contig9 from 292311 to 293684	m	79%	sp P04994 EX7L_ECOLI EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT (EXONUCLEASE VII LARGE SUBUNIT) pir NCEC7 exodeoxyribonuclease VII (EC 3.1.11.6) large chain - Escherichia coli (strain K-12) gb AAC75562.1 (AE000337) exonuclease VII, large subunit [Escherichia coli K12] dbj BAJ6396.1 (D90880) exodeoxyribonuclease VII (EC 3.1.11.6) large chain [Escherichia coli]	SEQ ID n-237
SEQ ID n° 6157	PL-1177.1	Contig9 from 293857 to 295323	p	86%	dbj BAAL6395.1 (D90880) IMP dehydrogenase (EC 1.1.1.205) [Escherichia coli]	SEQ ID n-238

TABLEAU II

SEQ ID n° 6148	PL-1169.1	Contig9 from 280354 to 281481	m	82%	sp P24176 DAPE_ECOLI SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (SDAP) pir A42959 succinyl- diaminopimelate desuccinylase (EC 3.5.1.18) - Escherichia coli emb CAA40665.1 (X57403) succinyl-diaminopimelate desuccinylase [Escherichia coli] gb AAB22798.1 (S41760) N- succinyl-L-diaminopimelic acid desuccinylase, DapE, MspB {EC 3.5.1.18} [Escherichia coli, Peptide, 375 aa] gb AAC75525.1 (AE000334) N-succinyl-diaminopimelate deacylase [Escherichia coli K12] dbj BAA16346.1 (D90875) succinyl- diaminopimelate desuccinylase (EC 3.5.1.18) [Escherichia coli] dbj BAA16350.1 (D90876) succinyl-diaminopimelate desuccinylase (EC 3.5.1.18) [Escherichia coli] SEQ ID n-229
SEQ ID n° 6149	PL-4546.1	Contig9 from 281483 to 281869	m	65%	sp P24178 YFFB_ECOLI PROTEIN YFFB pir B42959 14K hypothetical protein (5' of dapE) - Escherichia coli emb CAA40664.1 (X57403) orf [Escherichia coli] gb AAC75524.1 (AE000334) orf, hypothetical protein [Escherichia coli K12] dbj BAA16345.1 (D90875) similar to [PIR Accession Number B42959] [Escherichia coli] dbj BAA16349.1 (D90876) similar to [PIR Accession Number B42959] [Escherichia coli] #N/A
SEQ ID n° 6150	PL-1170.1	Contig9 from 282096 to 282731	m	74%	gb AAG57328.1 AE005452_1 (AE005452) nitrate/nitrite response regulator (sensor NarQ) [Escherichia coli O157:H7] SEQ ID n-231
SEQ ID n° 6151	PL-1171.1	Contig9 from 283418 to 285697	p	89%	gb AAG57572.1 AE005475_7 (AE005475) putative multimodular enzyme [Escherichia coli O157:H7] SEQ ID n-232

TABLEAU II

SEQ ID n° 6144 PL-3837.1	Contig9 from 277036 to 277488	P 69%	sp P76240 YEAL_ECOLI_HYPOTHETICAL_15.3 RD PROTEIN IN GAPA-RND INTERGENIC REGION pir E64939 hypothetical protein b1789 - Escherichia coli (strain K-12) dbj BAA15588.1 (D90822) ORF_ID:0331#5; similar to [SwissProt Accession Number P44110] [Escherichia coli] dbj BAA15590.1 (D90823) ORF_ID:0331#5; similar to [SwissProt Accession Number P44110] [Escherichia coli] gb AAC74859.1 (AE000274) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-3010
SEQ ID n° 6145 PL-1167.1	Contig9 from 277493 to 279541	P 61%	gb AAG57584.1 AE005477_2 (AE005477) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-227
SEQ ID n° 6146 PL-4548.1	Contig9 from 279492 to 279680	M 71%	dbj BAA16347.1 (D90875) similar to [PIR Accession Number D42959] [Escherichia coli] dbj BAA16351.1 (D90876) similar to [PIR Accession Number D42959] [Escherichia coli]	#N/A
SEQ ID n° 6147 PL-1168.1	Contig9 from 279680 to 280357	M 61%	gb AAK03105.1 (AE006143) unknown [Pasteurella multocida]	SEQ ID n-238

TABLEAU II

SEQ ID n°	Contig9 from	m	No Hits found	SEQ ID n-222
6139 PL-1162.1	270392 to 271402	m		
6140 PL-1163.1	272145 to 273209	m	29%	<p>pir E70091 hypothetical protein yydG - Bacillus subtilis dbj BAAL1275.1 (D78193) yydG [Bacillus subtilis] emb CAB16054.1 (Z99124) yydG [Bacillus subtilis]</p>
6141 PL-1164.1	273588 to 275207	p	70%	<p>emb CAA70529.1 (Y09356) ATP-dependent activating enzyme [Pseudomonas fluorescens] sp PI5048 ENTB_ECOLI ISOCHORISMATASE (2,3 DIHYDRO-2,3 DIHYDROXYBENZOATE SYNTHASE) pir YXECIC isochorismatase (EC 3.3.2.1) - Escherichia coli gb AA16102.1 (M24148) isochorismatase [Escherichia coli] gb AA76835.1 (M24143) 2,3-dihydro-2,3-dihydroxybenzoate synthase [Escherichia coli] gb AAB40795.1 (U82598) isochorismatase [Escherichia coli] gb AAC73696.1 (AE000165) 2,3-dihydro-2,3-dihydroxybenzoate synthetase, isochorismatase [Escherichia coli K12] gb AAG54930.1 AE005239_5 (AE005239) 2,3-dihydro-2,3-dihydroxybenzoate synthetase, isochorismatase [Escherichia coli O157:H7] gb AAG54931.1 AE005239_6 (AE005239) 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase, enterochelin biosynthesis [Escherichia coli O157:H7 EDL933] dbj BAB34058.1 (AP002552) 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase [Escherichia coli O157:H7]</p>
6142 PL-1165.1	275230 to 275883	p	71%	
6143 PL-1166.2	275951 to 276697	p	68%	#N/A

TABLEAU II

SEQ ID n°	Contig9 from	P	No Hits found	#N/A
6131 PL-4550.1	260669 to 260875	p		
6132 PL-1157.1	260983 to 262158	p	34%	<p>pir B72391 conserved hypothetical protein - Thermotoga maritima (strain MSB8)</p> <p>gb AAD35423.1 AE001714_14 (AE001714) conserved hypothetical protein [Thermotoga maritima]</p> <p>sp P45743 DHBB_BACSU ISOCHORISMATASE (2,3 DIHYDRO-2,3 DIHYDROXYBENZOATE SYNTHASE) (SUPEROXIDE-INDUCIBLE PROTEIN 1) (SOIL)</p> <p>pir B69615 isochorismatase (EC 3.3.2.1) dhbb - Bacillus subtilis gb AAC44633.1 (U26444) isochorismatase [Bacillus subtilis]</p> <p>emb CAB15187.1 (Z99120) isochorismatase [Bacillus subtilis]</p>
6133 PL-4549.1	262170 to 262400	m	28%	<p>pir H83346 probable ATP-binding/permease fusion ABC transporter PA2390 [imported] - Pseudomonas aeruginosa (strain PAO1)</p> <p>gb AAG05778.1 AE004665_5 (AE004665) probable ATP-binding/permease fusion ABC transporter [Pseudomonas aeruginosa]</p>
6134 PL-1158.1	262435 to 263658	m	48%	<p>emb CAA11724.1 (AJ223978) putative ABC transporter, Yvrc [Bacillus subtilis]</p> <p>sp P75830 YBJY_ECOLI HYPOTHETICAL 41.7 KDA PROTEIN IN AQPZ-CSPD INTERGENIC REGION dbj BAA35597.1 (D90725) MtrC protein [Escherichia coli]</p>
6135 PL-1159.1	263661 to 264326	m	57%	<p>emb CAC01604.1 (AJ269505) peptidase synthetase [Anabaena sp. 90]</p>
6136 PL-1160.1	264310 to 265467	m	51%	
6137 PL-1161.1	265492 to 269883	m	42%	
6138 PL-3838.1	269901 to 270395	m		

TABLEAU II

SEQ ID n° 6126 PL-1153.1	Contig9 from 254432 to 255145	P	91%	sp P21155 PUR7_ECOLI PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE (SAICAR pir C36146 SYNTHETASE)	SEQ ID n-212
				phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) - Escherichia coli gb AA24448.1 [M33928] 5'-phosphoribosyl- 5-aminoimidazole-4- N-succinocarboxamide synthetase (EC 6.3.2.6) [Escherichia coli] gb AAC75529.1 (AE000334)	
SEQ ID n° 6127 PL-1154.1	Contig9 from 255522 to 256547	P	21%	phosphoribosylaminoimidazole-succinocarboxamide synthetase = SAICAR synthetase [Escherichia coli K12] dbj BAA16353.1 (D90876)	SEQ ID n-213
				phosphoribosylaminoimidazole-succinocarboxamide synthase coli dbj BAA16363.1 (D90877)	
SEQ ID n° 6128 PL-1155.1	Contig9 from 256943 to 258580	P	48%	phosphoribosylaminoimidazole-succinocarboxamide synthase coli gb AAG57586.1 AE005477_4 (AE005477)	SEQ ID n-214
				phosphoribosylaminoimidazole-succinocarboxamide synthetase = SAICAR synthetase [Escherichia coli O157:H7]	
SEQ ID n° 6129 PL-1156.1	Contig9 from 258577 to 260232	P	48%	dbj BAH06239.1 (AF001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-215
				pir S74455 ABC-type transport protein slr1488 - 6803 Synechocystis sp. (strain PCC dbj BAA16607.1 (D90899) ABC transporter [Synechocystis sp.]	
SEQ ID n° 6130 PL-4551.1	Contig9 from 260476 to 260676	P	No Hits found	pir S74461 ABC transporter slr1494 - Synechocystis sp. (strain PCC 6803) dbj BAA16613.1 (D90899) ABC transporter [Synechocystis sp.]	#N/A

TABLEAU II

SEQ ID n° 6124 PL-1151.1	Contig9 from 252187 to 253086	P 82%	<p>sp P05640 DAPA_ECOLI_DIHYDRODIPICOLINATE SYNTHASE (DHDPS) pir SYECDP dihydrodipicolinate synthase (EC 4.2.1.52) [validated] - Escherichia coli</p> <p>pdb 1DHP A Chain A, Dihydrodipicolinate Synthase pdb 1DHP B Chain B, Dihydrodipicolinate Synthase gb AAC75531.1 (AE000335) dihydrodipicolinate synthase [Escherichia coli K12] dbj BAAL6355.1 (D90876) dihydrodipicolinate synthase (EC 4.2.1.52) [Escherichia coli] -dbj BAAL6365.1 (D90877) dihydrodipicolinate synthase (EC 4.2.1.52) [Escherichia coli]</p>	SEQ ID n-210
			<p>pir D65023 lipoprotein-34 precursor - Escherichia coli gb AAC75530.1 (AE000335) lipoprotein-34 [Escherichia coli K12]</p>	
SEQ ID n° 6125 PL-1152.1	Contig9 from 253103 to 254152	P 68%	<p>SEQ ID n-211</p>	SEQ ID n-211

TABLEAU II

SEQ ID n° 6122 PL-3841.1	Contig9 from 250761 to 251231	m 82*	sp P23480 BCP_ECOLI BACTERIOFERRITIN COMIGRATORY PROTEIN pir [B49749 thioredoxin-dependent hydroperoxide peroxidase (EC 1.11.1.-) [validated] - Escherichia coli gb AAC75533.1 (AE000335) bacterioferritin comigratory protein [Escherichia coli K12]
			dbj BAA16358.1 (D90876) bacterioferritin comigratory protein [Escherichia coli] dbj BAA16368.1 (D90877) bacterioferritin comigratory protein [Escherichia coli] gb AAE88562.1 (M63654) bacterioferritin comigratory protein [Escherichia coli] gb AAG57590.1 AE005477_8 (AE005477) bacterioferritin comigratory protein [Escherichia coli O157:H7]
SEQ ID n° 6123 PL-3840.1	Contig9 from 251258 to 251803	m 72*	pir [P65023 gcvR protein - Escherichia coli gb AAC75532.1 (AE000335) transcriptional regulation of gcv operon [Escherichia coli K12] dbj BAA16356.1 (D90876) GCV OPERON TRANSCRIPTIONAL REGULATOR. [Escherichia coli] dbj BAA16366.1 (D90877) GCV OPERON TRANSCRIPTIONAL REGULATOR. [Escherichia coli] gb AAG57589.1 AE005477_7 (AE005477) transcriptional regulation of gcv operon [Escherichia coli O157:H7]
			SEQ ID n~3014
SEQ ID n° 6123 PL-3840.1	Contig9 from 251258 to 251803	m 72*	SEQ ID n~9013
			SEQ ID n~9013

TABLEAU II

SEQ ID n° 6118 PL-1148.1	Contig9 from 246734 to 247435	p	87%	sp P76570 YFGE_ECOLI_HYPOTHETICAL_28.4_KDA PROTEIN_IN_FOCB-URAA_INTERGENIC_REGION pir G65025_hypothetical_protein_b2496_- Escherichia_coli_(strain_K-12)_gb AAC75549.1 (AE0000336)_putative_DNA_replication_factor [Escherichia_coli_K12]_gb AGS7606.1 AE005479_4 (AE005479)_putative_DNA_replication_factor [Escherichia_coli_O157:H7] SEQ ID n-206
SEQ ID n° 6119 PL-4554.1	Contig9 from 247590 to ... 247946	m	76%	gb AAG57605.1 AE005479_3_(AE005479)_putative oxidoreductase_[Escherichia_coli_O157:H7] #N/A
SEQ ID n° 6120 PL-1149.1	Contig9 from 247956 to 249419	m	74%	pir E65025_hypothetical_protein_b2494_- Escherichia_coli_(strain_K-12)_gb AAC75547.1 (AE0000336)_orf_hypothetical_protein [Escherichia_coli_K12] sp P77406 PERM_ECOLI_PUTATIVE_PERMEASE_PERM pir D65025_hypothetical_protein_b2493_- Escherichia_coli_(strain_K-12)_gb AAC75546.1 (AE0000335)_putative_permease_[Escherichia_coli_K12] dbj BAAL6382.1 (D90878)_similar_to [SwissProt_Accession_Number_P43970] [Escherichia_coli] SEQ ID n-207
SEQ ID n° 6121 PL-1150.1	Contig9 from 249556 to 250635	p	79%	SEQ ID n-209

TABLEAU II

SEQ ID n° 6110	PL-1144.1	Contig9 from 240545 to 241171	p	94%	pir A65026 uracil phosphoribosyltransferase (EC 2.4.2.9) upp - Escherichia coli gb AAC7551.1 (AE000336) uracil phosphoribosyltransferase [Escherichia coli K12] gb AAG57608.1 AE005479_6 (AE005479) uracil phosphoribosyltransferase [Escherichia coli O157:H7]	SEQ ID n-202
SEQ ID n° 6111	PL-4558.1	Contig9 from 241409 to 241756	m	64%	gb AAC35810.1 (AF071757) HicB [Haemophilus influenzae]	#N/A
SEQ ID n° 6112	PL-4557.3	Contig9 from 241897 to 242001	m	38%	gb AAC35821.1 (AF071760) HicA [Haemophilus influenzae]	#N/A
SEQ ID n° 6113	PL-1145.1	Contig9 from 242220 to 243527	m	71%	pir G82219 6-phospho-beta-glucosidase VC1284 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94443.1 (AE004207) 6- phospho-beta-glucosidase [Vibrio cholerae]	SEQ ID n-203
SEQ ID n° 6114	PL-4556.1	Contig9 from 243524 to 243883	m	64%	gb AA23559.1 (M93573) PTS enzyme III cel [Escherichia coli]	#N/A
SEQ ID n° 6115	PL-1146.1	Contig9 from 243902 to 245230	m	69%	pir E82219 PTS system, cellobiose-specific IIC component VC1282 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94441.1 (AE004207) PTS system, cellobiose- specific IIC component [Vibrio cholerae]	SEQ ID n-204
SEQ ID n° 6116	PL-4555.1	Contig9 from 245260 to 245565	m	61%	pir D82219 PTS system, cellobiose-specific IIB component VC1281 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94440.1 (AE004207) PTS system, cellobiose- specific IIB component [Vibrio cholerae]	#N/A
SEQ ID n° 6117	PL-1147.1	Contig9 from 245825 to 246451	p	No Hits found		SEQ ID n-205

TABLEAU II

SEQ ID n° 6104	PL-1140.1	Contig9 from 234286 to 235818	m	84%	gb AAC34891.1 (AF085682) exopolyphosphatase [Salmonella typhimurium]	SEQ ID n-198
SEQ ID n° 6105	PL-1141.1	Contig9 from 235822 to 237891	m	87%	sp P28688 PPK_ECOLI POLYPHOSPHATE KINASE p1x A44306 polyphosphate kinase (EC 2.7.4.1) - Escherichia coli gb AAC7554.1 (AE000336) polyphosphate kinase [Escherichia coli K12] dbj BA16389.1 (D90878) polyphosphate kinase (EC 2.7.4.1) [Escherichia coli] gb AAG57611.1 AE005479_9 (AE005479) polyphosphate kinase [Escherichia coli O157:H7] dbj BA15286.1 (D90799) Spermidine N1- acetyltransferase (EC 2.3.1.57) (Diamine acetyltransferase) (SAT). [Escherichia coli] dbj BA15308.1 (D90800) Spermidine N1- acetyltransferase (EC 2.3.1.57) (Diamine acetyltransferase) (SAT). [Escherichia coli] dbj BA15310.1 (D90801) Spermidine N1- acetyltransferase (EC 2.3.1.57) (Diamine acetyltransferase) (SAT). [Escherichia coli] pdb 3GAR A Ph-Dependent Stabilization Of An Active Site Loop Observed From Low And High Ph Crystal Structures Of Mutant Monomeric Glycinamide Ribonucleotide Transformylase pdb 2GAR A Ph-Dependent Stabilization Of An Active Site Loop Observed From Low And High Ph Crystal Structures Of Mutant Monomeric Glycinamide Ribonucleotide Transformylase gb AAG14577.1 AF293164_1 (AF293164) phosphoribosylaminoimidazole synthetase [Escherichia coli]	SEQ ID n-200
SEQ ID n° 6108	PL-1143.1	Contig9 from 239278 to 240318	m	86%		SEQ ID n-201
SEQ ID n° 6109	PL-4560.1	Contig9 from 240393 to 240548	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6097	PL-1134.1	Contig9 from 225724 to 226386	p	38%	pir F72285 transcription regulator, crp family Thermotoga maritima (strain MSB8) gb AAD36246.1 AE001774_3 (AE001774) transcriptional regulator, crp family [Thermotoga maritima] SEQ ID n-191
SEQ ID n° 6098	PL-1135.1	Contig9 from 226575 to 228107	m	47%	sp P22106 ASNB_ECOLI ASPARAGINE SYNTHETASE B [GLUTAMINE-HYDROLYZING] pir AJECN asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - Escherichia coli gb AA23498.1 (J05554) asparagine synthetase B [Escherichia coli] dbj BAA35317.1 (D90706) Asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) [Escherichia coli] gb AAC73768.1 (AE000171) asparagine synthetase B [Escherichia coli K12] sp Q9RVD3 AROA_DEIRA 3-PHOSPHOSHIKIMATE 1- CARBOXYVINYLTRANSFERASE (5- ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS) SEQ ID n-192
SEQ ID n° 6099	PL-1136.1	Contig9 from 228143 to 229498	m	49%	sp Q57925 AROA_METUA PROBABLE 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (5- ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS) gb AAB98493.1 (U67500) 3- phosphoshikimate-1-carboxyvinyltransferase (aroA) [Methanococcus jannaschii] pir A75567 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb AAF09626.1 AE001867_1 (AE001867) conserved hypothetical protein [Deinococcus radiodurans] sp P55641 Y4RH_RHISN HYPOTHETICAL 52.5 KDA PROTEIN Y4RH gb AAB91833.1 (AE000094) Y4RH [Rhizobium sp. NGR234] SEQ ID n-194
SEQ ID n° 6100	PL-1137.1	Contig9 from 229526 to 230830	m	43%	pir C75275 hypothetical protein - Deinococcus radiodurans (strain R1) gb AAF11982.1 AE002073_12 (AE002073) hypothetical protein [Deinococcus radiodurans] #N/A
SEQ ID n° 6101	PL-4562.1	Contig9 from 230881 to 231279	m	50%	
SEQ ID n° 6102	PL-1138.1	Contig9 from 231852 to 233090	p	33%	
SEQ ID n° 6103	PL-1139.1	Contig9 from 233160 to 233951	p	40%	

TABLEAU II

SEQ ID n° 6090	PL-1127.1	Contig9 from 213283 to 213987	m	81%	gb AAG57142.1 AE005434_6 (AE005434) transcriptional response regulatory protein (sensor Baes) [Escherichia coli O157:H7]	SEQ ID n-283
SEQ ID n° 6091	PL-1128.1	Contig9 from 213984 to 215372	m	71%	gb AAG57141.1 AE005434_5 (AE005434) sensor protein (for Baer) [Escherichia coli O157:H7] sp P76399 YEGO_ECOLI HYPOTHETICAL 111.0 KDA PROTEIN IN ALKA-BAES INTERGENIC REGION pir C64974 hypothetical protein b2076 - Escherichia coli (strain K-12) dbj BAAL5932.1 (D90846) Acriflavin resistance protein P (EnvD protein) . [Escherichia coli] gb AAC75137.1 (AE000297) orf, hypothetical protein [Escherichia coli K12] sp P76398 YEGN_ECOLI HYPOTHETICAL 112.1 KDA PROTEIN IN ALKA-BAES INTERGENIC REGION pir B64974 hypothetical protein b2075 - Escherichia coli (strain K-12) dbj BAAL5929.1 (D90845) Acriflavin resistance protein D. [Escherichia coli] gb AAC75136.1 (AE000297) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-287 sp P76397 YEGM_ECOLI HYPOTHETICAL 44.5 KDA PROTEIN IN ALKA-BAES INTERGENIC REGION PRECURSOR emb CAB91168.1 (AL355920) putative inosine- uridine preferring nucleoside hydrolase [Schizosaccharomyces pombe] pir T35340 probable adenosine deaminase - Streptomyces coelicolor emb CAB42949.1 (AL049863) putative adenosine deaminase (Streptomyces coelicolor A3(2))	SEQ ID n-284
SEQ ID n° 6092	PL-1129.1	Contig9 from 215493 to 218603	m	86%		
SEQ ID n° 6093	PL-1130.1	Contig9 from 218600 to 221746	m	86%		
SEQ ID n° 6094	PL-1131.1	Contig9 from 221746 to 222951	m	74%		
SEQ ID n° 6095	PL-1132.1	Contig9 from 223442 to 224371	p	51%		
SEQ ID n° 6096	PL-1133.1	Contig9 from 224397 to 225404	p	46%		

TABLEAU II

SEQ ID n° 6083	PL-1123.1	Contig9 from 203507 to 204886	p	77%	gp AAG54416.1 AE005187_9 (AE005187) aromatic amino acid transport protein [Escherichia coli O157:H7]	SEQ ID n-278
SEQ ID n° 6084	PL-1123.1	Contig9 from 205205 to 205828	m	55%	sp P37001 CRCA_ECOLI CRCA PROTEIN pir D64796 craA protein - Escherichia coli gb AA67555.1 (L29054) putative [Escherichia coli] gb AAB40822.1 (U82598) hypothetical protein [Escherichia coli] gb AAC73723.1 (AE000167) orf., hypothetical protein [Escherichia coli K12] SEQ ID n-279 sp P36996 CSPC_ECOLI COLD SHOCK-LIKE PROTEIN CSPC (CSP-C) pir S43618 cold shock protein homolog cspC - Escherichia coli dbj BAA05854.1 (D28496) cspC (MsmB) [Escherichia coli] gb AA23619.1 (L28430) cold-shock protein [Escherichia coli] dbj BAA15634.1 (D90826) Cold shock protein cspC [Escherichia coli] gb AAC74893.1 (AE000276) cold shock protein [Escherichia coli K12] gb AAG56812.1 AE005405_3 (AE005405) cold shock protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6085	PL-4568.1	Contig9 from 206429 to 206638	p	55%	sp P55882 THID_SALTY PHOSPHOMETHYLPIRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE) gb AAB66492.1 (U87940) HMP-P kinase [Salmonella typhimurium]	SEQ ID n-280
SEQ ID n° 6087	PL-1125.1	Contig9 from 208030 to 209079	m	92%	sp P71295 ALF1_ECOLI FRUCTOSE-BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)	SEQ ID n-281
SEQ ID n° 6088	PL-1126.1	Contig9 from 211266 to 212642	m	87%	gb AAG57144.1 AE005435_2 (AE005435) orf., hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-282
SEQ ID n° 6089	PL-4566.1	Contig9 from 212841 to 213185	m	67%	gb AAK02603.1 (AE006087) unknown [Pasteurella multocida]	#N/A

TABLEAU II

SEQ ID n° 6074	PL-1118.1	Contig9 from 193280 to 193984	m	37%	dbj BA93678.1 (AB029431) GTP cyclohydrolase I [Tetrahymena pyriformis]	SEQ ID n-173
SEQ ID n° 6075	PL-1119.1	Contig9 from 194668 to 195561	p	70%	emb CAB72138.1 (AJ0111922) BphR protein [Ralstonia eutropha]	SEQ ID n-174
SEQ ID n° 6076	PL-1120.1	Contig9 from 197959 to 199431	p	81%	pir H82085 sodium/alanine symporter VC2356 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95499.1 (AE004306) sodium/alanine symporter [Vibrio cholerae]	SEQ ID n-176
SEQ ID n° 6077	PL-1121.1	Contig9 from 199732 to 200553	p	58%	gb AAG55249.1 AE005268_2 (AE005268) putative regulator [Escherichia coli O157:H7]	SEQ ID n-177
SEQ ID n° 6078	PL-4570.1	Contig9 from 200816 to 201244	m	No Hits found		#N/A
SEQ ID n° 6079	PL-3845.1	Contig9 from 201583 to 202077	p	49%	emb CAB88438.1 (AL353815) putative integral membrane protein [Streptomyces coelicolor A3(2)]	SEQ ID n-3017
SEQ ID n° 6080	PL-7043.1	Contig9 from 202207 to 202341	m	No Hits found		#N/A
SEQ ID n° 6081	PL-3844.1	Contig9 from 202364 to 202753	m	37%	pdb 1DSY A Chain A, Crystal Structure Of The E. Coli Rob Transcription Factor In Complex With Dna pdb 1DSY C Chain C, Crystal Structure Of The E. Coli Rob Transcription Factor In Complex With Dna pdb 1DSY B Chain B, Crystal Structure Of The E. Coli Rob Transcription Factor In Complex With Dna pdb 1DSY D Chain D, Crystal Structure Of The E. Coli Rob Transcription Factor In Complex With Dna	SEQ ID n-3016
SEQ ID n° 6082	PL-4569.1	Contig9 from 203064 to 203207	p	No Hits found		#N/A

TABLEAU II

SEQ. ID n° 6068	PL-3847.1	Contig9 from 185063 to 185605	-m- 40%	<p> pdb 1DY3 A Chain A, Ternary Complex Of 7,8-Dihydro-6- Hydroxymethylpterinpyrophosphokinase From Escherichia Coli With Atp And A Substrate Analogue. pdb 1EQ0 A Chain A, Crystal Structure Of A Ternary Complex Of 6- Hydroxymethyl-7, 8-Dihydropterin Pyrophosphokinase From E. Coli With Mgampcpp And 6-Hydroxymethyl-7,8- Dihydropterin At 1.25 Angstrom Resolution pdb 1HKA 6-Hydroxymethyl-7,8- Dihydropterin Pyrophosphokinase pir B82680 pteridine reductase 1 XF1457 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84266.1 AE003975_9 (AE003975) pteridine reductase 1 [Xylella fastidiosa] </p>	SEQ ID n-3019
SEQ ID n° 6069	PL-1114.1	Contig9 from 185686 to 186450	m 59%	<p> emb CAC01604.1 (AJ269505) peptide synthetase [Anabaena sp. 90] pir C81683 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain TC0618 [similarity] - Chlamydia muridarum (strain Nigg) gb AAF39449.1 (AE002330) 2-oxoisovalerate dehydrogenase; E1 component, alpha and beta subunit [Chlamydia muridarum] sp Q9ZDY5 Y178_RICPR HYPOTHETICAL PROTEIN RP178 pir F71728 hypothetical protein RP178 - Rickettsia prowazekii emb CAA14645.1 (AJ235270) unknown [Rickettsia prowazekii] </p>	SEQ ID n-169
SEQ ID n° 6070	PL-1115.1	Contig9 from 186495 to 187856	m No Hits found	SEQ ID n-170	
SEQ ID n° 6071	PL-1116.1	Contig9 from 187863 to 190670	m 29%	SEQ ID n-171	
SEQ ID n° 6072	PL-1117.1	Contig9 from 190712 to 192664	m 47%	SEQ ID n-172	
SEQ ID n° 6073	PL-3846.1	Contig9 from 192699 to 193283	m 36%	SEQ ID n-3018	

TABLEAU II

SEQ ID n° 6065 PL-4576.1	Contig9 from 182307 to 182843	m	78%	sp P75966 YMF_ECOLI_HYPOTHETICAL_24.9_KDA PROTEIN IN TRMU-ICDA INTERGENIC REGION dbj BAA35957.1 (D90748) Hypothetical protein HI0694 [Escherichia coli] dbj BAA35966.1 (D90749) Hypothetical protein HI0694 [Escherichia coli]	#N/A
SEQ ID n° 6066 PL-1113.2	Contig9 from 183076 to 184329	p	95%	sp P08200 IDH_ECOLI_ISOCITRATE_DEHYDROGENASE [NADP] (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP) pir [DCECIS isocitrate dehydrogenase (NADP+)] (EC 1.1.1.42) [validated] - Escherichia coli pdb 1AI2 Isocitrate Dehydrogenase Complexed With Isocitrate, NADP+, And Calcium (Flash-Cooled) pdb 1AI3 Orbital Steering In The Catalytic Power Of Enzymes: Small Structural Changes With Large Catalytic Consequences pdb 1IKA Isocitrate Dehydrogenase (E.C.1.1.1.42) Complexed With Alpha-Ketoglutarate pdb 1SJS Access To Phosphorylation In Isocitrate Dehydrogenase May Occur By Domain Shifting pdb 5ICD Isocitrate Dehydrogenase (E.C.1.1.1.42) Complex With Mg2+ And Isocitrate pdb 9ICD Isocitrate Dehydrogenase (E.C.1.1.1.42) Complex With NADP+ pdb 3ICD Isocitrate dehydrogenase (E.C.1.1.1.42) gb AAA24006.1 (J02799) isocitrate dehydrogenase (icd; EC 1.1.1.42) [Escherichia coli] dbj BAA35958.1 (D90748) Isocitrate dehydrogenase (NADP) (EC emb CAC22108.1 (AL512862) hypothetical repeat containing protein; duplicated in S pombe [Schizosaccharomyces pombe]	#N/A
SEQ ID n° 6067 PL-4574.1	Contig9 from 184449 to 184844	p	33%		#N/A

TABLEAU II

SEQ ID n° 6059 PL-1109.1	Contig9 from 177748 to 178416	m	79%	emb CAA47148.1 (X66587) phop [Versinia pseudotuberculosis]	SEQ ID n-163
SEQ ID n° 6060 PL-4577.1	Contig9 from 178508 to 178696	p	No Hits found		#N/A
SEQ ID n° 6061 PL-1110.1	Contig9 from 178654 to 180024	m	81%	gb AAG55957.1 AE005329_1 (AE005329) adenylosuccinate lyase [Escherichia coli O157:H7]	SEQ ID n-165
SEQ ID n° 6062 PL-1111.1	Contig9 from 180048 to 180674	m	72%	sp P25746 YCFC_ECOLI HYPOTHETICAL 22.9 KDA PROTEIN IN PURB-ICDA INTERGENIC REGION (ORF-23) pir S19211 ycfC protein - Escherichia coli emb CAA41995.1 (X59307) ORF-23 [Escherichia coli] gb AAC74216.1 (AE000213) orf, hypothetical protein [Escherichia coli K12] dbj BAA35954.1 (D90748) Hypothetical protein 23. [Escherichia coli] dbj BAA35963.1 (D90749) Hypothetical protein 23. [Escherichia coli]	SEQ ID n-166
SEQ ID n° 6063 PL-1112.1	Contig9 from 180677 to 181780	m	90%	gb AAG55959.1 AE005329_3 (AE005329) orf, hypothetical protein [Escherichia coli O157:H7] sp P75965 YMF8_ECOLI HYPOTHETICAL 17.4 KDA PROTEIN IN TRMU-ICD INTERGENIC REGION pir C64858 probable dNTP pyrophosphohydrolase b1134 - Escherichia coli gb AAC74218.1 (AE000213) putative phosphohydrolase [Escherichia coli K12] dbj BAA35956.1 (D90748) Hypothetical protein YGL067w [Escherichia coli] dbj BAA35965.1 (D90749) Hypothetical protein YGL067w [Escherichia coli]	SEQ ID n-167
SEQ ID n° 6064 PL-3848.2	Contig9 from 181865 to 182335	m	74%	gb AAG55960.1 AE005329_4 (AE005329) putative phosphohydrolase [Escherichia coli O157:H7]	#N/A

TABLEAU II

SEQ ID n° 6051	PL-1101.1	Contig9 from 165827 to 169273	m	87%	sp P30958 MFD_ECOLI_TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) pir [G64855 transcription/repair-coupling protein - Escherichia coli dbj BAA35929.1 (D90746) transcription-repair coupling protein mfd [Escherichia coli] dbj BAA35934.1 (D90747) transcription-repair coupling protein mfd [Escherichia coli] gb AAC74198.1 (AE000211) transcription-repair coupling factor; mutation frequency decline [Escherichia coli K12]	SEQ ID n-255
SEQ ID n° 6052	PL-1102.1	Contig9 from 169471 to 170673	p	82%	dbj BAA35936.1 (D90747) Hypothetical protein HI1555 [Escherichia coli]	SEQ ID n-256
SEQ ID n° 6053	PL-1103.1	Contig9 from 170666 to 171370	p	75%	dbj BAA35937.1 (D90747) Heterocyst maturation protein (devA) homolog [Escherichia coli]	SEQ ID n-257
SEQ ID n° 6054	PL-1104.1	Contig9 from 171370 to 172617	p	82%	gb AAG55864.1 AE005321.7 (AE005321) putative kinase [Escherichia coli O157:H7]	SEQ ID n-258
SEQ ID n° 6055	PL-1105.1	Contig9 from 172709 to 173560	p	77%	pir [E64856 hypothetical protein b1120 - Escherichia coli gb AAC74204.1 (AE000212) putative nicotinic acid mononucleotide:5,6-dimethylbenzimidazole (DMB) phosphoribosyltransferase [Escherichia coli K12] dbj BAA35940.1 (D90747) ORF_ID:0238#9 [Escherichia coli]	SEQ ID n-259
SEQ ID n° 6056	PL-1106.1	Contig9 from 173616 to 174881	p	80%	gb AAG55931.1 AE005327.1 (AE005327) putative peptidase T [Escherichia coli O157:H7]	SEQ ID n-260
SEQ ID n° 6057	PL-1107.1	Contig9 from 175060 to 176181	m	80%	pir [E64857 ycfD protein - Escherichia coli gb AAC74212.1 (AE000213) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-261
SEQ ID n° 6058	PL-1108.1	Contig9 from 176265 to 177728	m	82%	gb AAC38776.1 (AF041833) putative sensor kinase [Providencia stuartii]	SEQ ID n-262

TABLEAU II

SEQ ID n° 57679	NTPA_METJA NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE) (NTPASE) pir C64328 conserved hypothetical protein MJ0226 - Methanococcus jannaschii pdb 2MJP A Chain A, Structure-Based Identification Of The Biochemical Function Of A Hypothetical Protein From Methanococcus Jannaschii:mj0226 pdb 2MJP B Chain B, Structure- Based Identification Of The Biochemical Function Of A Hypothetical Protein From Methanococcus Jannaschii:mj0226 pdb 1B78 A Chain A, Structure- Based Identification Of The Biochemical Function Of A Hypothetical Protein From Methanococcus Jannaschii:mj0226 pdb 1B78 B Chain B, Structure- Based Identification Of The Biochemical Function Of A Hypothetical Protein From Methanococcus Jannaschii:mj0226 gb AAB98211.1 (U67478) conserved hypothetical protein [Methanococcus jannaschii]	Contig9 from 161608 to 162114	m	31%	SEQ ID n-3021
SEQ ID n° 6048	PL-4579.1	Contig9 from 162507 to 162794	p	No Hits found	#N/A
SEQ ID n° 6049	PL-1099.1	Contig9 from 163274 to 164119	m	53%	SEQ ID n-151
SEQ ID n° 6050	PL-1100.1	Contig9 from 164131 to 165108	m	67%	SEQ ID n-154

TABLEAU II

SEQ ID n° 6043	PL-1095.1	Contig9 from 155330 to 156193	P 42%	gp AAG55852.1 AE005320_6 (AE005320) putative beta-glucosidase (EC 3.2.1.21) [Escherichia coli O157:H7] sp P75949 YCFO_EC01 HYPOTHETICAL 37.6 KDA PROTEIN IN FHUE-NDH INTERGENIC REGION pir H64854 probable glucosidase (EC 3.2.1.-) ycfo - Escherichia coli gb AAC74191.1 (AE000211) orf, hypothetical protein [Escherichia coli K12] dbj BAA35914.1 (D90745) Hypothetical protein HI0959 [Escherichia coli] dbj BAA35922.1 (D90746) Hypothetical protein HI0959 [Escherichia coli] sp P00393 DHNA_EC01 NADH DEHYDROGENASE pir DEECR NADH dehydrogenase (EC 1.6.99.3) [validated] - Escherichia coli emb CAA23586.1 (V00306) NADH dehydrogenase [Escherichia coli] dbj BAA35924.1 (D90746) NADH dehydrogenase (EC 1.6.99.3) [Escherichia coli] gb AAC74193.1 (AE000211) respiratory NADH dehydrogenase [Escherichia coli K12] emb CAB69803.1 (AJ243711) putative subtilase family serine protease [Bacillus cereus]	SEQ ID n-147
SEQ ID n° 6044	PL-1096.1	Contig9 from 156316 to 157338	P 80%		SEQ ID n-148
SEQ ID n° 6045	PL-1097.1	Contig9 from 157744 to 159048	P 87%		
SEQ ID n° 6046	PL-1098.1	Contig9 from 159135 to 160811	M 24%		SEQ ID n-150

TABLEAU II

SEQ ID n° 6039	PL-1092.1	Contig9 from 152239 to 153228	p 62%	sp P28631 HOLB_ECOLI DNA POLYMERASE III, DELTA' SUBUNIT pir S35523 DNA-directed DNA polymerase (EC 2.7.7.7) III delta' chain - Escherichia coli pdb 1A5T Crystal Structure Of The Delta Prime Subunit Of The Clamp-Loader Complex Of Escherichia Coli Dna Polymerase Iii gb AAA23696.1 [I01483] DNA polymerase III delta prime subunit [Escherichia coli] dbj BAA35906.1 (D90745) DNA-directed dna polymerase (EC 2.7.7.7) III delta' chain [Escherichia coli] gb AAC74183.1 (AE000210) DNA polymerase III, delta prime subunit [Escherichia coli K12] SEQ ID n-144
SEQ ID n° 6040	PL-1093.1	Contig9 from 153254 to 154039	p 78%	sp P37346 YCFH_ECOLI PUTATIVE DEOXYRIBONUCLEASE ycfH pir A64854 probable metal-dependent hydrolase (EC 3.-.-.-) ycfH - Escherichia coli gb AAC74184.1 (AE000210) orf, hypothetical protein [Escherichia coli K12] dbj BAA35907.1 (D90745) Hypothetical protein in holB 3'region . [Escherichia coli] gb AAG55846.1 AE005319_15 (AE005319) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-145 sp P36950 YCFH_ECOLI HIT-LIKE PROTEIN YCFH pir JCS685 histidine triad-like protein ycfH - Escherichia coli gb AAC74187.1 (AE000211) orf, hypothetical protein [Escherichia coli K12] dbj BAA35910.1 (D90745) Hypothetical protein HI0961 [Escherichia coli] dbj BAA35918.1 (D90746) Hypothetical protein HI0961 [Escherichia coli] gb AAG55849.1 AE005320_3 (AE005320) orf, hypothetical protein [Escherichia coli O157:H7] dbj BAA35912.1 (D90745) Fibronectin-binding protein B [Escherichia coli] dbj BAA35920.1 (D90746) Fibronectin-binding protein B [Escherichia coli] SEQ ID n-146
SEQ ID n° 6041	PL-4580.1	Contig9 from 154110 to 154466	p 86%	
SEQ ID n° 6042	PL-1094.1	Contig9 from 154774 to 155343	p 56%	#N/A

TABLEAU II

SEQ ID n° 6035	PL-1088.1	Contig9 from 148085 to 149335	P 86%	sp F39435 FABF_ECOLI 3-OXOACYL-[ACYL-CARRIER- PROTEIN] SYNTHASE II (BETA-KETOACYL-ACP SYNTHASE II) (KAS II) pir I41060 3-oxoacyl- [acyl-carrier-protein] synthase (EC 2.3.1.41) II Escherichia coli emb CAA84431.1 (Z34979) beta ketoacyl-acyl carrier protein synthase [Escherichia coli] gb AAA83255.1 (U20767) beta-ketoacyl-acyl carrier protein synthase II [Escherichia coli] gb AAC74179.1 (AE000210) 3- oxoacyl-[acyl-carrier-protein] synthase II [Escherichia coli K12] dbj BAA35903.1 (D90745) 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II [Escherichia coli] gb AAG55841.1 AE005319_10 (AE005319) 3-oxoacyl- [acyl-carrier-protein] synthase II [Escherichia coli O157:H7] gb AAG55842.1 AE005319_11 (AE005319) 4-amino-4- deoxychorismate lyase [Escherichia coli O157:H7] sp P28306 YCEG_ECOLI HYPOTHETICAL 38.2 KD PROTEIN IN PABC-HOLB INTERGENIC REGION pir P64853 yceG protein precursor - Escherichia coli gb AAC74181.1 (AE000210) putative thymidylate kinase (EC 2.7.4.9) [Escherichia coli K12] sp O69169 KTHY_YERPE THYMIDYLATE KINASE (DTMP KINASE) gb AAC18855.1 (AF065312) thymidylate kinase [Yersinia pestis]	SEQ ID n-139
SEQ ID n° 6036	PL-1089.1	Contig9 from 149690 to 150514	P 65%	SEQ ID n-140	
SEQ ID n° 6037	PL-1090.1	Contig9 from 150579 to 151595	P 70%		
SEQ ID n° 6038	PL-1091.1	Contig9 from 151601 to 152239	P 80%	SEQ ID n-142	
				SEQ ID n-143	

TABLEAU II

SEQ ID n° 6032	PL-1086.1	Contig9 from 145946 to 146878	P	84%	sp P25715 FABD_ECOLI MALONYL COA-ACYL CARRIER PROTEIN TRANSACYLASE (MCT) pir B41856 [acyl- carrier-protein] s-malonyltransferase (EC 2.3.1.39) fabD [validated] - Escherichia coli pdb 1MLA Mol_id: 1; Molecule: Malonyl-Coenzyme A Acyl Carrier Protein Transacylase; Chain: Null; Synonym: Malonyl-CoA Acp Transacylase; Engineered: Yes emb CAA7658.1 (z11565) malonyl CoA-acyl carrier protein transacylase [Escherichia coli] gb AA23742.1 (M87040) malonyl coenzyme A-acyl carrier protein transacylase [Escherichia coli] dbj BAA35900.1 (D90745) [Acyl-carrier-protein] s-malonyltransferase (EC 2.3.1.39). [Escherichia coli] gb AAC74176.1 (AE000210) malonyl-CoA-[acyl- carrier-protein] transacylase [Escherichia coli K12]	SEQ ID n-137
SEQ ID n° 6033	PL-1087.1	Contig9 from 146886 to 147620	P	80%	sp P25716 FABG_ECOLI 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE) pir B42147 3-oxoacyl-[acyl- carrier-protein] reductase (EC 1.1.1.100) - Escherichia coli dbj BAA35901.1 (D90745) 3- oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100). [Escherichia coli] gb AAC74177.1 (AE000210) 3-oxoacyl-[acyl- carrier-protein] reductase [Escherichia coli K12]	SEQ ID n-338
SEQ ID n° 6034	PL-4582.1	Contig9 from 147775 to 148011	P	74%	gb AAG42370.1 AF294440_2 (AF294440) acyl carrier protein [Xanthomonas albilineans]	#N/A

TABLEAU II

SEQ ID n° 6028	PL-3850.1	Contig9 from 143188 to 143712	P	84%	sp P14189 YCED_ECOLI_HYPOTHETICAL_19.3_KDA PROTEIN IN RNE-RPMF INTERGENIC REGION (G30K) pir JV0047_probable membrane protein yced - Escherichia coli gb AAA24574.1 (M29698) g30k protein [Escherichia coli] gb AAC74172.1 (AE000209) orf, hypothetical protein [Escherichia coli K12] dbj BAA35896.1 (D90744) Hypothetical 19.3 kd protein in rne-rpmf intergenic region (g30k). [Escherichia coli] gb AAG55834.1 AE005319_3 (AE005319) orf, hypothetical protein [Escherichia coli O157:H7] sp P02435 RL32_ECOLI_50S_RIBOSOMAL_PROTEIN_L32 pir RSEC32_ribosomal protein L32 [validated] - Escherichia coli gb AA24575.1 (M29698) ribosomal protein L32 [Escherichia coli] dbj BAA35897.1 (D90744) Ribosomal protein L32. [Escherichia coli] gb AAC74173.1 (AE000209) 50S ribosomal subunit protein L32 [Escherichia coli K12] gb AAC38646.1 (AF044668) 50S ribosomal protein L32 [Salmonella typhimurium] gb AAG55835.1 AE005319_4 (AE005319) 50S ribosomal subunit protein L32 [Escherichia coli O157:H7] #N/A SEQ ID n° 3023
SEQ ID n° 6029	PL-4585.1	Contig9 from 143725 to 143895	P	85%	sp O85139 FABH_SALTY_FATTY_ACID/PHOSPHOLIPID SYNTHESIS PROTEIN PLSX sp O85139 FABH_SALTY_3-OXOACYL-[ACYL-CARRIER- PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) gb AAC38648.1 (AF044668) 3-oxoacyl-acyl carrier protein synthase III [Salmonella typhimurium] SEQ ID n° 136
SEQ ID n° 6030	PL-1084.1	Contig9 from 143924 to 144961	P	84%	sp O85138 PLSX_SALTY_FATTY_ACID/PHOSPHOLIPID SYNTHESIS PROTEIN PLSX sp O85139 FABH_SALTY_3-OXOACYL-[ACYL-CARRIER- PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) gb AAC38648.1 (AF044668) 3-oxoacyl-acyl carrier protein synthase III [Salmonella typhimurium] SEQ ID n° 136
SEQ ID n° 6031	PL-1085.1	Contig9 from 144968 to 145921	P	85%	sp O85139 FABH_SALTY_3-OXOACYL-[ACYL-CARRIER- PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) gb AAC38648.1 (AF044668) 3-oxoacyl-acyl carrier protein synthase III [Salmonella typhimurium] SEQ ID n° 136

TABLEAU II

SEQ ID n° 6023 PL-4587.1	Contig9 from 136656 to 136973	p 88%	pir [F64965 hypothetical protein b2007 - Escherichia coli dbj BAA15828.1 (D90838) ORF_ID:0348#19-similar to [SwissProt Accession Number P44117] [Escherichia coli] dbj BAA15835.1 (D90839) ORF_ID:0348#19; similar to [SwissProt Accession Number P44117] [Escherichia coli] gb AAC75068.1 (AE000292) putative alpha helix protein [Escherichia coli K12] gb AGS7066.1 AE005426_8 (AE005426) putative alpha helix protein [Escherichia coli O157:H7] pir T12067 hypothetical protein Y - Yersinia pestis gb AAC64864.1 (U60647) unknown [Yersinia pestis] gb AAG55830.1 AE005318_7 (AE005318) RNase E, membrane attachment, mRNA turnover, maturation 5S RNA [Escherichia coli O157:H7] sp P23851 RLUC_ECOLI RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) pir [C64852 probable pseudouridylylate synthase yceC - Escherichia coli gb AAC74170.1 (AE000209) orf, hypothetical protein [Escherichia coli K12] dbj BAA35894.1 (D90744) Hypothetical 36.0 kd protein in rne-rpmF intergenic region (orf). [Escherichia coli] sp P27244 YCEF_ECOLI HYPOTHETICAL 23.2 KDA PROTEIN IN RNE-RPMF INTERGENIC REGION (ORFY) pir [D64852 ycef protein - Escherichia coli gb AAA23829.1 (M96791) orfy [Escherichia coli] gb AAC74171.1 (AE000209) orf, hypothetical protein [Escherichia coli K12] dbj BAA35895.1 (D90744) Hypothetical 23.2 kd protein in rne- rpmF intergenic region (orf). [Escherichia coli]	#N/A	SEQ ID n-130
SEQ ID n° 6024 PL-1079.1	Contig9 from 137018 to 137650	m 66%			SEQ ID n-132
SEQ ID n° 6025 PL-1080.1	Contig9 from 137835 to 140939	m 76%			
SEQ ID n° 6026 PL-1081.1	Contig9 from 141499 to 142458	p 83%			
SEQ ID n° 6027 PL-1082.1	Contig9 from 142455 to 143063	m 73%			SEQ ID n-134

TABLEAU II

SEQ ID n° 6019	PL-1077.1	Contig9 from 131984 to 133414	m	80%	sp P04995 EX1_ECOLI EXODEOXYRIBONUCLEASE I (EXONUCLEASE I) (DNA DEOXYRIBOPHOSPHODIESTERASE) (DRPASE) pir [NCECX1 exodeoxyribonuclease I (EC 3.1.11.1) - Escherichia coli gb AA16417.1 (U00009) exonuclease I [Escherichia coli] dbj BAA15839.1 (D90839) Exodeoxyribonuclease I (EC 3.1.11.1) (Exonuclease I) (DNA deoxyribophosphodiesterase) (DRPase). [Escherichia coli] dbj BAA15844.1 (D90840) Exodeoxyribonuclease I (EC 3.1.11.1) (Exonuclease I) (DNA deoxyribophosphodiesterase) (DRPase). [Escherichia coli] gb AAC75072.1 (AF000292) exonuclease I, 3' --> 5' specific; deoxyribophosphodiesterase [Escherichia coli K12] ref NP_046944.1 gp48 [Bacteriophage N15] pir [T13135 protein gp48 - phage N15 gb AAC19087.1 (AF064539) gp48 [Bacteriophage N15] ref NP_046945.1 gp49 [Bacteriophage N15] pir [T13136 protein gp49 - phage N15 gb AAC19088.1 (AF064539) gp49 [Bacteriophage N15]	SEQ ID n°128
SEQ ID n° 6020	PL-4592.1	Contig9 from 133570 to 133851	m	51%		#N/A
SEQ ID n° 6021	PL-4591.1	Contig9 from 133868 to 134197	m	47%		#N/A
SEQ ID n° 6022	PL-4590.1	Contig9 from 134279 to 134479	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6016 PL-1074.1	Contig9 from 125866 to 127845	p 64%	sp P27772 IRGA_VIBCH IRON-REGULATED OUTER MEMBRANE VIRULENCE PROTEIN PRECURSOR	SEQ ID n-125
			pir D82317 iron-regulated outer membrane virulence protein, TonB receptor	
			family VC0475 [imported] - Vibrio cholerae (group O1 strain N16961)	
SEQ ID n° 6017 PL-1075.1	Contig9 from 128564 to 129946	p 80%	gb AAF93648.1 (AE004134) iron-regulated outer membrane virulence protein, TonB receptor family [Vibrio cholerae] sp P33016 YEEF_ECOLI HYPOTHETICAL 49.8 KD TRANSPORT PROTEIN IN SBCB-HISL INTERGENIC REGION pir [E64966 probable amino acid permease yeef - Escherichia coli gb AA16420.1 (U00009) yeef [Escherichia coli] dbj BAA15842.1 (D90839) Proline transport protein [Escherichia coli] dbj BAA15847.1 (D90840) Proline transport protein [Escherichia coli] gb AAC75075.1 (AE000293) putative amino acid/amine transport protein [Escherichia coli K12] gb AAG57073.1 AE005427.1 (AE005427) putative amino acid/amine transport protein [Escherichia coli O157:H7] sp P06149 DLD_ECOLI D-LACTATE DEHYDROGENASE pir [DEECDL D-lactate dehydrogenase (EC 1.1.1.28) - Escherichia coli pdb 1FOX A Chain A, Crystal Structure Of D-lactate Dehydrogenase, A Peripheral Membrane Respiratory Enzyme. pdb 1FOX B Chain B, Crystal Structure Of D-lactate Dehydrogenase, A Peripheral Membrane Respiratory Enzyme. emb CAA25531.1 (X01067) D-lactate dehydrogenase [Escherichia coli] gb AAA23698.1 (M10038) D-lactate dehydrogenase [Escherichia coli] gb AAC75194.1 (AE000302) D-lactate dehydrogenase, FAD protein, NADH independent [Escherichia coli K12]	SEQ ID n-126
SEQ ID n° 6018 PL-1076.1	Contig9 from 130141 to 131856	p 81%		SEQ ID n-127

TABLEAU II

SEQ ID n° 6011	PL-1069.1	Contig9 from 119742 to 120605	p	81%	sp P32484 YEIE_ECOLI_HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN LYSP-NFO INTERGENIC REGION pir D64984 hypothetical transcription regulator lyss-nfo intergenic region - Escherichia coli (strain K-12) gb AA060508.1 (U00007) yeie [Escherichia coli] gb AA017052.1 (M89774) ORF 1 function unknown [Escherichia coli] gb AAC75218.1 (AE000305) putative transcriptional regulator LYSR-type [Escherichia coli K12] gb AAG57295.1 AE005448_2 (AE005448) putative transcriptional regulator LYSR-type [Escherichia coli O157:H7] prf 2014253BC yeie gene [Escherichia coli] SEQ ID n-119 pir C64984 lysine-specific permease - Escherichia coli gb AA017053.1 (M89774) lysine specific permease [Escherichia coli] gb AAC75217.1 (AE000305) lysine-specific permease [Escherichia coli K12] pir E72406 hypothetical protein TM0189 - Thermotoga maritima (strain MSB8) gb AAD35281.1 AE001704_2 (AE001704) iron(III) ABC transporter, periplasmic iron-binding protein, putative [Thermotoga maritima] pir F71067 probable ferrichrome transport permease protein - Pyrococcus horikoshii dbj BAA30336.1 (AP000005) 343aa long hypothetical ferrichrome transport permease protein [Pyrococcus horikoshii] sp Q57554 Y089_METHA_HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0089 pir A64311 ferric enterobactin transport ATP- binding protein homolog - Methanococcus jannaschii gb AAB98070.1 (U67466) ferric enterobactin transport ATP- binding protein [Methanococcus jannaschii] SEQ ID n-124
SEQ ID n° 6012	PL-1070.1	Contig9 from 120760 to 122241	p	85%	pir E72406 hypothetical protein TM0189 - Thermotoga maritima (strain MSB8) gb AAD35281.1 AE001704_2 (AE001704) iron(III) ABC transporter, periplasmic iron-binding protein, putative [Thermotoga maritima] pir F71067 probable ferrichrome transport permease protein - Pyrococcus horikoshii dbj BAA30336.1 (AP000005) 343aa long hypothetical ferrichrome transport permease protein [Pyrococcus horikoshii] sp Q57554 Y089_METHA_HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0089 pir A64311 ferric enterobactin transport ATP- binding protein homolog - Methanococcus jannaschii gb AAB98070.1 (U67466) ferric enterobactin transport ATP- binding protein [Methanococcus jannaschii] SEQ ID n-124
SEQ ID n° 6013	PL-1071.1	Contig9 from 122704 to 123828	p	40%	pir E72406 hypothetical protein TM0189 - Thermotoga maritima (strain MSB8) gb AAD35281.1 AE001704_2 (AE001704) iron(III) ABC transporter, periplasmic iron-binding protein, putative [Thermotoga maritima] pir F71067 probable ferrichrome transport permease protein - Pyrococcus horikoshii dbj BAA30336.1 (AP000005) 343aa long hypothetical ferrichrome transport permease protein [Pyrococcus horikoshii] sp Q57554 Y089_METHA_HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0089 pir A64311 ferric enterobactin transport ATP- binding protein homolog - Methanococcus jannaschii gb AAB98070.1 (U67466) ferric enterobactin transport ATP- binding protein [Methanococcus jannaschii] SEQ ID n-124
SEQ ID n° 6014	PL-1072.1	Contig9 from 123952 to 124938	p	54%	pir E72406 hypothetical protein TM0189 - Thermotoga maritima (strain MSB8) gb AAD35281.1 AE001704_2 (AE001704) iron(III) ABC transporter, periplasmic iron-binding protein, putative [Thermotoga maritima] pir F71067 probable ferrichrome transport permease protein - Pyrococcus horikoshii dbj BAA30336.1 (AP000005) 343aa long hypothetical ferrichrome transport permease protein [Pyrococcus horikoshii] sp Q57554 Y089_METHA_HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0089 pir A64311 ferric enterobactin transport ATP- binding protein homolog - Methanococcus jannaschii gb AAB98070.1 (U67466) ferric enterobactin transport ATP- binding protein [Methanococcus jannaschii] SEQ ID n-124
SEQ ID n° 6015	PL-1073.1	Contig9 from 124935 to 125735	p	57%	pir E72406 hypothetical protein TM0189 - Thermotoga maritima (strain MSB8) gb AAD35281.1 AE001704_2 (AE001704) iron(III) ABC transporter, periplasmic iron-binding protein, putative [Thermotoga maritima] pir F71067 probable ferrichrome transport permease protein - Pyrococcus horikoshii dbj BAA30336.1 (AP000005) 343aa long hypothetical ferrichrome transport permease protein [Pyrococcus horikoshii] sp Q57554 Y089_METHA_HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN MJ0089 pir A64311 ferric enterobactin transport ATP- binding protein homolog - Methanococcus jannaschii gb AAB98070.1 (U67466) ferric enterobactin transport ATP- binding protein [Methanococcus jannaschii] SEQ ID n-124

TABLEAU II

SEQ ID n° 6008 PL-1066.1	Contig9 from 116547 to 117485	p	85%	sp P23539 K1PF_ECOLI_1-PHOSPHOFRUCTOKINASE (FRUCTOSE 1-PHOSPHATE KINASE) pir B37245 1- phosphofructokinase (EC 2.7.1.56) - Escherichia coli emb CAA37896.1 (X53948) 1- phosphofructokinase [Escherichia coli] gb AA60525.1 (U00007) 1-phosphofructokinase [Escherichia coli] dbj BA15977.1 (D90849) 1- phosphofructokinase (EC 2.7.1.56) (Fructose 1- phosphate kinase). [Escherichia coli] gb AAC75229.1 (AE000306) fructose-1-phosphate kinase [Escherichia coli K12] gb AAG57306.1 AB005449_4 (AE005449) fructose-1- phosphate kinase [Escherichia coli O157:H7] prf 2014253BP fruk gene [Escherichia coli] SEQ ID n-216
				sp P12638 END4_ECOLI_ENDONUCLEASE IV (ENDODEOXYRIBONUCLEASE IV) pir NDEC4 deoxyribonuclease IV (phage-T4-induced) (EC 3.1.21.2) - Escherichia coli pdb 1QUM A Chain A, Crystal Structure Of Escherichia Coli Endonuclease IV In Complex With Damaged Dna gb AAC75220.1 (AE000305) endonuclease IV [Escherichia coli K12] SEQ ID n-217
SEQ ID n° 6009 PL-1067.1	Contig9 from 117505 to 118347	m	82%	sp P33019 YEIH_ECOLI_HYPOTHETICAL 36.9 KD PROTEIN IN LYSP-NFO INTERGENIC REGION pir B64984 hypothetical 36.9 kD protein in lyssp- nfo intergenic region - Escherichia coli (strain X-12) gb AA60511.1 (U00007) yeih [Escherichia coli] gb AAC75219.1 (AE000305) orf, hypothetical protein [Escherichia coli K12] prf 2014253BD yeih gene [Escherichia coli] SEQ ID n-218
				Contig9 from 118470 to 119552

TABLEAU II

SEQ ID n° 6002	PL-1062.1	Contig9 from 111099 to 111689	m	74%	sp F77685 SER_ECOLI LIPOPROTEIN SPR PRECURSOR pir E64986 hypothetical protein b2175 - Escherichia coli (strain K-12) dbj BAI13140.1 (D86610) Spr [Escherichia coli] dbj BAI15983.1 (D90849) Probable lipoprotein NlpC homolog precursor. [Escherichia coli] gb AAC75236.1 (AE000307) putative lipoprotein [Escherichia coli K12] gb AAG57313.1 AE005450_3 (AE005450) putative lipoprotein [Escherichia coli O157:H7]	SEQ ID n-212
SEQ ID n° 6003	PL-1063.1	Contig9 from 112038 to 112742	m	70%	pir E64986 hypothetical protein b2174 - Escherichia coli (strain K-12) gb AAC75235.1 (AE000307) orf, hypothetical protein [Escherichia coli K12] gb AAG57312.1 AE005450_2 (AE005450) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-213
SEQ ID n° 6004	PL-4595.1	Contig9 from 113181 to 113492	p	No Hits found		#N/A
SEQ ID n° 6005	PL-1064.1	Contig9 from 113843 to 114415	m	85%	gb AAG57309.1 AE005449_7 (AE005449) putative elongation factor [Escherichia coli O157:H7] pir E82966 tryptophan permease PA5434 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08819.1 AE004956_3 (AE004956) tryptophan permease [Pseudomonas aeruginosa]	SEQ ID n-214
SEQ ID n° 6006	PL-1065.1	Contig9 from 114548 to 115807	m	64%	gb AAG52038.1 AC011914_8 (AC011914) putative mutT protein; 68398-67881 [Arabidopsis thaliana]	SEQ ID n-215
SEQ ID n° 6007	PL-4594.1	Contig9 from 115923 to 116342	m	47%		#N/A

TABLEAU II

SEQ ID n° 5998	PL-1059.1	Contig9 from 105467 to 107224	m	79%	gd AAG57322.1 AE005451.3 (AE005451) putative ATP- dependent helicase [Escherichia coli O157:H7]	SEQ ID n°108
SEQ ID n° 5999	PL-1060.1	Contig9 from 107514 to 108215	p	79%	sp P33918 RSUA_ECOLI_RIBOSOMAL_SMALL_SUBUNIT PSEUDOURIDINE SYNTHASE A (16S PSEUDOURIDYLATE 516 SYNTHASE) (16S PSEUDOURIDINE 516 SYNTHASE) (URACIL HYDROLASE) pir P64987 hypothetical 25.9 kD protein in bcr- xply intergenic region - Escherichia coli (strain K-12) gb AAAL6377.1 (U00008) yejD [Escherichia coli] gb AB34905.1 16S RNA pseudouridine 516 synthase, 16S RNA psi 516 synthase-rsua gene product [Escherichia coli, Peptide, 231 aa] gb AAC75244.1 (AE000308) 16S pseudouridylylate 516 synthase [Escherichia coli K12] gb AAG57321.1 AE005451.2 (AE005451) 16S pseudouridylylate 516 synthase [Escherichia coli O157:H7]	SEQ ID n°110
SEQ ID n° 6000	PL-1061.1	Contig9 from 108259 to 109443	p	77%	gb AAG57320.1 AE005451.1 (AE005451) bicyclomycin resistance protein; transmembrane protein [Escherichia coli O157:H7] sp P33917 YEJG_ECOLI_HYPOTHETICAL_12.5_KD PROTEIN IN RTN-BCR INTERGENIC REGION pir D64987 hypothetical 12.5 kD protein in bcr 5' region - Escherichia coli (strain K- 12) gb AAAL6380.1 (U00008) yejG [Escherichia coli] gb AAC75242.1 (AE000307) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n°111
SEQ ID n° 6001	PL-4596.1	Contig9 from 110543 to 110887	p	71%		#N/A

TABLEAU II

SEQ ID n° 5992	PL-1055.1	Contig9 from 99412 to 100734	p	19%	pir SI8687 Sc/SVN protein - Escherichia coli plasmid p15B emb CAA44050.1 (X62121) DNA inversion product [Escherichia coli] gb AAG56009.1 AE005333.6 (AE005333) putative tail fiber protein of prophage CP-933X [Escherichia coli O157:H7] sp P33922 YEJM_ECOLI HYPOTHETICAL 67.3 KD PROTEIN IN RPLY-PROL INTERGENIC REGION	SEQ ID n-204
SEQ ID n° 5993	PL-1056.1	Contig9 from 100734 to 101360	p	47%	pir C64988 hypothetical 67.3 kD protein in rply- proL intergenic region - Escherichia coli (strain K-12) gb AAA16384.1 (U00008) yejM [Escherichia coli] gb AAC75249.1 (AE000308) putative sulfatase [Escherichia coli K12] gb AAG57326.1 AE005451.7 (AE005451) putative sulfatase [Escherichia coli O157:H7] sp P33921 YEJL_ECOLI HYPOTHETICAL 8.3 KD PROTEIN IN RPLY-PROL INTERGENIC REGION pir B64988 hypothetical 8.3 kD protein in rply-proL intergenic region - Escherichia coli (strain K-12) gb AAA16383.1 (U00008) yejL [Escherichia coli] gb AAC75248.1 (AE000308) orf, hypothetical protein [Escherichia coli K12] gb AAG57325.1 AE005451.6 (AE005451) orf, hypothetical protein [Escherichia coli O157:H7] sp P33920 NA37_ECOLI 37 KD NUCLEOID-ASSOCIATED PROTEIN pir A64988 hypothetical 37.8 kD protein in rply-proL intergenic region - Escherichia coli (strain K-12) gb AAA16382.1 (U00008) yejK [Escherichia coli] gb AAC75247.1 (AE000308) orf, hypothetical protein [Escherichia coli K12] pdb 487D N Chain N, Seven Ribosomal Proteins Fitted To A Cryo-Electron Microscopic Map Of The Large 50s Subunit At 7.5 Angstroms Resolution	SEQ ID n-205
SEQ ID n° 5994	PL-1057.1	Contig9 from 101676 to 103415	m	73%	Contig9 from 103448 to 103675	SEQ ID n-206
SEQ ID n° 5995	PL-4598.1	Contig9 from 103448 to 103675	m	84%	Contig9 from 103947 to 104951	SEQ ID n-207
SEQ ID n° 5996	PL-1058.1	Contig9 from 103947 to 104951	p	86%	Contig9 from 105024 to 105308	SEQ ID n-208
SEQ ID n° 5997	PL-4597.1	Contig9 from 105024 to 105308	m	85%		

TABLEAU II

SEQ ID n° 5985 PL-1050.1	Contig9 from 94780 to 95499	P 56%	pir B82661 hypothetical protein XF1591 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84400.1 AE003987_4 (AE003987) hypothetical protein [Xylella fastidiosa]	SEQ ID n-99
SEQ ID n° 5986 PL-4601.1	Contig9 from 95496 to 95834	P 41%	pir C82648 hypothetical protein XF1698 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84507.1 AE003994_6 (AE003994) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 5987 PL-1051.1	Contig9 from 95809 to 96654	P 65%	pir D82661 hypothetical protein XF1593 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84402.1 AE003987_6 (AE003987) hypothetical protein [Xylella fastidiosa]	SEQ ID n-100
SEQ ID n° 5988 PL-1052.1	Contig9 from 96629 to 97300	P 49%	pir E82661 hypothetical protein XF1594 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84403.1 AE003987_7 (AE003987) hypothetical protein [Xylella fastidiosa]	SEQ ID n-101
SEQ ID n° 5989 PL-4600.1	Contig9 from 97297 to 97659	P 52%	pir F82661 hypothetical protein XF1595 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84404.1 AE003987_8 (AE003987) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 5990 PL-1053.1	Contig9 from 97643 to 98776	P 50%	pir A82649 hypothetical protein XF1704 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84513.1 AE003994_12 (AE003994) hypothetical protein [Xylella fastidiosa]	SEQ ID n-102
SEQ ID n° 5991 PL-1054.1	Contig9 from 98769 to 99425	P 46%	pir B82649 hypothetical protein XF1705 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84514.1 AE003994_13 (AE003994) hypothetical protein [Xylella fastidiosa]	SEQ ID n-103

TABLEAU II

SEQ ID n° 5977	PL-4607.1	Contig9 from 89851 to 90246	p 47%	H82651 hypothetical protein XF1690 XF1585 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84394.1 AE003986_24 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84499.1 AE003993_18 (AE003993) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 5978	PL-4606.1	Contig9 from 90282 to 90419	p No Hits found	pir B82652 hypothetical protein XF1692 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84501.1 AE003993_20 (AE003993) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 5979	PL-1048.1	Contig9 from 90394 to 92382	p 31%	pir D83221 hypothetical protein PA3385 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAD55364.1 (AF139988) DNA binding-protein; AlgZ [Pseudomonas aeruginosa] gb AAG06773.1 AE004760_1 (AE004760) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-96 #N/A
SEQ ID n° 5980	PL-4605.1	Contig9 from 92451 to 92738	p No Hits found	ref NP_050115.1 hypothetical protein [Lactobacillus bacteriophage phi adh] emb CAB52485.1 (AJ131519) hypothetical protein [Lactobacillus bacteriophage phi adh] SEQ ID n-97 gb AAG55887.1 AE005323_3 (AE005323) putative Gef. like protein encoded by prophage CP-933N [Escherichia coli O157:H7]	#N/A
SEQ ID n° 5981	PL-4604.1	Contig9 from 92756 to 93031	m 29%		
SEQ ID n° 5982	PL-4603.1	Contig9 from 93142 to 93315	p No Hits found		#N/A
SEQ ID n° 5983	PL-1049.1	Contig9 from 93302 to 94246	p 17%		
SEQ ID n° 5984	PL-4602.1	Contig9 from 94427 to 94633	p 69%		

TABLEAU II

SEQ ID n° 5972 PL-1046.1	Contig9 from 86557 to 87150	p 42%	<p>pir C82651 hypothetical protein XF1685 XF1580 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84389.1 AE003986_19 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84494.1 AE003993_13 (AE003993) hypothetical protein [Xylella fastidiosa] fastidiosa] SEQ ID n-94</p>
SEQ ID n° 5973 PL-4609.1	Contig9 from 87131 to 87481	p 47%	<p>pir C82665 hypothetical protein XF1581 XF1686 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84390.1 AE003986_20 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84495.1 AE003993_14 (AE003993) hypothetical protein [Xylella fastidiosa] fastidiosa] #N/A</p>
SEQ ID n° 5974 PL-3853.1	Contig9 from 87468 to 87899	p 39%	<p>pir E82651 hypothetical protein XF1687 XF1582 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84391.1 AE003986_21 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84496.1 AE003993_15 (AE003993) hypothetical protein [Xylella fastidiosa] fastidiosa] SEQ ID n-3025</p>
SEQ ID n° 5975 PL-1047.1	Contig9 from 87902 to 89413	p 56%	<p>pir F82651 hypothetical protein XF1688 XF1583 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84392.1 AE003986_22 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84497.1 AE003993_16 (AE003993) hypothetical protein [Xylella fastidiosa] fastidiosa] SEQ ID n-95</p>
SEQ ID n° 5976 PL-4608.1	Contig9 from 89423 to 89851	p 52%	<p>pir F82665 hypothetical protein XF1584 XF1689 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84393.1 AE003986_23 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84498.1 AE003993_17 (AE003993) hypothetical protein [Xylella fastidiosa] fastidiosa] #N/A</p>

TABLEAU II

SEQ ID n° 5966 PL-1042.1	Contig9 from 81410 to 82798	p 46%	sp F44183 YE09_HAEMIN HYPOTHETICAL PROTEIN HI1409 pir D64028 hypothetical protein HI1409 - Haemophilus influenzae (strain Rd KW20) gb AAC23057.1 (U32820) H. influenzae predicted coding region HI1409 [Haemophilus influenzae Rd] pir E82650 plasmid-related protein XF1679 XF1574 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84383.1 AE003986_13 (AE003986) plasmid- related protein [Xylella fastidiosa] gb AAF84488.1 AE003993_7 (AE003993) plasmid- related protein [Xylella fastidiosa] sp P44180 YE05_HAEMIN HYPOTHETICAL PROTEIN HI1405 pir A64028 hypothetical protein HI1405 - Haemophilus influenzae (strain Rd KW20) gb AAC23055.1 (U32820) H. influenzae predicted coding region HI1405 [Haemophilus influenzae Rd] SEQ ID n-90
SEQ ID n° 5967 PL-1043.1	Contig9 from 82758 to 83570	p 48%	sp P44180 YE05_HAEMIN HYPOTHETICAL PROTEIN HI1405 pir A64028 hypothetical protein HI1405 - Haemophilus influenzae (strain Rd KW20) gb AAC23055.1 (U32820) H. influenzae predicted coding region HI1405 [Haemophilus influenzae Rd] SEQ ID n-91
SEQ ID n° 5968 PL-1044.1	Contig9 from 83574 to 84731	p 48%	sp P44180 YE05_HAEMIN HYPOTHETICAL PROTEIN HI1405 pir A64028 hypothetical protein HI1405 - Haemophilus influenzae (strain Rd KW20) gb AAC23055.1 (U32820) H. influenzae predicted coding region HI1405 [Haemophilus influenzae Rd] SEQ ID n-92
SEQ ID n° 5969 PL-3854.1	Contig9 from 84734 to 85219	p No Hits found	sp P44180 YE05_HAEMIN HYPOTHETICAL PROTEIN HI1405 pir A64028 hypothetical protein HI1405 - Haemophilus influenzae (strain Rd KW20) gb AAC23055.1 (U32820) H. influenzae predicted coding region HI1405 [Haemophilus influenzae Rd] SEQ ID n-93
SEQ ID n° 5970 PL-1045.1	Contig9 from 85224 to 86183	p No Hits found	sp P44180 YE05_HAEMIN HYPOTHETICAL PROTEIN HI1405 pir A64028 hypothetical protein HI1405 - Haemophilus influenzae (strain Rd KW20) gb AAC23055.1 (U32820) H. influenzae predicted coding region HI1405 [Haemophilus influenzae Rd] SEQ ID n-94
SEQ ID n° 5971 PL-4610.1	Contig9 from 86198 to 86560	p 49%	sp P44180 YE05_HAEMIN HYPOTHETICAL PROTEIN HI1405 pir A64028 hypothetical protein HI1405 - Haemophilus influenzae (strain Rd KW20) gb AAC23055.1 (U32820) H. influenzae predicted coding region HI1405 [Haemophilus influenzae Rd] SEQ ID n-95

#N/A

TABLEAU II

SEQ ID n° 5956	PL-4621.1	Contig9 from 76213 to 76398	m	46%	seq P76195 YDIH_ECOLI_HYPOTHETICAL 10.5 KD PROTEIN IN LPP-AROD INTERGENIC REGION pir E64926 hypothetical protein b1685 - Escherichia coli gb AAC74755.1 (AE000263) orf, hypothetical protein [Escherichia coli K12] gb AAG56672.1 AE005391_9 (AE005391) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 5957	PL-4620.1	Contig9 from 76370 to 76468	m	No Hits found		#N/A
SEQ ID n° 5958	PL-4619.1	Contig9 from 76550 to 76873	p	64%	emb CAB58444.1 (AJ133022) hypothetical protein [Xenorhabdus nematophilus]	#N/A
SEQ ID n° 5959	PL-4618.1	Contig9 from 76870 to 77280	p	58%	ref NP_049909.1 structural protein P5 [Alteromonas phage PM2] gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2]	#N/A
SEQ ID n° 5960	PL-4617.1	Contig9 from 77292 to 77516	p	No Hits found		#N/A
SEQ ID n° 5961	PL-3855.1	Contig9 from 77513 to 77962	p	46%	gb AAB40752.1 (U82598) hypothetical protein [Escherichia coli]	SEQ ID n-3027
SEQ ID n° 5962	PL-4616.1	Contig9 from 78159 to 78437	m	43%	ref NP_065305.1 yaja [Escherichia coli] dbj BAB12598.1 (AP002527) yaja [Escherichia coli]	#N/A
SEQ ID n° 5963	PL-1040.1	Contig9 from 79085 to 79753	p	No Hits found		SEQ ID n-88
SEQ ID n° 5964	PL-4614.1	Contig9 from 79798 to 80199	p	60%	ref NP_050978.1 P17 [Bacteriophage APSE-1] sp Q9TIT1 VP17_BPAPS PUTATIVE PROTEIN P17 gb AAF03960.1 AF157835_17 (AF157835) P17 [Bacteriophage APSE-1]	#N/A
SEQ ID n° 5965	PL-1041.1	Contig9 from 80196 to 81425	p	23%	ref NP_050979.1 P18 [Bacteriophage APSE-1] gb AAF03961.1 AF157835_18 (AF157835) P18 [Bacteriophage APSE-1]	SEQ ID n-89

TABLEAU II

SEQ ID n° 5947	PL-3857.1	Contig9 from 59763 to 70044	P	No Hits found		emb CAC04160.1 (AJ292531) putative helicase [Lactococcus bacteriophage phi31]	SEQ ID n-3029
SEQ ID n° 5948	PL-1037.1	Contig9 from 70116 to 71657	P	36%			
SEQ ID n° 5949	PL-1038.1	Contig9 from 71812 to 72576	P	34%		gb AAG54598.1 AE005204.8 (AE005204) alpha replication protein of prophage CP-933I [Escherichia coli O157:H7]	SEQ ID n-84
SEQ ID n° 5950	PL-4628.1	Contig9 from 72629 to 72781	P	No Hits found			SEQ ID n-85
SEQ ID n° 5951	PL-4627.1	Contig9 from 72989 to 73432	P	60%		sp Q37870 YBCN_BP82 HYPOTHETICAL 17.5 KDA PROTEIN IN RUSA 5'REGION (ORF151) pir S66580 hypothetical protein ybcN - phage 82 emb CAA63327.1 (X92588) orf151 [Bacteriophage 82]	#N/A
SEQ ID n° 5952	PL-4626.1	Contig9 from 73432 to 73668	P	No Hits found			#N/A
SEQ ID n° 5953	PL-4625.1	Contig9 from 73777 to 74157	P	48%		ref NP_047915.1 unknown [Yersinia pestis] pir T15030 hypothetical protein Y1115 - Yersinia pestis plasmid pMT1 gb AAC82773.1 (AF074611) unknown [Yersinia pestis] emb CAB55230.1 (AL117211) hypothetical protein YPMT1.48c [Yersinia pestis] pir B64911 hypothetical protein b1559 - Escherichia coli gb AAC74632.1 (AE000253) orf, hypothetical protein [Escherichia coli K12]	#N/A
SEQ ID n° 5954	PL-1039.1	Contig9 from 74526 to 75341	P	53%			SEQ ID n-86
SEQ ID n° 5955	PL-3856.1	Contig9 from 75579 to 75989	P	No Hits found			SEQ ID n-3028

TABLEAU II

SEQ ID n° 5940	PL-7071.2	Contig9 from 66201 to 66419	m	No Hits found	#N/A
SEQ ID n° 5941	PL-7264.1	Contig9 from 66403 to 66576	p	No Hits found	#N/A
SEQ ID n° 5942	PL-7263.1	Contig9 from 66747 to 67157	m	46%	#N/A

SEQ ID n° 5943	PL-1036.2	Contig9 from 67551 to 68189	m	58%	#N/A

SEQ ID n° 5944	PL-4634.1	Contig9 from 68299 to 68502	p	68%	#N/A

SEQ ID n° 5945	PL-4633.1	Contig9 from 68625 to 68942	p	42%	#N/A
SEQ ID n° 5946	PL-4632.1	Contig9 from 68987 to 69349	p	No Hits found	#N/A

gb|AAG57243.1|AE005443_11 (AE005443) unknown
 protein encoded within prophage CP-933V
 [Escherichia coli O157:H7 EDL933]
 ref|NP_049485.1| repressor protein CI
 [Bacteriophage 933W] gb|AAD25430.1|AF125520_25
 (AF125520) repressor protein CI [Bacteriophage
 933W] gb|AAG55574.1|AE005295_14 (AE005295)
 putative repressor protein CI of bacteriophage
 BP-933W [Escherichia coli O157:H7
 EDL933]
 sp|P03036|RCRO_BP434 REGULATORY PROTEIN CRO
 (ANTIREPRESSOR) pir||RCEP4 regulatory protein
 cro - phage 434 pdb|1ZUG| Structure Of Phage
 434 Cro Protein, Nmr, 20 Structures pdb|3CRO|L
 Chain L, 434 Cro Protein Complex With 20 Base
 Pair Piece Of DNA Containing Operator
 OR1 pdb|2CRO| 434 Cro Protein pdb|3CRO|R
 Chain R, 434 Cro Protein Complex With 20 Base
 Pair Piece Of DNA Containing Operator
 OR1 emb|CAA33908.1| (V00635) reading frame
 (cro) [Bacteriophage 434] gb|AAA32245.1|
 (J02460) cro [bacteriophage lambda]
 gb|AAB22480.1| transcription activator protein
 C1, P22 C1 [bacteriophage P22,
 Peptide, 92 aa]

TABLEAU II

SEQ ID n° 5931	PL-3172.1	Contig9 from 61071 to 61991	m	33%	ref NP_049474.1 Bet protein [Bacteriophage 933W] gb AAD25419.1 AF125520_14 (AF125520) Bet protein [Bacteriophage 933W] dbj BAB19616.1 (AP000400) Bet protein [Escherichia coli O157:H7] gb AAG55564.1 AE005295_4 (AE005295) putative Bet recombination protein of bacteriophage BP-933W [Escherichia coli O157:H7]	SEQ ID n~2420
SEQ ID n° 5932	PL-6859.1	Contig9 from 61988 to 62245	m	No Hits found	#N/A	
SEQ ID n° 5933	PL-3173.1	Contig9 from 62636 to 63538	m	58%	ref NP_061549.1 Orf53 [Pseudomonas phage D3] gb AAF80812.1 (AF165214) Orf53 [Pseudomonas phage D3]	SEQ ID n~2421
SEQ ID n° 5934	PL-6860.1	Contig9 from 63608 to 64030	m	No Hits found	#N/A	
SEQ ID n° 5935	PL-6861.2	Contig9 from 64060 to 64317	m	63%	gb AAG56433.1 AE005370_6 (AE005370) unknown protein encoded within prophage CP-933R [Escherichia coli O157:H7 EDL933] dbj BAB35373.1 (AP002556) hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 5936	PL-7067.1	Contig9 from 64536 to 64715	m	No Hits found	#N/A	
SEQ ID n° 5937	PL-7068.1	Contig9 from 64792 to 65322	m	43%	emb CAE38995.1 (AL034558) predicted using hexExon; MAL3P2.8 (PFC0195W), Hypothetical protein, len: 1424 aa [Plasmodium falciparum] sp P18683 VNUN_BPHK0 TRANSCRIPTION TERMINATION FACTOR NUN pir VNBPHK regulatory protein nun - phage HK022 emb CAA34221.1 (X16093) nun gene product (AA 1-112) [Enterobacteria phage HK022]	#N/A
SEQ ID n° 5938	PL-7069.1	Contig9 from 65429 to 65635	m	45%		
SEQ ID n° 5939	PL-7070.2	Contig9 from 65727 to 66011	m	No Hits found	#N/A	

TABLEAU II

SEQ ID n° 5922	PL-6849.1	Contig9 from 56052 to 56270	m	No Hits found	#N/A
SEQ ID n° 5923	PL-6852.1	Contig9 from 57148 to 57387	m	No Hits found	#N/A
SEQ ID n° 5924	PL-3169.1	Contig9 from 57374 to 58018	m	49%	gb AAF72345.1 AF192329_6 (AF192329) Muni-like protein [Enterococcus faecalis]
SEQ ID n° 5925	PL-6854.1	Contig9 from 58295 to 58525	m	No Hits found	#N/A
SEQ ID n° 5926	PL-3170.1	Contig9 from 58682 to 59338	m	No Hits found	SEQ ID n-2416
SEQ ID n° 5927	PL-6855.1	Contig9 from 59344 to 59781	m	No Hits found	#N/A
SEQ ID n° 5928	PL-6856.1	Contig9 from 59797 to 59976	m	No Hits found	#N/A
SEQ ID n° 5929	PL-6857.1	Contig9 from 59989 to 60396	m	20%	ref NP_050511.1 hypothetical protein [Bacteriophage VT2-Sa] dbj BAAS4295.1 (AP000363) hypothetical protein [Bacteriophage VT2-Sa] dbj BAAS4111.1 (AP000422) hypothetical protein [Escherichia coli O157:H7] pdb 1AVQ A Chain A, Toroidal Structure Of Lambda Exonuclease Determined At 2.4 Angstroms pdb 1AVQ B Chain B, Toroidal Structure Of Lambda Exonuclease Determined At 2.4 Angstroms pdb 1AVQ C Chain C, Toroidal Structure Of Lambda Exonuclease Determined At 2.4 Angstroms
SEQ ID n° 5930	PL-3171.1	Contig9 from 60387 to 61070	m	82%	SEQ ID n-2419

TABLEAU II

SEQ ID n° 5911	Contig9 from 49182 to 50087	PL-3165.1	p	24%	gd AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-2412
SEQ ID n° 5912	Contig9 from 50100 to 50522	PL-6840.1	p	60%	ref NP_050998.1 P37 [Bacteriophage APSE-1] sp Q9T1R1 TFA_BPAPS PROBABLE TAIL FIBER ASSEMBLY PROTEIN (P37) gb AAF03980.1 AF157835_37 (AF157835) P37 [Bacteriophage APSE-1]	#N/A
SEQ ID n° 5913	Contig9 from 50754 to 50918	PL-6841.1	m	No Hits found		#N/A
SEQ ID n° 5914	Contig9 from 51105 to 52130	PL-3166.1	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-2413
SEQ ID n° 5915	Contig9 from 52127 to 52531	PL-6913.1	p	37%	gb AAF23801.1 AF213822_16 (AF213822) unknown protein [Zymomonas mobilis]	#N/A
SEQ ID n° 5916	Contig9 from 52845 to 53660	PL-3167.1	p	61%	gb AAG55918.1 AE005325_11 (AE005325) putative antirepressor protein encoded by prophage CP-933N [Escherichia coli O157:H7]	SEQ ID n-2414
SEQ ID n° 5917	Contig9 from 53775 to 54071	PL-6845.1	p	No Hits found		#N/A
SEQ ID n° 5918	Contig9 from 54086 to 54217	PL-6846.1	p	No Hits found		#N/A
SEQ ID n° 5919	Contig9 from 54263 to 54373	PL-6847.1	p	No Hits found		#N/A
SEQ ID n° 5920	Contig9 from 54424 to 54606	PL-6848.1	p	46%	gb AAG56009.1 AE005333_6 (AE005333) putative tail fiber protein of prophage CP-933X [Escherichia coli O157:H7]	#N/A
SEQ ID n° 5921	Contig9 from 54872 to 56050	PL-3168.1	m	44%	dbj BAA75916.1 (AB024602) similar to integrase [Pseudomonas putida]	SEQ ID n-2415

TABLEAU II

SEQ ID n° 5903	PL-2774.1	Contig9 from 38764 to 39432	p 68%	gb AAG42457.1 AF308467_3 (AF308467) sircheme synthase [Klebsiella aerogenes] sp P13040 BTUR_ECOLI COB(I)ALAMIN ADENOSYLTRANSFERASE (CORRINOID ADENOSYLTRANSFERASE) pir A64875 cob(I)alamin adenosyltransferase (EC 2.5.1.17) - Escherichia coli gb AAA23530.1 (M21528) btur protein [Escherichia coli] dbj BAA14807.1 (D90764) Cob(I)alamin adenosyltransferase (EC 2.5.1.17) (Corrinoid adenosyltransferase). [Escherichia coli] dbj BAA14822.1 (D90765) Cob(I)alamin adenosyltransferase (EC 2.5.1.17) (Corrinoid adenosyltransferase). [Escherichia coli] gb AAC74352.1 (AE000225) cob(I)alamin adenosyltransferase [Escherichia coli K12]	SEQ ID n-1981
SEQ ID n° 5904	PL-4015.1	Contig9 from 39455 to 40012	p 71%	gb AAG58749.1 AE005587_7 (AE005587) putative adhesin [Escherichia coli O157:H7] dbj BAA76527.2 (AB017338) tail fiber [Pectobacterium carotovorum] dbj BAA76527.2 (AB017338) tail fiber [Pectobacterium carotovorum] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7] ref NP_050998.1 P37 [Bacteriophage APSE-1] sp Q9TIR1 TFA_BPAPS PROBABLE TAIL FIBER ASSEMBLY PROTEIN (P37) gb AAF03980.1 AF157835_37 (AF157835) P37 [Bacteriophage APSE-1]	SEQ ID n-1979
SEQ ID n° 5905	PL-2773.1	Contig9 from 40918 to 41556	p 42%		SEQ ID n-9166
SEQ ID n° 5906	PL-2772.2	Contig9 from 42742 to 44226	p 35%		SEQ ID n-1980
SEQ ID n° 5907	PL-3162.1	Contig9 from 44309 to 45724	p 22%		SEQ ID n-2409
SEQ ID n° 5908	PL-3163.1	Contig9 from 46168 to 46932	p 23%		SEQ ID n-2410
SEQ ID n° 5909	PL-3164.1	Contig9 from 47466 to 48053	p 25%		SEQ ID n-2411
SEQ ID n° 5910	PL-4016.1	Contig9 from 48056 to 48478	p 57%		SEQ ID n-3167

TABLEAU II

SEQ ID n° 5894	PL-4014.1	Contig9 from 27650 to 28129	p	57%	gb AAG54517.1 AE005197.6 (AE005197) Z0248 gene product [Escherichia coli O157:H7]	SEQ ID n-3165
SEQ ID n° 5895	PL-2782.1	Contig9 from 28137 to 28967	p	54%	gb AAG58551.1 AE005568_1 (AE005568) orf; hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-1990
SEQ ID n° 5896	PL-2781.1	Contig9 from 31272 to 31919	p	No Hits found	sp P19265 EUTC_SALTY ETHANOLAMINE AMMONIA-LYASE LIGHT CHAIN gb AAC78124.1 (AF093749) ethanolamine ammonia lyase small subunit [Salmonella typhimurium]	SEQ ID n-1989
SEQ ID n° 5897	PL-2780.1	Contig9 from 32013 to 32867	m	80%	sp P19635 EUTR_ECOLI ETHANOLAMINE AMMONIA-LYASE HEAVY CHAIN dbj BAAL6323.1 (D90873) ETHANOLAMINE AMMONIA-LYASE HEAVY CHAIN (EC 4.3.1.7) (FRAGMENT). [Escherichia coli] dbj BAAL6329.1 (D90874) ETHANOLAMINE AMMONIA-LYASE HEAVY CHAIN (EC 4.3.1.7) (FRAGMENT). [Escherichia coli]	SEQ ID n-1988
SEQ ID n° 5898	PL-2779.1	Contig9 from 32890 to 34251	m	93%	gb AAG57559.1 AE005474_7 (AE005474) ethanolamine ammonia-lyase, heavy chain [Escherichia coli O157:H7]	SEQ ID n-1986
SEQ ID n° 5899	PL-2778.1	Contig9 from 34264 to 35691	m	75%	sp Q92FV2 EUTA_SALTY ETHANOLAMINE UTILIZATION PROTEIN EUTA gb AAC78122.1 (AF093749) putative chaperonin [Salmonella typhimurium]	SEQ ID n-1985
SEQ ID n° 5900	PL-2777.1	Contig9 from 36004 to 36789	p	62%	gb AAC18603.2 (AF067123) uroporphyrinogen-III C- methyltransferase [Lactobacillus reuteri]	SEQ ID n-1984
SEQ ID n° 5901	PL-2776.1	Contig9 from 36818 to 37894	p	69%	gb AAC79515.1 (U90625) CobD [Salmonella typhimurium]	SEQ ID n-1983
SEQ ID n° 5902	PL-2775.1	Contig9 from 37842 to 38747	p	65%	gb AAD39022.1 (AF026270) Pdux [Salmonella enterica serovar Typhimurium]	SEQ ID n-1982

TABLEAU II

SEQ ID n° 5888	PL-2785.1	Contig9 from 22747 to 23493	p	76%	sp U05602 COBS_SALTY COBALAMIN [5'-PHOSPHATE] SYNTHASE gb AA27270.1 (L12006) cobalamin synthase [Salmonella typhimurium] SEQ ID n-1993 sp Q57089 YBAQ_HAEN HYPOTHETICAL PROTEIN H1251 pir H64112 virulence-associated protein vpa homolog H1251 - Haemophilus influenzae (strain Rd KW20) gb AAC22901.1 (U32805) virulence associated protein A (vpa) [Haemophilus influenzae Rd] #N/A
SEQ ID n° 5889	PL-6834.1	Contig9 from 23530 to 23838	m	38%	
SEQ ID n° 5890	PL-6832.1	Contig9 from 24313 to 24663	p	NO Hits found	#N/A
SEQ ID n° 5891	PL-6834.1	Contig9 from 24679 to 24903	p	31%	emb CAB54522.1 (AJ245959) Int protein [Bacteriophage WPhi] #N/A
SEQ ID n° 5892	PL-2784.1	Contig9 from 24944 to 25561	p	65%	sp P39701 COBC_SALTY ALPHA-RIBAZOLE-5'-PHOSPHATE PHOSPHATASE sp P36562 COBT_ECOLI NICOTINATE-NUCLEOTIDE-- DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE (NN:DBI PRT) (N1-ALPHA-PHOSPHORIBOSYLTRANSFERASE) pir F64963 nicotinate-nucleotide-- dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21) - Escherichia coli dbj BA15808.1 (D90837) Nicotinate-nucleotide-- dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21) (NN:DBI PRT) Phosphoribosyltransferase. [Escherichia coli] gb AAC75052.1 (AE000291) nicotinate-nucleotide dimethylbenzimidazole-P phosphoribosyl transferase [Escherichia coli K12] SEQ ID n-1991
SEQ ID n° 5893	PL-2783.1	Contig9 from 25566 to 26615	p	68%	

TABLEAU II

SEQ ID n° 5870	PL-6823.1	Contig9 from 5679 to 5969	m	56%	sp P76125 YDM_ECOLI_HYPOTHETICAL_13.3_KD PROTEIN IN FDN1-ADHP INTERGENIC REGION pir H64900_hypothetical protein b1477 - Escherichia coli gb AAD13441.1 (AE000244) orf, hypothetical protein [Escherichia coli K12] pir JC4693_proteic killer suppression protein hig A - plasmid Rts1 gb AAC43982.1 (U43847) killer protein [Plasmid Rts1] gb AAD00515.1 (U81366) killer protein [Plasmid Rts1] prf 2210234A_higB gene [Escherichia coli]	#N/A
SEQ ID n° 5871	PL-6824.1	Contig9 from 5969 to 6247	m	69%		#N/A
SEQ ID n° 5872	PL-2798.1	Contig9 from 7070 to 8596	m	No Hits found		SEQ ID n-2007
SEQ ID n° 5873	PL-6825.1	Contig9 from 9019 to 9423	m	53%	sp P44102 YNEI_HAEIN_HYPOTHETICAL_PROTEIN_H11044 pir C64019_ycdy protein homolog H11044 - Haemophilus influenzae (strain Rd KW20) gb AAC22703.1 (U32785) conserved hypothetical protein [Haemophilus influenzae Rd] sp P29946 CBIA_SALTY_COBYRINIC_ACID_A,C-DIAMIDE SYNTHASE gb AAA27252.1 (L12006) precorrin amidase [Salmonella typhimurium] sp Q05600 CBIB_SALTY_CBIB_PROTEIN gb AAA27253.1 (L12006) putative [Salmonella typhimurium]	#N/A
SEQ ID n° 5874	PL-2797.1	Contig9 from 10374 to 11756	p	65%		SEQ ID n-2006
SEQ ID n° 5875	PL-2796.1	Contig9 from 11753 to 12712	p	75%		SEQ ID n-2005
SEQ ID n° 5876	PL-2795.1	Contig9 from 12727 to 13359	p	65%	sp Q05601 CBIC_SALTY_PRECORRIN-8X_METHYLMUTASE (PRECORRIN ISOMERASE) gb AAA27254.1 (L12006) precorrin isomerase [Salmonella typhimurium] sp Q05628 CBID_SALTY_CBID_PROTEIN gb AAA27255.1 (L12006) putative [Salmonella typhimurium]	SEQ ID n-2004
SEQ ID n° 5877	PL-2794.1	Contig9 from 13356 to 14492	p	81%		SEQ ID n-2003
SEQ ID n° 5878	PL-2793.1	Contig9 from 14489 to 15091	p	65%	sp Q05629 CBIE_SALTY_PRECORRIN-6Y_C5,15- METHYLTRANSFERASE [DECARBOXYLATING] (PRECORRIN-6 METHYLTRANSFERASE) (PRECORRIN-6Y METHYLASE) gb AAA27256.1 (L12006) precorrin methylase [Salmonella typhimurium]	SEQ ID n-2002

TABLEAU II

SEQ ID n° 5861 PL-3392.1	Contig8 from 2236 to 2598	m	34%	pir C83640 probable transcription regulator PA0048 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AA03438.1 AE004444_7 (AE004444) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-2627
SEQ ID n° 5862 PL-7302.2	Contig8 from 2731 to 5193	p	20%	dbj BAB05094.1 (AP001511) DNA primase [Bacillus halodurans]	#N/A
SEQ ID n° 5863 PL-7272.1	Contig9 from 118 to 696	p	32%	dbj BAB03228.1 (AB046380) tail fiber protein [Pseudomonas aeruginosa] sp P77656 YFDK_ECOLI_HYPOTHETICAL_16.4_KDA PROTEIN IN INTC-DSDC INTERGENIC REGION pir G65008 hypothetical protein b2354 - Escherichia coli (strain K-12) gb AAC75413.1 (AE000324) orf, hypothetical protein [Escherichia coli K12] dbj BAAL6214.1 (D90865) similar to [SwissProt Accession Number P09154] [Escherichia coli] dbj BAAL6221.1 (D90866) similar to [SwissProt Accession Number P09154] [Escherichia coli]	#N/A
SEQ ID n° 5864 PL-6899.2	Contig9 from 699 to 1121	p	60%	gb AAG56009.1 AE005333_6 (AE005333) putative tail fiber protein of prophage CP-933X [Escherichia coli O157:H7]	SEQ ID n-2454
SEQ ID n° 5865 PL-3202.1	Contig9 from 1166 to 1792	m	54%	pir S18690 Sc/SvQ protein - Escherichia coli plasmid p15B emb CAA44053.1 (X62121) DNA inversion product [Escherichia coli]	#N/A
SEQ ID n° 5866 PL-3983.3	Contig9 from 1792 to 2550	m	38%		SEQ ID n-2008
SEQ ID n° 5867 PL-2799.1	Contig9 from 2994 to 3566	m	No Hits found		#N/A
SEQ ID n° 5868 PL-6821.1	Contig9 from 4963 to 5175	m	No Hits found		#N/A
SEQ ID n° 5869 PL-6823.1	Contig9 from 5256 to 5372	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 5852	PL-2802.2	Contig7 from 12438 to 13988	m	55%	sp P75785 YBIP_ECOLI HYPOTHETICAL 59.7 KDA PROTEIN IN OMPX-MOEB INTERGENIC REGION pir G64818 probable membrane protein ybip - Escherichia coli gb AAC73902.1 (AE000183) putative enzyme [Escherichia coli K12] dbj BAA35487.1 (D90718) Hypothetical protein HI1005 [Escherichia coli] dbj BAA35497.1 (D90719) Hypothetical protein HI1005 [Escherichia coli]	#N/A
SEQ ID n° 5853	PL-2801.1	Contig7 from 14404 to 14973	m	53%	gb AAG56009.1 AE005333_6 (AE005333) putative tail fiber protein of prophage CP-933X [Escherichia coli O157:H7]	SEQ ID n° 2012
SEQ ID n° 5854	PL-7063.1	Contig7 from 15030 to 15758	m	37%	pir S18687 Sc/SvN protein - Escherichia coli plasmid p15B emb CAA44050.1 (X62121) DNA inversion product [Escherichia coli]	#N/A
SEQ ID n° 5855	PL-7062.1	Contig7 from 16181 to 16300	m	No Hits found		#N/A
SEQ ID n° 5856	PL-7453.1	Contig8 from 1 to 189	m	54%	pdb 1F3I A Chain A, Crystal Structure Of Tn5 Transposase Complexed With Transposon End Dna	#N/A
SEQ ID n° 5857	PL-7451.1	Contig8 from 328 to 594	p	No Hits found		#N/A
SEQ ID n° 5858	PL-7449.1	Contig8 from 733 to 1521	p	14%	ref XP_046913.1 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 [Homo sapiens] pir D81221 hypothetical protein NMB0237 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF40692.1 (AE002381) hypothetical protein [Neisseria meningitidis MC58]	#N/A
SEQ ID n° 5859	PL-7448.1	Contig8 from 1536 to 1883	p	44%		#N/A
SEQ ID n° 5860	PL-7446.1	Contig8 from 1966 to 2196	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 5844	PL-3199.2	Contig7 from 3681 to 4637	m	44%	gb AAC38751.1 (AF030373) galactosyl transferase [Streptococcus pneumoniae] gb AAC69531.1 (AF057294) Cps23fH [Streptococcus pneumoniae] dbj BAB34316.1 (AP002553) putative enzyme [Escherichia coli O157:H7] pir H81120 transposase, IS30 family NMB1099 [imported] - Neisseria meningitidis (group B strain MD58) gb AAP41490.1 (AB002460) transposase, IS30 family [Neisseria meningitidis MC58] gb AAC69672.1 (AF019746) putative beta1,3- glucosyltransferase WaaV [Escherichia coli] ref NP_065324.1 31 pct identical (12 gaps) to sp:Y014_BPHP1[hypothetical 14.9kd protein of phage HP1] [Escherichia coli] dbj BAB12617.1 (AP002527) 31 pct identical (12 gaps) to sp:Y014_BPHP1[hypothetical 14.9kd protein of phage HP1] [Escherichia coli] dbj BAA76527.2 (AB017338) tail fiber [Pectobacterium carotovorum] ref NP_050654.1 U [Bacteriophage Mu] sp Q9T1U9 TFA_BPMU PROBABLE TAIL FIBER ASSEMBLY PROTEIN (GPU) gb AAF01128.1 AF083977_47 (AF083977) U [Bacteriophage Mu] pir E72354 probable hexosyltransferase (EC 2.4.1.-) TM0622 - Thermotoga maritima (strain MSB8) gb AAD35706.1 AE001736_4 (AE001736) lipopolysaccharide biosynthesis protein, putative [Thermotoga maritima]	#N/A
SEQ ID n° 5845	PL-2807.2	Contig7 from 4749 to 5519	m	39%		#N/A
SEQ ID n° 5846	PL-2806.1	Contig7 from 5915 to 6883	p	60%		
SEQ ID n° 5847	PL-2805.1	Contig7 from 7253 to 8230	m	51%		SEQ ID n-2017
SEQ ID n° 5848	PL-5321.1	Contig7 from 9075 to 9428	m	59%		SEQ ID n-2016
SEQ ID n° 5849	PL-2804.1	Contig7 from 9881 to 10684	p	32%		#N/A
SEQ ID n° 5850	PL-4011.1	Contig7 from 10694 to 11206	p	54%		SEQ ID n-2015
SEQ ID n° 5851	PL-2803.3	Contig7 from 11248 to 12345	m	44%		SEQ ID n-3162

TABLEAU II

SEQ ID	PROT NB	CONTIG	SENS % HOMOLOGIE	FONCTION OBTENUE PAR COMPARAISON SUR BANQUE DE HOMOLOGUE A LA DONNEES (BLAST P)	SEQ ID
SEQ ID n° 5835	PL-7466.1	Contig6 from 171 to 305	m --- No Hits found		#N/A
SEQ ID n° 5836	PL-7465.1	Contig6 from 328 to 570	p 41%	sp P39394 YJW_ECOLI_HYPOTHETICAL 14.6 KDA PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132) pir S56573 hypothetical 14.6K protein (mcrB-hads intergenic region) - Escherichia coli gb AAA97244.1 (U14003) ORF_f132 [Escherichia coli] gb AAC77303.1 (AE000505) orf, hypothetical protein [Escherichia coli K12] #N/A	
SEQ ID n° 5837	PL-7463.1	Contig6 from 1044 to 2099	m 13%	pir C69899 conserved hypothetical protein yobL Bacillus subtilis gb AAB84464.1 (AF027868) TopI homolog [Bacillus subtilis] emb CAB13792.1 (Z99114) similar to hypothetical proteins from B. subtilis [Bacillus subtilis] #N/A	
SEQ ID n° 5838	PL-7461.1	Contig6 from 2056 to 2148	m No Hits found		#N/A
SEQ ID n° 5839	PL-7454.1	Contig6 from 4056 to 4355	m No Hits found		#N/A
SEQ ID n° 5840	PL-3982.3	Contig7 from 1 to 423	m 33%	dbj BAB03228.1 (AB046380) tail fiber protein [Pseudomonas aeruginosa] ref NP_065324.1 31 pct identical (12 gaps) to sp:Y014_BPH1[hypothetical 14.9kd protein of phage HP1] [Escherichia coli] dbj BAB12617.1 (AP002527) 31 pct identical (12 gaps) to sp:Y014_BPH1[hypothetical 14.9kd protein of phage HP1] [Escherichia coli] #N/A	
SEQ ID n° 5841	PL-6900.1	Contig7 from 905 to 1333	p 70%		
SEQ ID n° 5842	PL-3201.1	Contig7 from 1784 to 2554	m No Hits found		SEQ ID n-2453
SEQ ID n° 5843	PL-3200.1	Contig7 from 2714 to 3469	m 37%	gb AAB49623.1 (U58147) LOS biosynthesis enzyme LEGA [Haemophilus ducreyi] gb AAC45592.1 (AF004712) LosA [Haemophilus ducreyi] #N/A	SEQ ID n-2452

TABLEAU I

SEQ ID n°3848	Prot n°PL-992.1	Contig40	586930	587514	84%	<p>Identities = 155/189 (82%), Positives = 173/189 (91%)</p> <p>sp P09550 UBIX_ECOLI_3-OCTAPRENYL-4-HYDROXYBENZOATE CARBOXY-LYASE (POLYPRENYL P-HYDROXYBENZOATE DECARBOXYLASE) pir JXMECFD 3-octaprenyl-4-hydroxybenzoate carboxylase [EC 4.1.1.-] - Escherichia coli gb AAC75371.1 (AE000320) 3-octaprenyl-4-hydroxybenzoate carboxylase [Escherichia coli] dbj BAA16157.1 (D90862) 3-OCTAPRENYL-4-HYDROXYBENZOATE CARBOXY-LYASE (EC 4.1.1.-) (POLYPRENYL P-HYDROXYBENZOATE DECARBOXYLASE). [Escherichia coli]</p> <p>Identities = 188/297 (63%), Positives = 232/297 (77%), Gaps = 1/297 (0%)</p> <p>sp P7775 YFCH_ECOLI_HYPOTHETICAL 32.7 KDA PROTEIN IN FOLX-HISP INTERGENIC REGION pir JF65002 hypothetical protein b2304 - Escherichia coli (strain K-12) gb AAC75364.1 (AE000319) putative sugar nucleotide epimerase [Escherichia coli] dbj BAA16141.1 (D90861) similar to [SwissProt Accession Number Q10403] [Escherichia coli]</p> <p>dbj BAA16150.1 (D90862) similar to [SwissProt Accession Number Q10403] [Escherichia coli] Length = 297</p>
SEQ ID n°3849	Prot n°PL-993.1	Contig40	587495	588409	74%	<p>Identities = 138/207 (66%), Positives = 163/207 (78%)</p> <p>sp P77526 YFCG_ECOLI_HYPOTHETICAL 24.5 KD PROTEIN IN PTA-FOLX INTERGENIC REGION pir JF65002 hypothetical protein b2302 - Escherichia coli (strain K-12) gb AAC75362.1 (AE000319) putative S-transferase [Escherichia coli] dbj BAA16139.1 (D90861) URE2 PROTEIN. [Escherichia coli] dbj BAA16148.1 (D90862) URE2 PROTEIN. [Escherichia coli]</p>
SEQ ID n°3850	Prot n°PL-994.1	Contig40	588562	589182	64%	<p>Identities = 198/347 (57%), Positives = 257/347 (74%), Gaps = 3/347 (0%)</p> <p>dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] Length = 345</p>
SEQ ID n°3851	Prot n°PL-995.1	Contig40	589352	590950	No Hits found	Identities = 108/439 (24%), Positives = 190/439 (42%), Gaps = 71/439 (16%) gb AAF94575.1 (AE004220) hypothetical protein [Vibrio cholerae] Length = 641
SEQ ID n°3852	Prot n°PL-996.1	Contig40	591803	592843	73%	Identities = 131/168 (77%), Positives = 147/168 (88%) pir JAE5002 hypothetical protein b2289 - Escherichia coli (strain K-12) gb AAC75359.1 (AE000319) putative regulator [Escherichia coli] Length = 180
SEQ ID n°3853	Prot n°PL-997.1	Contig40	593464	595404	29%	
SEQ ID n°3854	Prot n°PL-998.1	Contig40	595886	596452	71%	
SEQ ID n°3855	Prot n°PL-999.1	Contig40	597484	598263	No Hits found	

TABLEAU I

SEQ ID n°3844	Prot n°PL-989.1	Contig40	582659	583957	70%	<p>Identities = 258/425 (60%), Positives = 310/425 (72%), Gaps = 9/425 (2%)</p> <p>sp P08192 FOLC_ECOLI FOLC BIFUNCTIONAL PROTEIN [INCLUDES: FOLYLPOLYGLUTAMATE SYNTHASE (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS); DIHYDROFOLATE SYNTHASE] pir SYECFG tetrahydrofolypolyglutamate synthase (EC 6.3.2.17) / dihydrofolate synthase (EC 6.3.2.12) - Escherichia coli gb AAC75375.1 (AE000320) dihydrofolate:folypolyglutamate synthetase; dihydrofolate synthetase [Escherichia coli] dbj BAA16164.1 (D90862) FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) / DIHYDROFOLATE SYNTHASE (EC 6.3.2.12) [Escherichia coli] dbj BAA16172.1 (D90863) FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) / DIHYDROFOLATE SYNTHASE (EC 6.3.2.12) [Escherichia coli] Length = 422 "</p>
SEQ ID n°3845	Prot n°PL-99.1	Contig41	169638	170336	83%	<p>Identities = 182/231 (78%), Positives = 203/231 (87%), Gaps = 1/231 (0%)</p> <p>sp P7756 YBAX_ECOLI HYPOTHETICAL 25.5 KD PROTEIN IN HUPB-COF INTERGENIC REGION pir D64774 YbaX protein - Escherichia coli dbj BAA11648.1 (D82943) YbaX [Escherichia coli] gb AAB40200.1 (U82664) similar to H. Influenzae H11191 [Escherichia coli] gb AAC73547.1 (AE000150) orf, hypothetical protein [Escherichia coli] Length = 231</p>
SEQ ID n°3846	Prot n°PL-990.1	Contig40	583947	584630	57%	<p>Identities = 106/229 (46%), Positives = 139/229 (60%), Gaps = 30/229 (13%)</p> <p>sp P09549 DEDD_ECOLI DEDD PROTEIN pir XMECDD dedD protein - Escherichia coli gb AAA23967.1 (M68935) dedD protein (gig start codon) [Escherichia coli] gb AAC75374.1 (AE000320) putative lipoprotein [Escherichia coli] dbj BAA16162.1 (D90862) dedD protein [Escherichia coli] dbj BAA16170.1 (D90863) dedD protein [Escherichia coli] Length = 211</p>
SEQ ID n°3847	Prot n°PL-991.1	Contig40	585366	586883	86%	<p>Identities = 422/505 (83%), Positives = 457/505 (91%)</p> <p>sp P00498 PUR1_ECOLI AMIDOPHOSPHORIBOSYLTRANSFERASE (GLUTAMINE PHOSPHORIBOSYLPYRIPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPATASE) pir XQEC amidophosphoribosyltransferase (EC 2.4.2.14) - Escherichia coli gb AAC75372.1 (AE000320) amidophosphoribosyltransferase = PRPP</p>

TABLEAU I

SEQ ID n°3839	Prot n°PL-984.1	Contig40	577858	578985	80%	<p>Identities = 262/371 (70%), Positives = 301/371 (80%)</p> <p>sp P05459 PDXB_ECOLI_ERYTHRONATE-4-PHOSPHATE DEHYDROGENASE pir IDEECP probable erythronate-4-phosphate dehydrogenase (EC 1.1.1.-) - Escherichia coli gb AAA24308.1 (M29982) erythronate-4-phosphate dehydrogenase [Escherichia coli] gb AAB36530.1 (U76961) 4-phosphoerythronate dehydrogenase [Escherichia coli] gb AAC75380.1 (AE000321) erythronate-4-phosphate dehydrogenase [Escherichia coli] dbj BAA16177.1 (D90863) probable erythronate-4-phosphate dehydrogenase (EC 1.1.1.-) [Escherichia coli] Length = 371</p>
SEQ ID n°3840	Prot n°PL-985.1	Contig40	579037	580047	79%	<p>Identities = 224/337 (66%), Positives = 271/337 (79%), Gaps = 1/337 (0%)</p> <p>sp P08390 USG_ECOLI_USG-1-PROTEIN pir IQECH3 probable dehydrogenase (EC 1.2.1.-) usg1 - Escherichia coli emb CAA26521.1 (X02743) usg protein (aa 1-337) [Escherichia coli] gb AAC75379.1 (AE000320) putative PTS system enzyme II A component [Escherichia coli] dbj BAA16176.1 (D90863) usg1 protein [Escherichia coli] Length = 337</p>
SEQ ID n°3841	Prot n°PL-986.1	Contig40	580074	580883	79%	<p>Identities = 206/260 (79%), Positives = 231/260 (88%) pdb 1DJOA Chain A, The Crystal Structure Of E. Coli Pseudouridine Synthase I At 1.5 Angstrom Resolution pdb 1DJOB Chain B, The Crystal Structure Of E. Coli Pseudouridine Synthase I At 1.5 Angstrom Resolution Length = 260</p>
SEQ ID n°3842	Prot n°PL-987.1	Contig40	580879	581619	79%	<p>Identities = 175/216 (81%), Positives = 196/216 (90%)</p> <p>sp P09548 DEDA_ECOLI_DEDA PROTEIN (DSG-1 PROTEIN) pir XMECAD dedA protein - Escherichia coli gb AAA23984.1 (M68935) dedA [Escherichia coli] gb AAC75377.1 (AE000320) orf, hypothetical protein [Escherichia coli] dbj BAA16174.1 (D90863) dedA protein [Escherichia coli] Length = 219</p>
SEQ ID n°3843	Prot n°PL-988.1	Contig40	581722	582666	80%	<p>Identities = 242/285 (84%), Positives = 261/285 (90%), Gaps = 2/285 (0%)</p> <p>sp P08183 ACCD_ECOLI_ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA (ACCASE BETA CHAIN) pir XMECBD acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase beta chain - Escherichia coli gb AAC75376.1 (AE000320) acetylCoA carboxylase, carboxyltransferase component, beta subunit [Escherichia coli] dbj BAA16173.1 (D90863) acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase beta chain [Escherichia coli] Length = 304</p>

TABLEAU I

SEQ ID n°3829	Prot n°PL-975.1	Contig40	562403	563208	73%	<p>Identities = 158/250 (63%), Positives = 197/250 (78%)</p> <p>sp P14008 YFCA_ECOLI_HYPOTHETICAL 28.6 KD PROTEIN IN FABE-MEPA INTERGENIC_REGION pir J08346 hypothetical 28.6 K protein (meaA 3' region) - Escherichia coli emb CAA34783.1 (X16909) unidentified ORF (269 AA) [Escherichia coli] gb AAC75387.1 (AE000321) putative structural protein [Escherichia coli] dbj BAA16183.1 (D90863) similar to [PIR Accession Number S08346] [Escherichia coli] Length = 289</p> <p>Identities = 393/676 (58%), Positives = 480/676 (70%), Gaps = 10/676 (1%)</p> <p>pir B65005 hypothetical protein b2324 - Escherichia coli (strain K-12) gb AAC75384.1 (AE000321) putative peptidase [Escherichia coli] dbj BAA16181.1 (D90863) similar to [SwissProt Accession Number P44246] [Escherichia coli] Length = 688</p>
SEQ ID n°3830	Prot n°PL-976.1	Contig40	564155	566197	69%	<p>Identities = 325/403 (80%), Positives = 363/403 (89%), Gaps = 2/403 (0%)</p> <p>pdb 1DD8 A Chain A, Crystal Structure Of Beta-Ketoacyl-[acyl Carrier Protein] Synthase I From Escherichia coli pdb 1DD8 B Chain B, Crystal Structure Of Beta-Ketoacyl-[acyl Carrier Protein] Synthase I From Escherichia coli</p> <p>Identities = 195/320 (60%), Positives = 254/320 (78%), Gaps = 5/320 (1%)</p> <p>gb AAG04141.1 (AE004510) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 505</p> <p>Identities = 195/320 (60%), Positives = 254/320 (78%), Gaps = 5/320 (1%)</p> <p>gb AAG04143.1 (AE004510) hypothetical protein [Pseudomonas aeruginosa] Length = 327</p> <p>Identities = 253/344 (73%), Positives = 289/344 (83%) gb AAF94220.1 (AE004187) cysteine synthase/cystathionine beta-synthase family protein [Vibrio cholerae] Length = 355</p>
SEQ ID n°3831	Prot n°PL-977.1	Contig40	566935	568149	88%	<p>Identities = 143/219 (65%), Positives = 181/219 (82%)</p> <p>sp P22104 TCTD_SALTY_TRANSCRIPTIONAL_REGULATORY_PROTEIN TCTD pir A33861 trans-activating transcription regulator tctD - Salmonella typhimurium gb AAA27232.1 (M28368) membrane associated regulatory protein [Salmonella typhimurium] Length = 224</p> <p>Identities = 256/418 (61%), Positives = 317/418 (75%), Gaps = 4/418 (0%)</p> <p>gb AAC05919.1 (AF029846) TcE [Salmonella typhimurium] Length = 439</p> <p>Identities = 130/282 (46%), Positives = 189/282 (66%)</p> <p>gb AAG07675.1 (AE004845) hypothetical protein [Pseudomonas aeruginosa] Length = 296</p>
SEQ ID n°3832	Prot n°PL-978.1	Contig40	568636	570156	80%	Identities = 338/502 (66%), Positives = 420/502 (82%), Gaps = 2/502 (0%)
SEQ ID n°3833	Prot n°PL-979.1	Contig40	570612	571655	72%	Identities = 195/320 (60%), Positives = 254/320 (78%), Gaps = 5/320 (1%)
SEQ ID n°3834	Prot n°PL-98.1	Contig41	168553	169605	82%	Identities = 253/344 (73%), Positives = 289/344 (83%) gb AAF94220.1 (AE004187) cysteine synthase/cystathionine beta-synthase family protein [Vibrio cholerae] Length = 355
SEQ ID n°3835	Prot n°PL-980.1	Contig40	571960	572625	No Hits found	
SEQ ID n°3836	Prot n°PL-981.1	Contig40	573078	573755	76%	Identities = 143/219 (65%), Positives = 181/219 (82%)
SEQ ID n°3837	Prot n°PL-982.1	Contig40	573742	575163	65%	Identities = 256/418 (61%), Positives = 317/418 (75%), Gaps = 4/418 (0%)
SEQ ID n°3838	Prot n°PL-983.1	Contig40	575160	576047	61%	Identities = 130/282 (46%), Positives = 189/282 (66%)

TABLEAU I

SEQ ID n°3821	Prot n°PL-968.1	Contig40	552514	553470	50%	<p>Identities = 134/217 (61%), Positives = 160/217 (72%) sp P19452 HUTG_KLEAE FORMINOGUTAMASE (FORMINOGUTAMATE-HYDROLASE) (HISTIDINE PROTEIN G) p I JH64774 hutG protein - Klebsiella pneumoniae (fragment) gb AA25074.1 (M34604) histidine utilization repressor G [Klebsiella Identities = 159/232 (68%), Positives = 182/232 (77%) sp P12380 HUTC_KLEAE HISTIDINE UTILIZATION REPRESSOR p I JH64774 hutC protein - Klebsiella pneumoniae gb AA25075.1 (M34604) histidine utilization repressor C (hutC) [Klebsiella aerogenes] Length = 241</p>
SEQ ID n°3822	Prot n°PL-969.1	Contig40	553576	554307	68%	<p>Identities = 419/578 (72%), Positives = 491/578 (84%) sp P77265 MDLA_ECOLI MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDLA p I JH64774 ABC-type transport protein mdla - Escherichia coli gb AAB40204.1 (U82664) multidrug resistance-like ATP-binding protein Mdl [Escherichia coli] gb AAC73551.1 (AE000151) ATP-binding component of a transport system [Escherichia coli] Length = 590 Identities = 481/554 (88%), Positives = 518/554 (92%) gb AAG08485.1 AE004923.1 (AE004923) urocanase [Pseudomonas aeruginosa] Length = 559</p>
SEQ ID n°3823	Prot n°PL-97.1	Contig41	166108	167877	81%	<p>Identities = 319/445 (71%), Positives = 367/445 (81%), Gaps = 3/445 (0%) gb AAG08482.1 AE004922.7 (AE004922) probable amino acid permease [Pseudomonas aeruginosa] Length = 467 sp P21310 HUTH_PSEPU HISTIDINE AMMONIA-LYASE (HISTIDASE) Length = 510</p>
SEQ ID n°3824	Prot n°PL-970.1	Contig40	555276	556955	88%	<p>Identities = 251/314 (79%), Positives = 285/314 (89%) sp P39189 YFCB_ECOLI HYPOTHETICAL ADENINE-SPECIFIC METHYLASE IN AROC-FADL INTERGENIC REGION p I JH65005 site-specific DNA- methyltransferase (adenine-specific) (EC 2.1.1.72), hypothetical, aroC 3'region - Escherichia coli (strain K-12) gb AAC75390.1 (AE000321) putative adenine-specific methylase [Escherichia coli] db BAA16188.1 (D90884) similar to [SwissProt Accession Number P39189] [Escherichia Identities = 308/361 (85%), Positives = 330/361 (91%) sp P12008 AROC_ECOLI CHORISMATE SYNTHASE (5- ENOLPYRUVYL-SHIKIMATE-3-PHOSPHATE PHOSPHOLYASE) p I JH65005 site-specific DNA- methyltransferase (adenine-specific) (EC 4.6.1.4) - Escherichia coli gb AA23487.1 (M27714) chorismate synthase (EC 4.6.1.4) [Escherichia coli] gb AAC75389.1 (AE000321) chorismate synthase [Escherichia coli]</p>
SEQ ID n°3825	Prot n°PL-971.1	Contig40	556964	558508	84%	
SEQ ID n°3826	Prot n°PL-972.1	Contig40	558596	559990	78%	
SEQ ID n°3827	Prot n°PL-973.1	Contig40	560210	561154	88%	
SEQ ID n°3828	Prot n°PL-974.1	Contig40	561229	562314	89%	

TABLEAU I

SEQ ID n°3814	Prot n°PL-981.1	Contig40	540538	541791	94%	<p>Identities = 356/415 (85%), Positives = 396/415 (94%)</p> <p>sp P37312 DCTA_ECOLI C4-DICARBOXYLATE TRANSPORT PROTEIN pir S47749 C4-dicarboxylate transport protein dcta - Escherichia coli gb AA18505.1 (U00039) CG site No. 872 [Escherichia coli] gb AAC76553.1 (AE000429) uptake of C4-dicarboxylic acids [Escherichia coli] Length = 1250 (0%)</p> <p>Identities = 182/250 (72%), Positives = 208/250 (82%), Gaps = 1250 (0%)</p> <p>sp P43262 VACJ_SHIFL VACJ LIPOPROTEIN PRECURSOR db BAA03788.1 (D16283) VacJ [Shigella flexneri] Length = 251</p> <p>Identities = 282/453 (62%), Positives = 355/453 (78%), Gaps = 17/453 (3%)</p> <p>gb AAG17182.1 AF181030.1 (AF181030) outer membrane protein FadL [Enterobacter cloacae] Length = 442</p>
SEQ ID n°3815	Prot n°PL-962.1	Contig40	543151	543915	71%	
SEQ ID n°3816	Prot n°PL-963.1	Contig40	544119	545462	78%	
SEQ ID n°3817	Prot n°PL-964.1	Contig40	546041	547351	84%	<p>Identities = 338/436 (77%), Positives = 379/436 (86%)</p> <p>sp P76503 YFCY_ECOLI PROBABLE 3-KETOACYL-COA THIOLASE (ACETYL-COA ACYLTRANSFERASE) (BETA-KETOTHIOLASE) pir D65007 hypothetical protein b2342 - Escherichia coli (strain K-12) gb AAC75402.1 (AE000322) putative acyltransferase [Escherichia coli] Identities = 450/711 (63%), Positives = 549/711 (76%), Gaps = 7/711 (0%)</p> <p>sp P77398 YFCX_ECOLI PUTATIVE FATTY OXIDATION COMPLEX ALPHA SUBUNIT [INCLUDES: ENOYL-COA HYDRATASE; 3-HYDROXYBUTYRYL-COA EPIMERASE] COA DEHYDROGENASE; 3-HYDROXYBUTYRYL-COA EPIMERASE] pir C65007 hypothetical protein b2341 - Escherichia coli (strain K-12) gb AAC75401.1 (AE000322) putative enzyme [Escherichia coli] db BAA16195.1 (D90864) MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (CONTAINS: LONG-CHAIN ENOYL- COA HYDRATASE (EC 4.2.1.17) / LONG CHAIN 3-HYDROXYACYL- COA DEHYDROGENASE (EC 1.1.1.35)) [Escherichia coli] db BAA16201.1 (D90865) MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (CONTAINS: LONG-CHAIN ENOYL- COA HYDRATASE (EC 4.2.1.17) / LONG CHAIN 3-HYDROXYACYL- COA DEHYDROGENASE (EC 1.1.1.35)) [Escherichia coli]</p>
SEQ ID n°3818	Prot n°PL-965.1	Contig40	547303	549534	72%	
SEQ ID n°3819	Prot n°PL-966.1	Contig40	549841	550423	56%	<p>Identities = 95/156 (60%), Positives = 115/156 (72%), Gaps = 1/156 (0%)</p> <p>sp P76502 SIXA_ECOLI PHOSPHOHISTIDINE PHOSPHATASE SIXA (RX6) pir B65007 hypothetical protein b2340 - Escherichia coli (strain K-12) gb AAC75400.1 (AE000322) orf. hypothetical protein [Escherichia coli] db BAA24878.1 (D86298) RX6 [Escherichia coli] Length = 161</p> <p>Identities = 202/397 (50%), Positives = 274/397 (68%), Gaps = 2/397 (0%)</p> <p>gb AAAF94364.1 (AE004200) imidazoloneprolase [Vibrio cholerae] Length = 402</p>
SEQ ID n°3820	Prot n°PL-967.1	Contig40	551250	552503	63%	

TABLEAU I

SEQ ID n°3801	Prot n°PL-95.1	Contig41	162506	163789	72%	<p>Identities = 304/412 (73%), Positives = 350/412 (84%)</p> <p>spIP37905JAMTB_ECOLI PROBABLE AMMONIUM TRANSPORTER pir C64775 ammonium transport protein amB - Escherichia coli gb AAD14837.1 (U40429) AmB [Escherichia coli] gb AAB40207.1 (U82664) putative ammonium transporter [Escherichia coli] gb AAC73554.1 (AE000151) probable ammonium transporter [Escherichia coli] Length = Identities = 54/230 (23%), Positives = 99/230 (42%), Gaps = 13/230 (5%) gb AAG04736.1 (AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230</p>
SEQ ID n°3802	Prot n°PL-950.1	Contig40	505955	506815	34%	<p>Identities = 1018/1453 (70%), Positives = 1195/1453 (82%), Gaps = 22/1453 (1%) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558</p>
SEQ ID n°3803	Prot n°PL-951.1	Contig40	507583	508245	No Hits found	
SEQ ID n°3804	Prot n°PL-952.1	Contig40	509381	519976	33%	
SEQ ID n°3805	Prot n°PL-953.1	Contig40	520365	521030	No Hits found	
SEQ ID n°3806	Prot n°PL-954.1	Contig40	521950	523530	51%	<p>Identities = 167/505 (33%), Positives = 273/505 (53%); Gaps = 19/505 (3%) dbj BAB16235.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes] Length = 521</p>
SEQ ID n°3807	Prot n°PL-955.1	Contig40	523989	525005	71%	<p>Identities = 212/326 (65%), Positives = 258/326 (79%), Gaps = 1/326 (0%) pir F84674 aliphatic amidase - Helicobacter pylori (strain 26695) gb AAD08283.1 (AE000629) aliphatic amidase (aimE) [Helicobacter pylori 26695] Length = 334</p>
SEQ ID n°3808	Prot n°PL-956.1	Contig40	525496	526434	71%	<p>Identities = 163/313 (52%), Positives = 231/313 (73%), Gaps = 4/313 (1%) gb AAF81206.1 (AF247502_1 (AF247502) Yti2 [Salmonella dublin] Length = 318</p>
SEQ ID n°3809	Prot n°PL-957.1	Contig40	528077	535276	63%	<p>Identities = 1230/1909 (64%), Positives = 1513/1909 (78%), Gaps = 48/1909 (2%) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] Length = 4558</p>
SEQ ID n°3810	Prot n°PL-958.1	Contig40	535264	536148	59%	<p>Identities = 133/285 (46%), Positives = 190/285 (66%), Gaps = 4/285 (1%) gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] Length = 300</p>
SEQ ID n°3811	Prot n°PL-959.1	Contig40	536088	539219	79%	<p>Identities = 698/1039 (67%), Positives = 829/1039 (79%), Gaps = 21/1039 (2%) gb AAD21057.1 (AF119150) RtxA protein [Vibrio cholerae] Length Identities = 440/625 (70%), Positives = 521/625 (82%), Gaps = 3/625 (0%) gb AAB40205.1 (U82664) multidrug resistance-like ATP-binding protein Mdl [Escherichia coli] Length = 631</p>
SEQ ID n°3812	Prot n°PL-96.1	Contig41	164331	166115	81%	
SEQ ID n°3813	Prot n°PL-960.1	Contig40	539286	540095	70%	<p>Identities = 152/251 (60%), Positives = 190/251 (75%) sp P57536 YBFF_ECOLI PUTATIVE ESTERASE/LIPASE YBFF pir E64803 ybIF protein - Escherichia coli gb AAC73780.1 (AE000172) orf, hypothetical protein [Escherichia coli] dbj BAA35335.1 (D90707) Dihydrolipoamide acetyltransferase (acoC) homolog [Escherichia coli] dbj BAA35343.1 (D90708) Dihydrolipoamide acetyltransferase (acoC) homolog</p>

TABLEAU I

SEQ ID n°3788	Prot n°PL-938.1	Contig40	479762	483154	27%	Identities = 164/805 (20%), Positives = 309/805 (38%), Gaps = 80/805 (9%) gb AAG05058.1 AE004594_10 (AE004594) hypothetical protein [Pseudomonas aeruginosa] Length = 1175	Unknown, similar to toxins
SEQ ID n°3789	Prot n°PL-939.1	Contig40	483963	486518	45%	Identities = 231/862 (26%), Positives = 388/862 (44%), Gaps = 78/862 (9%) gb AAG04900.1 AE004579_12 (AE004579) conserved hypothetical protein [Pseudomonas aeruginosa] Length = 842	
SEQ ID n°3790	Prot n°PL-94.1	Contig41	161570	162433	78%	Identities = 188/286 (65%), Positives = 234/286 (81%) sp P23911 TESB_ECOLI_ACYL-COA_THIOESTERASE_II (TEII) pir D64775 acyl-CoA thioesterase (EC 3.1.2.-) II - Escherichia coli gb AAA24665.1 (M63308) thioesterase II [Escherichia coli] gb AAB40208.1 (U82684) acyl-CoA thioesterase II [Escherichia coli] gb AAC73555.1 (AE00151) acyl-CoA thioesterase II [Escherichia coli] Length = 286	
SEQ ID n°3791	Prot n°PL-940.1	Contig40	486519	488135	43%	Identities = 153/459 (33%), Positives = 233/459 (50%), Gaps = 55/459 (11%) gb AAG04899.1 AE004579_11 (AE004579) hypothetical protein [Pseudomonas aeruginosa] Length = 569	
SEQ ID n°3792	Prot n°PL-941.1	Contig40	488129	489238	33%	Identities = 78/329 (23%), Positives = 125/329 (37%), Gaps = 50/329 (15%) gb AAG04898.1 AE004579_10 (AE004579) hypothetical protein [Pseudomonas aeruginosa] Length = 380	
SEQ ID n°3793	Prot n°PL-942.1	Contig40	489777	490910	No Hits found	Identities = 169/784 (21%), Positives = 295/784 (37%), Gaps = 103/784 (13%) gb AAG03467.1 AE004446_15 (AE004446) hypothetical protein [Pseudomonas aeruginosa] Length = 1101	Unknown, similar to toxins
SEQ ID n°3794	Prot n°PL-943.1	Contig40	490895	494278	26%	Identities = 303/822 (36%), Positives = 416/822 (49%), Gaps = 107/822 (13%) gb AAG06678.1 AE004751_4 (AE004751) hypothetical protein [Pseudomonas aeruginosa] Length = 882	
SEQ ID n°3796	Prot n°PL-944.1	Contig40	496100	498607	49%		
SEQ ID n°3796	Prot n°PL-945.1	Contig40	498651	499634	No Hits found	Identities = 183/591 (30%), Positives = 295/591 (48%), Gaps = 31/591 (5%) gb AAF96024.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 589	
SEQ ID n°3797	Prot n°PL-946.1	Contig40	500161	501921	48%	Identities = 80/317 (25%), Positives = 133/317 (41%), Gaps = 8/317 (2%) gb AAF96025.1 (AE004353) hypothetical protein [Vibrio cholerae] Length = 338	
SEQ ID n°3798	Prot n°PL-947.1	Contig40	501843	502973	35%	Identities = 51/212 (24%), Positives = 98/212 (46%), Gaps = 14/212 (6%) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] Length = 230	
SEQ ID n°3798	Prot n°PL-948.1	Contig40	504248	505036	37%	Identities = 60/219 (27%), Positives = 101/219 (45%), Gaps = 10/219 (4%) gb AAF96971.1 (AE004433) transcriptional regulator, LsdR family [Vibrio cholerae] Length = 319	
SEQ ID n°3800	Prot n°PL-949.1	Contig40	505229	505924	43%		

TABLEAU II

SEQ ID n° 6386	PL-4035.1	Contig9 from 588601 to 589146	p	76%	sp P16454 AIL_YEREN ATTACHMENT INVASION LOCUS PROTEIN PRECURSOR pir A35123 ail protein precursor - Yersinia enterocolitica gb AAA88694.1 (M29945) attachment invasion locus protein [Yersinia enterocolitica] prf 1807234A ail gene [Yersinia enterocolitica] SEQ ID n-3184
SEQ ID n° 6387	PL-4034.1	Contig9 from 589663 to 590190	p	72%	sp P16454 AIL_YEREN ATTACHMENT INVASION LOCUS PROTEIN PRECURSOR pir A35123 ail protein precursor - Yersinia enterocolitica gb AAA88694.1 (M29945) attachment invasion locus protein [Yersinia enterocolitica] prf 1807234A ail gene [Yersinia enterocolitica] SEQ ID n-3183
SEQ ID n° 6388	PL-2896.1	Contig9 from 590358 to 591128	m	64%	pir B64873 probable membrane protein yciC - Escherichia coli dbj BAA14787.1 (D90763) ORF_ID:0252#13; similar to [SwissProt Accession Number P21365] [Escherichia coli] gb AAC74337.1 (AE000223) orf, hypothetical protein [Escherichia coli K12] gb AAG56111.1 AE005343_1 (AE005343) putative outer membrane protein [Escherichia coli O157:H7] SEQ ID n-2114
SEQ ID n° 6389	PL-2895.1	Contig9 from 591559 to 592200	p	71%	emb CAB922261.1 (AL356595) hypothetical protein [Streptomyces coelicolor A3(2)] SEQ ID n-2113
SEQ ID n° 6390	PL-2894.1	Contig9 from 592745 to 593773	m	39%	emb CAB922258.1 (AL356595) putative repetitive protein [Streptomyces coelicolor A3(2)] SEQ ID n-2112
SEQ ID n° 6391	PL-2893.2	Contig9 from 593766 to 595451	m	42%	pir B82222 GTP cyclohydrolase II VC1263 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94422.1 (AE004205) GTP cyclohydrolase II [Vibrio cholerae] #N/A
SEQ ID n° 6392	PL-2892.2	Contig9 from 595464 to 596060	m	69%	emb CAB922258.1 (AL356595) putative repetitive protein [Streptomyces coelicolor A3(2)] #N/A

TABLEAU II

SEQ ID n° 6393	PL-2891.2	Contig9 from 596351 to 597391	P	73%	ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-2109
SEQ ID n° 6394	PL-4032.1	Contig9 from 597396 to 597872	m	47%	dbj BAB05769.1 (AP001514) BH2050-unknown conserved protein [Bacillus halodurans]	SEQ ID n-3182
SEQ ID n° 6395	PL-4031.2	Contig9 from 597882 to 598637	m	33%	pir H75377 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb AAFL11145.1 AF002002.3 (AF002002) conserved hypothetical protein [Deinococcus radiodurans] pir H71196 hypothetical protein PH1846 - Pyrococcus horikoshii dbj BAA30967.1 (AP000007) 273aa long hypothetical protein [Pyrococcus horikoshii]	#N/A
SEQ ID n° 6396	PL-4431.1	Contig9 from 598645 to 599397	m	38%	emb CAB8835.1 (AL353832) putative ABC-transport protein, ATP-binding component. [Streptomyces coelicolor A3(2)]	#N/A
SEQ ID n° 6397	PL-4430.1	Contig9 from 599387 to 600151	m	43%		
SEQ ID n° 6398	PL-3213.2	Contig9 from 600153 to 601799	m	No Hits found		SEQ ID n-2466

TABLEAU II

sp P00929 TRPA_SALTY TRYPTOPHAN SYNTHASE ALPHA CHAIN pir TSEBAT tryptophan synthase (EC 4.2.1.20) alpha chain - Salmonella typhimurium pdb 1QOQ A Chain A, Crystal structure Of Wild-Type Tryptophan Synthase Complexed With Indole Glycerol Phosphate pdb 1CW2 A Chain A, Crystal Structure Of The Complex Of Bacterial Tryptophan Synthase With The Transition State Analogue Inhibitor 4-(2- Hydroxyphenylsulfanyl)-Butylphosphonic Acid pdb 1C8V A Chain A, Crystal Structure Of The Complex Of Bacterial Tryptophan Synthase With The Transition State Analogue Inhibitor 4-(2- Hydroxyphenylthio)- Butylphosphonic Acid pdb 1C29 A Chain A, Crystal Structure Of The Complex Of Bacterial Tryptophan Synthase With The Transition State Analogue Inhibitor 4- (2- Hydroxyphenylthio)-1-Butenylphosphonic Acid pdb 1C9D A Chain A, Crystal Structure Of The Complex Of Bacterial Tryptophan Synthase With The Transition State Analogue Inhibitor 4-(2- Hydroxy-4- pdb 1QOP B Chain B, Crystal structure Of Wild- Type Tryptophan Synthase Complexed With Indole Propanol phosphate	Contig9 from 603637 to 603443	SEQ ID n° 6399 PL-1462.2	m	81%	SEQ ID n-550
Contig9 from 603443 to 604633	SEQ ID n° 6400 PL-1461.1	m	91%	SEQ ID n-549	

TABLEAU II

SEQ ID n° 6401	PL-1460.1	Contig9 from 604710 to 606074	m	76%	sp P00910 TRPC_SALTY TRYPTOPHAN BIOSYNTHESIS PROTEIN TRPCF [INCLUDES: INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE (IGPS); N-(5'- PHOSPHO-RIBOSYL)ANTHRANILATE ISOMERASE (PRAI)] pir GWEBT indole-3-glycerol-phosphate synthase (EC 4.1.1.48) / phosphoribosylanthranilate isomerase (EC 5.3.1.24) - Salmonella typhimurium gb AA27237.1 (M30286) N-(5'-phosphoribosyl)- anthranilic acid isomerase/indole-3- glycerol phosphate synthetase [Salmonella typhimurium] sp P00904 TRPG_ECOLI ANTHRANILATE SYNTHASE COMPONENT II [INCLUDES: GLUTAMINE AMIDOTRANSFERASE; ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE 1 pir NNEC2 anthranilate synthase (EC 4.1.3.27) component II - Escherichia coli dbj BA14798.1 (D90764) Anthranilate synthase (EC 4.1.3.27) component II [Escherichia coli] gb AAC74345.1 (AE000224) anthranilate synthase component II, glutamine amidotransferase and phosphoribosylanthranilate transferase [Escherichia coli K12] sp P00900 TRPG_SERMA ANTHRANILATE SYNTHASE COMPONENT II (GLUTAMINE AMIDO-TRANSFERASE) gb AAA57309.1 (J01792) trpG [Serratia marcescens]	SEQ ID n-348
SEQ ID n° 6402	PL-1459.1	Contig9 from 606077 to 607093	m	81%	sp P00904 TRPG_ECOLI ANTHRANILATE SYNTHASE COMPONENT II [INCLUDES: GLUTAMINE AMIDOTRANSFERASE; ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE 1 pir NNEC2 anthranilate synthase (EC 4.1.3.27) component II - Escherichia coli dbj BA14798.1 (D90764) Anthranilate synthase (EC 4.1.3.27) component II [Escherichia coli] gb AAC74345.1 (AE000224) anthranilate synthase component II, glutamine amidotransferase and phosphoribosylanthranilate transferase [Escherichia coli K12] sp P00900 TRPG_SERMA ANTHRANILATE SYNTHASE COMPONENT II (GLUTAMINE AMIDO-TRANSFERASE) gb AAA57309.1 (J01792) trpG [Serratia marcescens]	SEQ ID n-346
SEQ ID n° 6403	PL-3803.1	Contig9 from 607089 to 607667	m	81%	sp P00904 TRPG_ECOLI ANTHRANILATE SYNTHASE COMPONENT II [INCLUDES: GLUTAMINE AMIDOTRANSFERASE; ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE 1 pir NNEC2 anthranilate synthase (EC 4.1.3.27) component II - Escherichia coli dbj BA14798.1 (D90764) Anthranilate synthase (EC 4.1.3.27) component II [Escherichia coli] gb AAC74345.1 (AE000224) anthranilate synthase component II, glutamine amidotransferase and phosphoribosylanthranilate transferase [Escherichia coli K12] sp P00900 TRPG_SERMA ANTHRANILATE SYNTHASE COMPONENT II (GLUTAMINE AMIDO-TRANSFERASE) gb AAA57309.1 (J01792) trpG [Serratia marcescens]	SEQ ID n-2981

TABLEAU II

SEQ ID n° 6404	PL-1458.1	Contig9 from 607667 to 609241	m	77%	sp P00895 TRPE_ECOLI_ ANTHRANILATE SYNTHASE COMPONENT I pir [NNEC1 anthranilate synthase (EC 4.1.3.27) component I - Escherichia coli dbj BAA14799.1 (D90764) Anthranilate synthase component I (EC 4.1.3.27). [Escherichia coli] dbj BAA14814.1 (D90765) Anthranilate synthase component I (EC 4.1.3.27). [Escherichia coli] gb AAC74346.1 (AE000224) anthranilate synthase component I [Escherichia coli K12]	SEQ ID n-545
SEQ ID n° 6405	PL-7035.1	Contig9 from 609306 to 609425	p	No Hits found		#N/A
SEQ ID n° 6406	PL-1457.1	Contig9 from 610098 to 611732	p	56%	emb CAA72201.1 (Y11391) exochitinase [Glossina morsitans S-endosymbiont]	SEQ ID n-544
SEQ ID n° 6407	PL-1456.2	Contig9 from 611829 to 615350	p	28%	gb AAC38628.1 (AF047028) insecticidal toxin complex protein Tcca [Photorhabdus luminescens]	SEQ ID n-943
SEQ ID n° 6408	PL-1455.1	Contig9 from 615343 to 619431	p	36%	gb AAC38629.1 (AF047028) insecticidal toxin complex protein Tccb [Photorhabdus luminescens]	SEQ ID n-542
SEQ ID n° 6409	PL-1454.1	Contig9 from 619559 to 621427	p	48%	emb CAA72201.1 (Y11391) exochitinase [Glossina morsitans S-endosymbiont]	SEQ ID n-541
SEQ ID n° 6410	PL-1453.1	Contig9 from 621737 to 622489	p	72%	sp O54453 TRPH_SALTY TRPH PROTEIN	SEQ ID n-540
SEQ ID n° 6411	PL-1452.1	Contig9 from 622517 to 623137	p	90%	sp P45847 YCIO_ECOLI_ 23.2 KDA PROTEIN IN TRPL- BTUR INTERGENIC REGION	SEQ ID n-539
SEQ ID n° 6412	PL-1451.1	Contig9 from 623451 to 624605	p	33%	gb AAC61764.1 (AF091998) calpain Lp82 [Mus musculus]	SEQ ID n-538

TABLEAU II

SEQ ID n° 6413	PL-4427.1	Contig9 from 625201 to 625437	m	40%	pir [E89931 hypothetical protein yozI - Bacillus subtilis emb CAB13779.1 (Z99114) yozI [Bacillus subtilis] #N/A
SEQ ID n° 6414	PL-1450.1	Contig9 from 625457 to 630520	m	34%	pir [C83339 hypothetical protein PA2462 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05850.1 AE004673_10 (AE004673) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-537
SEQ ID n° 6415	PL-1449.1	Contig9 from 631039 to 631971	p	81%	gb AAG56546.1 AE005380_5 (AE005380) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-535
SEQ ID n° 6416	PL-3802.1	Contig9 from 632008 to 632604	m	81%	sp P13040 BTUR_ECOLI COB(I) ALAMIN ADENOSYLTRANSFERASE (CORRINOID ADENOSYLTRANSFERASE) pir [A64875 cob(I) alamin adenosyltransferase (EC 2.5.1.17) - Escherichia coli gb AAA23530.1 (M21528) btur protein [Escherichia coli] dbj BAA14807.1 (D90764) cob(I) alamin adenosyltransferase (EC 2.5.1.17) (Corrinoid adenosyltransferase). [Escherichia coli] dbj BAA14822.1 (D90765) cob(I) alamin adenosyltransferase (EC 2.5.1.17) (Corrinoid adenosyltransferase). [Escherichia coli] gb AAC74352.1 (AE000225) cob(I) alamin adenoleyltransferase [Escherichia coli K12] SEQ ID n-2980
SEQ ID n° 6417	PL-1448.1	Contig9 from 632604 to 633368	m	73%	sp P31808 YCIK_ECOLI HYPOTHETICAL OXIDOREDUCTASE IN BTUR-SOHB INTERGENIC REGION pir [B64875 probable, dehydrogenase (EC 1.1.1.-) yciK - Escherichia coli dbj BAA14808.1 (D90764) Internalin B [Escherichia coli] dbj BAA14823.1 (D90765) Internalin B [Escherichia coli] gb AAC74353.1 (AE000225) putative oxidoreductase [Escherichia coli K12] SEQ ID n-534

TABLEAU II

SEQ ID n° 6418	PL-1447.1	Contig9 from 633698 to 634336	p	60%	sp P00484 CAT3_ECOLI_CHLORAMPHENICOL ACETYLTRANSFERASE III pir XXEBCF chloramphenicol O-acetyltransferase (EC 2.3.1.28) III - Shigella flexneri plasmid R387 pdb 3CLA Type III chloramphenicol Acetyltransferase (CATIII) (E.C.2.3.1.28) Complex With Chloramphenicol emb CAA30695.1 (X07848) chloramphenicol acetyltransferase (AA 1-213) [Enterobacteriaceae]	SEQ ID n-533
SEQ ID n° 6419	PL-7243.1	Contig9 from 634386 to 634502	p	No Hits found	#N/A	
SEQ ID n° 6420	PL-4421.1	Contig9 from 634665 to 635045	p	No Hits found	#N/A	
SEQ ID n° 6421	PL-1446.1	Contig9 from 635130 to 636134	p	84%	ref NP_044235.1 TnpA [Enterobacter aerogenes] pir T08494 probable transposase - Enterobacter aerogenes plasmid R751 gb AA03489.1 (U60777) transposase [Plasmid R751] gb AAC64438.1 (U67194) TnpA [Enterobacter aerogenes]	SEQ ID n-532
SEQ ID n° 6422	PL-3801.1	Contig9 from 636676 to 637056	m	68%	gb AAC98740.1 (AF052750) transposase [Pseudomonas putida]	SEQ ID n-2979
SEQ ID n° 6423	PL-3800.1	Contig9 from 637137 to 637685	m	59%	gb AAC98740.1 (AF052750) transposase [Pseudomonas putida]	SEQ ID n-2978
SEQ ID n° 6424	PL-4420.1	Contig9 from 638086 to 638244	m	No Hits found	#N/A	
SEQ ID n° 6425	PL-1445.1	Contig9 from 638278 to 638883	p	No Hits found		SEQ ID n-931
SEQ ID n° 6426	PL-3799.1	Contig9 from 639261 to 639788	p	No Hits found		SEQ ID n-2975

TABLEAU II

SEQ ID n° 6427	PL-1444.1	Contig9 from 639863 to 645190	p	41%	emb CAC19493.1 (AJ296651) nematocidal protein 2 [Xenorhabdus bovienii]	SEQ ID n°530
SEQ ID n° 6428	PL-4415.1	Contig9 from 645263 to 645445	p	No Hits found		#N/A
SEQ ID n° 6429	PL-4414.1	Contig9 from 645728 to 646084	m	No Hits found		#N/A
SEQ ID n° 6430	PL-4412.1	Contig9 from 646517 to 646744	p	No Hits found		#N/A
SEQ ID n° 6431	PL-1443.1	Contig9 from 647159 to 648205	p	77%	gb AAG56543.1 AE005380_2 (AE005380) putative protease [Escherichia coli O157:H7]	SEQ ID n°529
SEQ ID n° 6432	PL-4411.1	Contig9 from 648496 to 648675	m	No Hits found		#N/A
SEQ ID n° 6433	PL-1442.1	Contig9 from 648734 to 649564	p	33%	pir B75474 probable chloride peroxidase - Deinococcus radiodurans (strain R1) gb AAFI0370.1 AE001934_1 (AE001934) chloride peroxidase, putative [Deinococcus radiodurans] gb AAG56541.1 AE005379_9 (AE005379) DNA topoisomerase type I, omega protein [Escherichia coli O157:H7]	SEQ ID n°528 SEQ ID n°527
SEQ ID n° 6434	PL-1441.1	Contig9 from 650326 to 652926	p	90%		

TABLEAU II

SEQ ID n° 6435	PL-1440.1	Contig9 from 653231 to 654205	p	83%	sp P06613 CYSB_ECOLI_CYS REGULON TRANSCRIPTIONAL ACTIVATOR pir RSECCB regulatory protein cysB - Escherichia coli gb AAA23642.1 (M15041) cysB regulatory protein [Escherichia coli] gb AAA23643.1 (M34332) cysteine regulatory protein (cysB) [Escherichia coli] dbj BAA14827.1 (D90765) Regulatory protein CysB [Escherichia coli] gb AAC74357.1 (AE000225) positive transcriptional regulator for cysteine regulon [Escherichia coli K12] gb AAG56540.1 AE005379_8 (AE005379) positive transcriptional regulator for cysteine regulon [Escherichia coli O157:H7]	SEQ ID n-526
SEQ ID n° 6436	PL-1439.1	Contig9 from 654381 to 655208	m	No Hits found	pir G64875 aconitate hydratase (EC 4.2.1.3) - Escherichia coli gb AAC74358.1 (AE000225) aconitate hydratase 1 [Escherichia coli K12] sp P25523 GCH2_ECOLI_GTP CYCLOHYDROLASE II pir A40654 GTP cyclohydrolase II (EC 3.5.4.25) Escherichia coli emb CAA48075.1 (X67876) GTP cyclohydrolase II [Escherichia coli] dbj BAA14831.1 (D90766) GTP cyclohydrolase II (EC 3.5.4.25) [Escherichia coli] gb AAC74359.1 (AE000226) GTP cyclohydrolase II [Escherichia coli K12] gb AAG56536.1 AE005379_4 (AE005379) GTP cyclohydrolase II (EC 3.5.4.25) [Escherichia coli O157:H7]	SEQ ID n-524
SEQ ID n° 6437	PL-1438.1	Contig9 from 655461 to 658136	p	84%	sp P25523 GCH2_ECOLI_GTP CYCLOHYDROLASE II pir A40654 GTP cyclohydrolase II (EC 3.5.4.25) Escherichia coli emb CAA48075.1 (X67876) GTP cyclohydrolase II [Escherichia coli] dbj BAA14831.1 (D90766) GTP cyclohydrolase II (EC 3.5.4.25) [Escherichia coli] gb AAC74359.1 (AE000226) GTP cyclohydrolase II [Escherichia coli K12] gb AAG56536.1 AE005379_4 (AE005379) GTP cyclohydrolase II (EC 3.5.4.25) [Escherichia coli O157:H7]	SEQ ID n-523
SEQ ID n° 6438	PL-1437.1	Contig9 from 658286 to 658894	m	81%	sp P25523 GCH2_ECOLI_GTP CYCLOHYDROLASE II pir A40654 GTP cyclohydrolase II (EC 3.5.4.25) Escherichia coli emb CAA48075.1 (X67876) GTP cyclohydrolase II [Escherichia coli] dbj BAA14831.1 (D90766) GTP cyclohydrolase II (EC 3.5.4.25) [Escherichia coli] gb AAC74359.1 (AE000226) GTP cyclohydrolase II [Escherichia coli K12] gb AAG56536.1 AE005379_4 (AE005379) GTP cyclohydrolase II (EC 3.5.4.25) [Escherichia coli O157:H7]	SEQ ID n-522
SEQ ID n° 6439	PL-4408.1	Contig9 from 659096 to 659239	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6440	PL-4407.1	Contig9 from 659400 to 659711	P	73%	sp P77614 YCIS_ECOLI HYPOTHETICAL 11.4 KDA PROTEIN IN PGPB-PYRF INTERGENIC REGION pir B64876 probable membrane protein yciS - Escherichia coli dbj BAA14833.1 (D90766) ORF_ID:0255#4; similar to [SwissProt Accession Number P44129] [Escherichia coli] gb AAC74361.1 (AE000226) orf, hypothetical protein [Escherichia coli K12] sp P45576 YCIW_ECOLI HYPOTHETICAL 44.5 KD PROTEIN IN PGPB-PYRF INTERGENIC REGION PRECURSOR pir C64876 yciM protein precursor - Escherichia coli dbj BAA14834.1 (D90766) ORF_ID:0255#5; similar to [SwissProt Accession Number P45576] [Escherichia coli] gb AAC74362.1 (AE000226) putative heat shock protein [Escherichia coli K12] gb AAG56533.1 AE005379_1 (AE005379) putative heat shock protein [Escherichia coli O157:H7] gb AAG56532.1 AE005378_11 (AE005378) orotidine- 5'-phosphate decarboxylase [Escherichia coli O157:H7] pir Q3KCPF translation initiation factor SUI (similarity) - Escherichia coli gb AAC74364.1 (AE000226) orf, hypothetical protein [Escherichia coli K12] gb AAC25764.1 (AF072709) putative transcriptional regulator [Streptomyces lividans] emb CAC14337.1 (AL445945) putative regulatory protein [Streptomyces coelicolor] pir C82971 conserved hypothetical protein PAS395 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08780.1 AE004952_2 (AE004952) conserved hypothetical protein [Pseudomonas aeruginosa]	#N/A	SEQ ID n-521
SEQ ID n° 6441	PL-1436.2	Contig9 from 659718 to 660887	P	84%	SEQ ID n-520		
SEQ ID n° 6442	PL-1435.1	Contig9 from 660932 to 661678	P	80%	#N/A		
SEQ ID n° 6443	PL-4406.1	Contig9 from 661668 to 661994	P	84%	SEQ ID n-519		
SEQ ID n° 6444	PL-1434.1	Contig9 from 662384 to 662989	P	40%			
SEQ ID n° 6445	PL-3797.1	Contig9 from 663014 to 663493	P	77%			

TABLEAU II

SEQ ID n° 6446	PL-1433.1	Contig9 from 663593 to 664873	m	37%	gb AAG31049.1 AF264948.11 (AF264948) hypothetical protein [Erwinia amylovora]	SEQ ID n-518
SEQ ID n° 6447	PL-4402.1	Contig9 from 664870 to 665232	m	No Hits found		#N/A
SEQ ID n° 6448	PL-1432.1	Contig9 from 665500 to 666849	p	58%	pir F81046 hypothetical protein NMB1759 - Neisseria meningitidis (group B strain MD58) gb AAF42100.1 (AE002525) conserved hypothetical protein [Neisseria meningitidis MC58]	SEQ ID n-517
SEQ ID n° 6449	PL-1431.1	Contig9 from 666937 to 671847	m	14%	dbj BAA34597.1 (AB020025) dermonecrotizing toxin [Bordetella bronchiseptica]	SEQ ID n-516
SEQ ID n° 6450	PL-1430.1	Contig9 from 672123 to 673148	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-515
SEQ ID n° 6451	PL-4400.1	Contig9 from 673294 to 673674	m	44%	emb CAA72334.3 (Y11597) reverse transcriptase/maturase [Sinorhizobium meliloti]	#N/A
SEQ ID n° 6452	PL-4397.1	Contig9 from 673801 to 674025	m	52%	gb AAD29042.1 AF130439.1 (AF130439) transposase [Pseudomonas putida]	#N/A
SEQ ID n° 6453	PL-4396.1	Contig9 from 674251 to 674478	m	No Hits found		#N/A
SEQ ID n° 6454	PL-1429.1	Contig9 from 674447 to 675514	m	45%	pir E82175 conserved hypothetical protein VC1631 [imported] - Vibrio cholerae (group O1 strain N15961) gb AAF94782.1 (AE004241) conserved hypothetical protein [Vibrio cholerae]	SEQ ID n-513

TABLEAU II

SEQ ID n° 6455	PL-1428.2	Contig9 from 675602 to 676615	p	72%	ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAE20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	#N/A
SEQ ID n° 6456	PL-1427.1	Contig9 from 676958 to 678025	m	No Hits found		SEQ ID n-511
SEQ ID n° 6457	PL-1426.1	Contig9 from 678902 to 679681	p	40%	dbj BAB07432.1 (AP001519) glycosyltransferase [Bacillus halodurans]	SEQ ID n-510
SEQ ID n° 6458	PL-1425.2	Contig9 from 679762 to 680946	p	No Hits found		SEQ ID n-509
SEQ ID n° 6459	PL-1424.1	Contig9 from 680948 to 681820	p	No Hits found		SEQ ID n-508
SEQ ID n° 6460	PL-1423.1	Contig9 from 681805 to 683190	p	37%	pir E82182 enterobactin synthetase component F-related protein VC1579 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94733.1 (AE004235) enterobactin synthetase component F-related protein [Vibrio cholerae]	SEQ ID n-507
SEQ ID n° 6461	PL-4393.1	Contig9 from 683169 to 683390	p	No Hits found		#N/A
SEQ ID n° 6462	PL-1422.1	Contig9 from 683691 to 684761	p	No Hits found		SEQ ID n-506
SEQ ID n° 6463	PL-1421.1	Contig9 from 684748 to 685518	p	No Hits found		SEQ ID n-505

TABLEAU II

SEQ ID n° 6464	PL-1420.1	Contig9 from 685515 to 686600	p	48%	pir D75096 aspartate aminotransferase (aspb- like1) PAB0774 - Pyrococcus abyssi (strain Orsay) emb CAB50073.1 (AJ248286) aspartate aminotransferase (aspB-like1) [Pyrococcus abyssi] sp O26358 NDK_METH_NUCLEOSIDE_DIPHOSPHATE KINASE (NDK) (NDP KINASE) pir D69132 nucleoside-diphosphate kinase (EC 2.7.4.6) - Methanobacterium thermoautotrophicum (strain Delta H) gb AAB84764.1 (AE000812) nucleoside diphosphate kinase [Methanothermobacter thermautotrophicus]	SEQ ID n-504
SEQ ID n° 6465	PL-3795.1	Contig9 from 686594 to 687064	p	50%	sp P51565 TNP9_ECOLI_TRANSPPOSASE FOR TRANSPON TN1721 pir JQ1477 transposase - Escherichia coli transposon Tn1721 emb CAA43641.1 (X61367) transposase [Escherichia coli] emb CAA90481.1 (Z50120) transposase [synthetic construct] ref NP_054620.1 unknown [Yersinia pestis] ref NP_047619.1 Yop targeted effector [Yersinia pestis] pir T43601 yop targeted effector yopT Yersinia pestis plasmid pCD1 gb AAC62582.1 (AF053946) unknown [Yersinia pestis] gb AAC69833.1 (AF074612) Yop targeted effector [Yersinia pestis] emb CAB54897.1 (AL117189) putative cytotoxic effector protein [Yersinia pestis]	SEQ ID n-2972
SEQ ID n° 6467	PL-1419.1	Contig9 from 687609 to 688580	m	56%	emb CAA36717.1 (X52478) dermonecrotic toxin (AA 1-1285) [Pasteurella multocida] emb CAB77354.1 (AL160331) hypothetical protein SCD8A.33c (fragment) [Streptomyces coelicolor A3(2)] emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)]	SEQ ID n-501 SEQ ID n-500 SEQ ID n-499
SEQ ID n° 6468	PL-1418.1	Contig9 from 688857 to 690563	m	36%		
SEQ ID n° 6469	PL-1417.1	Contig9 from 690778 to 691680	m	23%		
SEQ ID n° 6470	PL-1416.2	Contig9 from 691705 to 693786	m	22%		

TABLEAU II

SEQ ID n° 6471	PL-1415.2	Contig9 from 693796 to 695226	m	No Hits found		SEQ ID n-498
SEQ ID n° 6472	PL-1414.1	Contig9 from 695269 to 698304	m	No Hits found		SEQ ID n-497
SEQ ID n° 6473	PL-1413.1	Contig9 from 698330 to 702382	m	No Hits found		SEQ ID n-496
SEQ ID n° 6474	PL-3794.1	Contig9 from 702466 to 702882	m	No Hits found		SEQ ID n-2971
SEQ ID n° 6475	PL-4389.1	Contig9 from 702879 to 703301	m	43%	emb CAB77339.1 (AL160331) hypothetical protein SCD8A.18c [Streptomyces coelicolor A3(2)]	#N/A
SEQ ID n° 6476	PL-1412.1	Contig9 from 703314 to 704918	m	39%	emb CAB77340.1 (AL160331) hypothetical protein SCD8A.19c [Streptomyces coelicolor A3(2)]	SEQ ID n-495
SEQ ID n° 6477	PL-1411.1	Contig9 from 704915 to 705598	m	No Hits found		SEQ ID n-494
SEQ ID n° 6478	PL-4386.1	Contig9 from 705585 to 705764	m	No Hits found		#N/A
SEQ ID n° 6479	PL-3793.1	Contig9 from 705761 to 706219	m	No Hits found		SEQ ID n-2970
SEQ ID n° 6480	PL-1410.1	Contig9 from 706238 to 707404	m	26%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-493
SEQ ID n° 6481	PL-1409.1	Contig9 from 707459 to 708751	m	24%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-491
SEQ ID n° 6482	PL-1408.1	Contig9 from 708809 to 709885	m	30%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-490

TABLEAU II

SEQ ID n° 6483	PL-3792.1	Contig9 from 709959 to 710408	m 35%	emb CAB77342.1 (A1160331) hypothetical protein SCD8A.21c [Streptomyces coelicolor A3(2)] SEQ ID n-2969
SEQ ID n° 6484	PL-1407.1	Contig9 from 710937 to 712880	m 80%	sp P30850 RNB_ECOLI EXORIBONUCLEASE II (RIBONUCLEASE II) (RNase II) pir A64877 exoribonuclease II (EC 3.1.13.1) - Escherichia coli dbj BAAL4840.1 (D90766) Exoribonuclease II (EC 3.1.13.1) (Ribonuclease II) (RNase II). [Escherichia coli] dbj BAAL4848.1 (D90767) Exoribonuclease II (EC 3.1.13.1) (Ribonuclease II) (RNase II). [Escherichia coli] gb AAC74368.1 (AE000226) RNase II, mRNA degradation [Escherichia coli K12] SEQ ID n-489
SEQ ID n° 6485	PL-1406.1	Contig9 from 713020 to 713658	m 88%	sp P20625 END3_ECOLI ENDONUCLEASE III (DNA- (APURINIC OR APYRIMIDINIC SITE) LYASE) pir A32412 DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) endonuclease III [validated] - Escherichia coli pdb 2ABK Refinement Of The Native Structure Of Endonuclease Iii To A Resolution Of 1.85 Angstrom gb AAA24227.1 (J02857) endonuclease III [Escherichia coli] dbj BAAL5387.1 (D90806) Deoxyribonuclease (pyrimidine dimer) (EC 3.1.25.1) [Escherichia coli] dbj BAAL5394.1 (D90807) Deoxyribonuclease (pyrimidine dimer) (EC 3.1.25.1) [Escherichia coli] dbj BAAL5417.1 (D90808) Deoxyribonuclease (pyrimidine dimer) (EC 3.1.25.1) [Escherichia coli] gb AAC74705.1 (AE000258) endonuclease III; specific for apurinic and/or apyrimidinic sites [Escherichia coli K12] SEQ ID n-488
SEQ ID n° 6486	PL-1405.1	Contig9 from 713660 to 714358	m 78%	gb AAG56621.1 AE005386_12 (AE005386) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-487

TABLEAU II

SEQ ID n° 6487	PL-1404.1	Contig9 from 714355 to 714984	m	78%	gb AAG56620.1 AE005386_11 (AE005386) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-486
SEQ ID n° 6488	PL-1403.1	Contig9 from 714994 to 716073	m	76%	sp P76182 YDGO_EC01 HYPOTHETICAL 38.1 KD PROTEIN IN ADD-NTH INTERGENIC REGION pir H64919 probable membrane protein ydgo precursor - Escherichia coli gb AAC74702.1 (AE000258) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-485
SEQ ID n° 6489	PL-1402.1	Contig9 from 716086 to 718644	m	63%	pir G64919 probable iron-sulfur protein b1629 - Escherichia coli dbj BAA15384.1 (D90806) Glucose repression mediator protein. [Escherichia coli] dbj BAA15391.1 (D90807) Glucose repression mediator protein. [Escherichia coli] dbj BAA15414.1 (D90808) Glucose repression mediator protein. [Escherichia coli] gb AAC74701.1 (AE000258) putative membrane protein [Escherichia coli K12]	SEQ ID n-484
SEQ ID n° 6490	PL-1401.1	Contig9 from 718637 to 719269	m	74%	sp P77223 YDGM_EC01 PUTATIVE FERREDOXIN-LIKE PROTEIN IN ADD-NTH INTERGENIC REGION pir F64919 probable iron-sulfur protein b1628 precursor - Escherichia coli dbj BAA15383.1 (D90806) Ferredoxin II. [Escherichia coli] dbj BAA15390.1 (D90807) Ferredoxin II. [Escherichia coli] dbj BAA15413.1 (D90808) Ferredoxin II. [Escherichia coli] gb AAC74700.1 (AE000258) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-483
SEQ ID n° 6491	PL-3789.1	Contig9 from 719269 to 719850	m	87%	pir E64919 probable membrane protein b1627 - Escherichia coli gb AAC74699.1 (AE000258) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-2967
SEQ ID n° 6492	PL-4385.1	Contig9 from 719977 to 720417	m	56%	gb AAG56615.1 AE005386_6 (AE005386) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A

TABLEAU II

SEQ ID n° 6493	PL-1400.1	Contig9 from 720601 to 721638	p	77%	gb AAG56613.1 AE005386_4 (AE005386)orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n° 482
SEQ ID n° 6494	PL-1399.1	Contig9 from 721847 to 722818	p	79%	gb AAG57528.1 AE005471_5 (AE005471) putative cytochrome oxidase [Escherichia coli O157:H7]	SEQ ID n° 479
SEQ ID n° 6495	PL-4383.1	Contig9 from 723254 to 723535	p	No Hits found		#N/A
SEQ ID n° 6496	PL-4381.1	Contig9 from 724052 to 724351	m	93%	pir A82602 conserved plasmid protein XF2066 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84865.1 AE004023_1 (AE004023) conserved plasmid protein [Xylella fastidiosa]	#N/A
SEQ ID n° 6497	PL-3787.1	Contig9 from 724369 to 724833	m	64%	pir C82602 hypothetical protein XF2068 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84867.1 AE004023_3 (AE004023) hypothetical protein [Xylella fastidiosa]	SEQ ID n° 2965
SEQ ID n° 6498	PL-4379.1	Contig9 from 724963 to 725088	m	No Hits found		#N/A
SEQ ID n° 6499	PL-4378.1	Contig9 from 725172 to 725375	p	36%	pir B70537 hypothetical protein Rv1113 - Mycobacterium tuberculosis (strain H37RV) emb CAB09045.1 (Z95585) hypothetical protein Rv1113 [Mycobacterium tuberculosis]	#N/A
SEQ ID n° 6500	PL-4377.1	Contig9 from 725375 to 725752	p	45%	pir C70537 hypothetical protein Rv1114 - Mycobacterium tuberculosis (strain H37RV) emb CAB09046.1 (Z95585) hypothetical protein Rv1114 [Mycobacterium tuberculosis]	#N/A
SEQ ID n° 6501	PL-4376.1	Contig9 from 725868 to 726020	p	No Hits found		#N/A
SEQ ID n° 6502	PL-4375.1	Contig9 from 726379 to 726636	p	96%	gb AAC82515.1 (AF027767) PemI [Morganella morganii]	#N/A

TABLEAU II

SEQ ID n° 6503 PL-3786.1	Contig9 from 726581 to 726970	p 72%	ref NP_052994.1 plasmid stable inheritance protein [Plasmid R100] sp P13976 PEMK_ECOLI PEMK PROTEIN pir I64784 hypothetical protein 3 - Escherichia coli plasmids emb CAA29585.1 (X06240) ORF 3 (AA 1-133) [Enterobacteriaceae] gb AA26070.1 (M26840) ORF3 [Escherichia coli] dbj BAA78898.1 (AP000342) plasmid stable inheritance protein [Plasmid R100]	SEQ ID n° 2964
SEQ ID n° 6504 PL-4374.1	Contig9 from 727060 to 727287	p 46%	gb AAC82521.1 (AF027768) Muca [serratia marcescens]	#N/A
SEQ ID n° 6505 PL-4371.1	Contig9 from 727514 to 727762	p No Hits found	sp P22333 ADD_ECOLI ADENOSINE DEAMINASE (ADENOSINE AMINOHYDROLASE) pir A64919 adenosine deaminase (EC 3.5.4.4) - Escherichia coli dbj BAAL5374.1 (D90805) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase). [Escherichia coli] dbj BAAL5381.1 (D90806) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase). [Escherichia coli] dbj BAAL5411.1 (D90808) Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase). [Escherichia coli] gb AAC74695.1 (AE000258) adenosine deaminase [Escherichia coli K12]	#N/A
SEQ ID n° 6506 PL-1398.1	Contig9 from 727971 to 728972	m 69%		SEQ ID n° 478

TABLEAU II

SEQ ID n° 6507	PL-1397.1	Contig9 from 729050 to 730597	m	54%	sp P77804 YDGA_ECOLI HYPOTHETICAL 54.7 KDA PROTEIN IM MANA-GUSC INTERGENIC REGION pir H64917 probable membrane protein ydga - Escherichia coli dbj BAA15362.1 (D90804) ORF ID:0312#14; similar to [SwissProt Accession Number P32128] [Escherichia coli] dbj BAA15366.1 (D90805) ORF_ID:0312#14; similar to [SwissProt Accession Number P32128] [Escherichia coli] gb AAC74686.1 (AE000257) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-477
SEQ ID n° 6508	PL-1396.1	Contig9 from 730737 to 731909	m	73%	gb AAG56600.1 AE005385_1 (AE005385) mannose-6- phosphate isomerase [Escherichia coli O157:H7]	SEQ ID n-476
SEQ ID n° 6509	PL-1395.1	Contig9 from 732214 to 733608	p	89%	gb AAG56598.1 AE005384_8 (AE005384) fumarase C= fumarate hydratase Class II; isozyme [Escherichia coli O157:H7]	SEQ ID n-475
SEQ ID n° 6510	PL-3785.1	Contig9 from 733676 to 734146	m	64%	gb AAG22119.1 (AY008264) hypothetical protein [Yersinia enterocolitica]	SEQ ID n-2963
SEQ ID n° 6511	PL-3784.1	Contig9 from 734143 to 734589	m	66%	gb AAG322120.1 (AY008264) hypothetical protein [Yersinia enterocolitica]	SEQ ID n-2962
SEQ ID n° 6512	PL-1394.1	Contig9 from 734662 to 735588	m	72%	gb AAF68950.1 (AF231032) DNA replication terminus site-binding protein [Yersinia pestis]	SEQ ID n-474
SEQ ID n° 6513	PL-3783.1	Contig9 from 736403 to 736870	p	No Hits found		
SEQ ID n° 6514	PL-4369.1	Contig9 from 736874 to 737092	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6515 PL-1393.1	Contig9 from 737363 to 738475	p 80%	pir D83174 probable acetylpolylamine aminohydrolase PA3774 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07161.1 AB004796_6 (AB004796) probable acetylpolylamine aminohydrolase [Pseudomonas aeruginosa] SEQ ID n-473
SEQ ID n° 6516 PL-1392.1	Contig9 from 738696 to 739295	m 54%	pir JW0070 chitin binding protein 21 precursor Serratia marcescens dbj BAA31569.1 (AB015998) CHP21 precursor [Serratia marcescens] SEQ ID n-472
SEQ ID n° 6517 PL-1391.1	Contig9 from 739488 to 740321	p 54%	pir H69795 conserved hypothetical protein yesf Bacillus subtilis emb CAB12507.1 (Z99107) alternate gene name: yeem, yfxB-similar to hypothetical proteins [Bacillus subtilis] SEQ ID n-471
SEQ ID n° 6518 PL-1390.2	Contig9 from 740404 to 742014	m 67%	sp P06202 OPPA_SALTY PERIPLASMIC OLIGOPEPTIDE- BINDING PROTEIN PRECURSOR pir QREBOA oligo peptide-binding protein precursor - Salmonella typhimurium emb CAA29039.1 (X05491) Opp A (AA1-542) [Salmonella typhimurium] emb CAA27785.1 (X04194) precursor polypeptide [Salmonella typhimurium] SEQ ID n-470
SEQ ID n° 6519 PL-1389.2	Contig9 from 742645 to 744075	p 72%	pir T35441 aldehyde dehydrogenase - Streptomyces coelicolor emb CAA19895.1 (AL031035) aldehyde dehydrogenase [Streptomyces coelicolor A3(2)] SEQ ID n-468
SEQ ID n° 6520 PL-1388.1	Contig9 from 744235 to 744864	p 19%	gb AAB97824.1 (AF013216) unknown [Mycococcus xanthus] SEQ ID n-467

TABLEAU II

SEQ ID n° 6521	PL-1387.1	Contig9 from 745159 to 746436	p	73%	sp P50457 GOAG_ECOLI_4-AMINO-BUTYRATE AMINOTRANSFERASE (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA TRANSAMINASE) (GLUTAMATE:SUCCINIC SEMIALDEHYDE TRANSAMINASE) (GABA AMINOTRANSFERASE) (GABA-AT) pir A64879 4-aminobutyrate transaminase (EC 2.6.1.19) goag - Escherichia coli gb AAC45301.1 (U38543) GABA- aminotransferase [Escherichia coli] dbj BAA14871.1 (D90768) 4-aminobutyrate aminotransferase (EC 2.6.1.19) (Gamma- amino-N-butyrate transaminase) (GABA transaminase) (Glutamate:succinic semialdehyde transaminase) (GABA aminotransferase). [Escherichia coli] gb AAC74384.1 (AE000228) 4-aminobutyrate aminotransferase [Escherichia coli K12]	SEQ ID n-466
SEQ ID n° 6522	PL-4366.1	Contig9 from 746475 to 746843	p	56%	sp P42621 YHAH_ECOLI_HYPOTHETICAL_14.3_KD PROTEIN IN EXUR-TDCC INTERGENIC REGION pir D65099 hypothetical 14.3 kD protein in exur- tdcc intergenic region - Escherichia coli (strain K-12) gb AAC76138.1 (AB000392) putative cytochrome [Escherichia coli K12] gb AAG58236.1 AE005540_1 (AE005540) putative cytochrome [Escherichia coli O157:H7] pir A83578 conserved hypothetical protein PA0534 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03923.1 AE004490_3 (AE004490) conserved hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 6523	PL-1386.1	Contig9 from 746901 to 748442	p	37%	gb AAG10092.1 U79570_1 (U79570) glucose dehydrogenase [Bacillus licheniformis]	SEQ ID n-465
SEQ ID n° 6524	PL-1385.1	Contig9 from 748641 to 749411	p	49%		SEQ ID n-464
SEQ ID n° 6525	PL-1384.2	Contig9 from 749565 to 750302	m	No Hits found		SEQ ID n-463

TABLEAU II

SEQ ID n° 6526	PL-1383.2	Contig9 from 750525 to 751541	p	64%	pir [E83504 probable oxidoreductase PA1137 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04526.1 AE004543_10 (AE004543) probable oxidoreductase [Pseudomonas aeruginosa] SEQ ID n-462
SEQ ID n° 6527	PL-1382.1	Contig9 from 751982 to 753907	p	34%	pir [H82234 probable glutamate decarboxylase VC1149 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94308.1 (AE004195) glutamate decarboxylase, putative [Vibrio cholerae] SEQ ID n-461
SEQ ID n° 6528	PL-1381.1	Contig9 from 753952 to 755160	p	83%	sp PI8199 TYRP_ECOLI TYROSINE-SPECIFIC TRANSPORT PROTEIN (TYROSINE PERMEASE) pir [GRECY tyrosine- specific transport protein - Escherichia coli dbj BAAL5730.1 (D90832) Tyrosine-specific transport protein (Tyrosine permease). [Escherichia coli] gb AAC74977.1 (AE000284) tyrosine-specific transport system [Escherichia coli K12] SEQ ID n-460
SEQ ID n° 6529	PL-3781.1	Contig9 from 755274 to 755708	p	72%	ref NP_052313.1 ORF C8 [Ralstonia solanacearum] dbj BAA32221.1 (AB015669) ORF C8 [Ralstonia solanacearum] SEQ ID n-2960
SEQ ID n° 6530	PL-1380.1	Contig9 from 755965 to 756474	p	27%	ref NP_073098.1 conserved hypothetical protein [Mycoplasma genitalium] sp P47666 Y427_MYCGE HYPOTHETICAL PROTEIN MG427 pir [B64247 conserved hypothetical protein MG427 - Mycoplasma genitalium gb AAC72448.1 (U39725) conserved hypothetical protein [Mycoplasma genitalium] SEQ ID n-459
SEQ ID n° 6531	PL-4364.1	Contig9 from 756635 to 756949	m	No Hits found	#N/A
SEQ ID n° 6532	PL-1379.1	Contig9 from 757474 to 759237	p	35%	pir [T44585 acyl-CoA oxidase homolog [imported] Streptomyces fradiae gb AAD40800.1 AF145049_1 (AF145049) acyl-CoA oxidase [Streptomyces fradiae] SEQ ID n-457

TABLEAU II

SEQ ID n° 6533	PL-1378.1	Contig9 from 759499 to 760281	m	57%	gb AAC38629.1 (AF047028) insecticidal toxin complex protein TccB [Photorhabdus luminescens]	SEQ ID n-456
SEQ ID n° 6534	PL-1377.1	Contig9 from 760146 to 761231	m	48%	gb AAC38629.1 (AF047028) insecticidal toxin complex protein TccB [Photorhabdus luminescens]	SEQ ID n-455
SEQ ID n° 6535	PL-4363.1	Contig9 from 761153 to 761314	m	52%	gb AAC38629.1 (AF047028) insecticidal toxin complex protein TccB [Photorhabdus luminescens]	#N/A
SEQ ID n° 6536	PL-4361.1	Contig9 from 761354 to 761590	m	57%	pir B47048 plasmid stabilization protein ParE - plasmid RK2	#N/A
SEQ ID n° 6537	PL-4360.1	Contig9 from 761503 to 761622	m	72%	pir B82608 plasmid stabilization protein XF2032 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84834.1 AE004021.11 (AE004021) plasmid stabilization protein [Xylella fastidiosa]	#N/A
SEQ ID n° 6538	PL-4359.1	Contig9 from 761659 to 761913	m	79%	sp P22995 PAD4_ECOLI PARD PROTEIN pir A37141 pard protein - Escherichia coli plasmid RP4 pir A47048 plasmid stabilization protein Pard - plasmid RK2 pir S70153 pard protein - Xanthomonas sp pir S32830 pard protein - Xanthomonas sp. plasmid RP1 transposon Tn5053 gb AAA91498.1 (L03728) putative [Escherichia coli] gb AAA92774.1 (L05507) pard gene product [Plasmid RK2] gb AAA26418.1 (M59825) pard [Plasmid RP4] gb AAA98334.1 (L40585) putative [Xanthomonas sp. W17] gb AAB67690.1 (U75325) pard [Cloning vector pJB321]	#N/A
SEQ ID n° 6539	PL-4358.1	Contig9 from 762764 to 762964	p	40%	pir T28654 transposase - Pseudomonas putida plasmid pPGH1 emb CAA70598.1 (V09450) transposase [Pseudomonas putida]	#N/A
SEQ ID n° 6540	PL-1376.1	Contig9 from 762971 to 763627	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6541	PL-1375.1	Contig9 from 763770 to 764681	p	44%	emb CAA07406.1 (AJ006986) transmembrane protein [Streptococcus pneumoniae]	SEQ ID n-454
SEQ ID n° 6542	PL-1374.1	Contig9 from 764998 to 766005	m	No Hits found	pir E70047 conserved hypothetical protein yvrK Bacillus subtilis emb CAB15314.1 (Z99120) similar to hypothetical proteins [Bacillus subtilis] emb CAB15329.1 (Z99121) similar to hypothetical proteins [Bacillus subtilis] emb CAA11727.1 (AJ223978) YvrK protein [Bacillus subtilis]	SEQ ID n-453
SEQ ID n° 6543	PL-1373.1	Contig9 from 766541 to 767707	m	52%	pir T17443 salicyl-AMP ligase (EC 6.2.1.-) ybte [similarity] - Yersinia pestis gb AA093464.1 (U50364) Ybte [Yersinia pestis] gb AAC69591.1 (AF091251) salicyl-AMP ligase Ybte [Yersinia pestis] emb CAA21394.1 (AL031866) ORF 71, len=525 aa, ybte, 100% identity in 525 aa overlap, with YPUS0364_2 Yersinia pestis yersiniabactin 2,3-dihydroxybenzoate- AMP ligase (ybte) (525 aa), Fasta scores: opt: 3451, E(): 0	SEQ ID n-452
SEQ ID n° 6544	PL-1372.1	Contig9 from 767900 to 770833	m	35%	pir T17442 ybtt protein - Yersinia pestis gb AAC69590.1 (AF091251) Ybtt [Yersinia pestis]	SEQ ID n-451
SEQ ID n° 6545	PL-1371.1	Contig9 from 770833 to 771609	m	56%	pir T30343 irp3 protein - Yersinia enterocolitica emb CAA73128.1 (Y12527) Irp3 protein [Yersinia enterocolitica]	SEQ ID n-450
SEQ ID n° 6546	PL-1370.1	Contig9 from 771636 to 772733	m	56%		SEQ ID n-449

TABLEAU II

SEQ ID n° 6547 PL-1369.1	Contig9 from 772730 to 784456	m 23%	<p>pir T17440 probable polyketide synthase - Yersinia pestis gb AAC69588.1 (AF091251) Ybt peptide/polyketide synthetase HMWP1 [Yersinia pestis] emb CAA21391.1 (AL031866) ORF68, len=3163 aa, irp1, function=synthesis of siderophore yersiniabactin, product=HMWP1 protein, 97.9% identity in 3163 aa overlap to YEIRPOP_1 Y.enterocolitica irp1, Fasta scores: opt: 2088, E(): 0 [Yersinia pestis]</p>	SEQ ID n-447
SEQ ID n° 6548 PL-1368.1	Contig9 from 784456 to 790605	m 61%	<p>pir T17439 peptide synthetase homolog irp2 - Yersinia pestis gb AAC69587.1 (AF091251) Ybt peptide synthetase HMWP2 [Yersinia pestis] emb CAA21390.1 (AL031866) ORF67, len=2041 aa, irp2, function=synthesis of siderophore yersiniabactin, product=HMWP2 protein 98.6% identity in 2035 aa overlap to HMP2_YEREN. also highly similar to ANGR_VIBAN, (1048 aa), 44.4% identity in 917 aa overlap, Fasta scores: > pir T47045 hypothetical protein ybtP [imported] - Yersinia pestis emb CAA21388.1 (AL031866) ORF 65, len=600 aa, yersiniabactin uptake, ABC Transporter, similar to many, eg. MTCV02B10_12 M. tuberculosis (859 aa), 35.7% identity in 577 aa overlap Fasta scores: opt: 1064, E(): 0 [Yersinia pestis]</p>	SEQ ID n-446
SEQ ID n° 6549 PL-1366.1	Contig9 from 790648 to 792450	m 47%	<p>pir T47045 hypothetical protein ybtP [imported] - Yersinia pestis emb CAA21388.1 (AL031866) ORF 65, len=600 aa, yersiniabactin uptake, ABC Transporter, similar to many, eg. MTCV02B10_12 M. tuberculosis (859 aa), 35.7% identity in 577 aa overlap Fasta scores: opt: 1064, E(): 0 [Yersinia pestis]</p>	SEQ ID n-445
SEQ ID n° 6550 PL-1365.1	Contig9 from 792395 to 794113	m 49%	<p>pir T47045 hypothetical protein ybtP [imported] - Yersinia pestis emb CAA21388.1 (AL031866) ORF 65, len=600 aa, yersiniabactin uptake, ABC Transporter, similar to many, eg. MTCV02B10_12 M. tuberculosis (859 aa), 35.7% identity in 577 aa overlap Fasta scores: opt: 1064, E(): 0 [Yersinia pestis]</p>	SEQ ID n-444

TABLEAU II

SEQ ID n° 6551	PL-1364.1	Contig9 from 794187 to 795395	m	51%	pir T47043 hypothetical protein ybtX [imported] - Yersinia pestis emb CAA21386.1 (AL031866) ORF63, len=462 aa, putative transmembrane protein, similarity to E. coli ECAMP03_1 E. coli ampG3 gene, 27.1% identity in 376 aa overlap, Fasta scores: opt: 311, E(): 1.1e-12 [Yersinia pestis] emb CAA86212.1 (Z38065) FyuA precursor [Escherichia coli] pir S74448 regulatory protein pcr - Synecocystis sp. (strain PCC 6803) dbj BAA16600.1 (D90899) regulatory protein pcr [Synecocystis sp.]	SEQ ID n-443
SEQ ID n° 6552	PL-1363.1	Contig9 from 795428 to 797434	m	49%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] gb AAA81002.1 (U11258) extracellular lipase [Serratia marcescens] pir B47055 DNA-invertase - Erwinia amylovora transposon Tn5393 gb AAC37003.1 (M77502) putative resolvase [Pseudomonas syringae] gb AA98411.2 (M96392) resolvase [Erwinia amylovora] gb AA27439.2 (M95402) resolvase [Transposon Tn5393] gb AAG39040.1 AF262622_2 (AF262622) putative resolvase [Aeromonas salmonicida subsp. salmonicida] sp P44190 YE19_HAEIN HYPOTHETICAL PROTEIN HI1419 pir B64029 hypothetical protein HI1419 - Haemophilus influenzae (strain Rd KW20) gb AAC23069.1 (U32821) H. influenzae predicted coding region HI1419 [Haemophilus influenzae Rd]	SEQ ID n-442
SEQ ID n° 6553	PL-1362.1	Contig9 from 797731 to 798702	p	24%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] gb AAA81002.1 (U11258) extracellular lipase [Serratia marcescens] pir B47055 DNA-invertase - Erwinia amylovora transposon Tn5393 gb AAC37003.1 (M77502) putative resolvase [Pseudomonas syringae] gb AA98411.2 (M96392) resolvase [Erwinia amylovora] gb AA27439.2 (M95402) resolvase [Transposon Tn5393] gb AAG39040.1 AF262622_2 (AF262622) putative resolvase [Aeromonas salmonicida subsp. salmonicida] sp P44190 YE19_HAEIN HYPOTHETICAL PROTEIN HI1419 pir B64029 hypothetical protein HI1419 - Haemophilus influenzae (strain Rd KW20) gb AAC23069.1 (U32821) H. influenzae predicted coding region HI1419 [Haemophilus influenzae Rd]	SEQ ID n-441
SEQ ID n° 6554	PL-1361.1	Contig9 from 798990 to 800015	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] gb AAA81002.1 (U11258) extracellular lipase [Serratia marcescens] pir B47055 DNA-invertase - Erwinia amylovora transposon Tn5393 gb AAC37003.1 (M77502) putative resolvase [Pseudomonas syringae] gb AA98411.2 (M96392) resolvase [Erwinia amylovora] gb AA27439.2 (M95402) resolvase [Transposon Tn5393] gb AAG39040.1 AF262622_2 (AF262622) putative resolvase [Aeromonas salmonicida subsp. salmonicida] sp P44190 YE19_HAEIN HYPOTHETICAL PROTEIN HI1419 pir B64029 hypothetical protein HI1419 - Haemophilus influenzae (strain Rd KW20) gb AAC23069.1 (U32821) H. influenzae predicted coding region HI1419 [Haemophilus influenzae Rd]	SEQ ID n-440
SEQ ID n° 6555	PL-1360.1	Contig9 from 800033 to 801886	m	79%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] gb AAA81002.1 (U11258) extracellular lipase [Serratia marcescens] pir B47055 DNA-invertase - Erwinia amylovora transposon Tn5393 gb AAC37003.1 (M77502) putative resolvase [Pseudomonas syringae] gb AA98411.2 (M96392) resolvase [Erwinia amylovora] gb AA27439.2 (M95402) resolvase [Transposon Tn5393] gb AAG39040.1 AF262622_2 (AF262622) putative resolvase [Aeromonas salmonicida subsp. salmonicida] sp P44190 YE19_HAEIN HYPOTHETICAL PROTEIN HI1419 pir B64029 hypothetical protein HI1419 - Haemophilus influenzae (strain Rd KW20) gb AAC23069.1 (U32821) H. influenzae predicted coding region HI1419 [Haemophilus influenzae Rd]	SEQ ID n-439
SEQ ID n° 6556	PL-4344.1	Contig9 from 802645 to 803025	p	39%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] gb AAA81002.1 (U11258) extracellular lipase [Serratia marcescens] pir B47055 DNA-invertase - Erwinia amylovora transposon Tn5393 gb AAC37003.1 (M77502) putative resolvase [Pseudomonas syringae] gb AA98411.2 (M96392) resolvase [Erwinia amylovora] gb AA27439.2 (M95402) resolvase [Transposon Tn5393] gb AAG39040.1 AF262622_2 (AF262622) putative resolvase [Aeromonas salmonicida subsp. salmonicida] sp P44190 YE19_HAEIN HYPOTHETICAL PROTEIN HI1419 pir B64029 hypothetical protein HI1419 - Haemophilus influenzae (strain Rd KW20) gb AAC23069.1 (U32821) H. influenzae predicted coding region HI1419 [Haemophilus influenzae Rd]	SEQ ID n-438
SEQ ID n° 6557	PL-3780.1	Contig9 from 803079 to 803381	p	47%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] gb AAA81002.1 (U11258) extracellular lipase [Serratia marcescens] pir B47055 DNA-invertase - Erwinia amylovora transposon Tn5393 gb AAC37003.1 (M77502) putative resolvase [Pseudomonas syringae] gb AA98411.2 (M96392) resolvase [Erwinia amylovora] gb AA27439.2 (M95402) resolvase [Transposon Tn5393] gb AAG39040.1 AF262622_2 (AF262622) putative resolvase [Aeromonas salmonicida subsp. salmonicida] sp P44190 YE19_HAEIN HYPOTHETICAL PROTEIN HI1419 pir B64029 hypothetical protein HI1419 - Haemophilus influenzae (strain Rd KW20) gb AAC23069.1 (U32821) H. influenzae predicted coding region HI1419 [Haemophilus influenzae Rd]	SEQ ID n-2959

TABLEAU II

SEQ ID n° 6558	PL-4341.1	Contig9 from 803378 to 803656	p	78%	sp P44191 YE20_HAEM HYPOTHETICAL PROTEIN HI1420 pir C64029 hypothetical protein HI1420 - Haemophilus influenzae (strain Rd KW20) gb AAC23070.1 (U32821) H. influenzae predicted coding region HI1420 [Haemophilus influenzae Rd] gb AAC80183.1 (U73041) plasmid stability-like protein [Acidithiobacillus ferrooxidans] pir A82603 hypothetical protein XF2074 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84873.1 AE004023_9 (AE004023) hypothetical protein [Xylella fastidiosa] pir B82603 hypothetical protein XF2075 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84874.1 AE004023_10 (AE004023) hypothetical protein [Xylella fastidiosa] gb AAC80183.1 (U73041) plasmid stability-like protein [Acidithiobacillus ferrooxidans] ref NP_037718.1 tail fiber [Bacteriophage HK97] gb AAF31111.1 (AF069529) tail fiber [Bacteriophage HK97]	#N/A
SEQ ID n° 6559	PL-4339.1	Contig9 from 803869 to 804003	p	46%		#N/A
SEQ ID n° 6560	PL-4337.1	Contig9 from 804094 to 804384	m	70%		#N/A
SEQ ID n° 6561	PL-4336.1	Contig9 from 804372 to 804644	m	63%		#N/A
SEQ ID n° 6562	PL-4335.1	Contig9 from 804739 to 804873	p	43%		#N/A
SEQ ID n° 6563	PL-1359.1	Contig9 from 805289 to 806164	p	34%		SEQ ID n-437
SEQ ID n° 6564	PL-4333.1	Contig9 from 806409 to 806663	m	No Hits found		#N/A
SEQ ID n° 6565	PL-1358.1	Contig9 from 807388 to 807939	p	52%	gb AAB92577.1 (AF037441) putative 19.5 kDa protein [Edwardsiella ictaluri]	SEQ ID n-436
SEQ ID n° 6566	PL-1357.1	Contig9 from 807947 to 809428	p	73%	gb AAB92576.1 (AF037441) putative 54.5 kDa protein [Edwardsiella ictaluri]	SEQ ID n-435

TABLEAU II

SEQ ID n° 6567	PL-3779.1	Contig9 from 809485 to 809979	p	53%	gb AAB92575.1 (AF037441) putative 17.8 kDa protein [Edwardsiella ictaluri]	SEQ ID n-2957
SEQ ID n° 6568	PL-4332.1	Contig9 from 810031 to 810474	p	45%	gb AAB92574.1 (AF037441) putative 18.8 kDa protein [Edwardsiella ictaluri]	#N/A
SEQ ID n° 6569	PL-1356.1	Contig9 from 810479 to 812290	p	46%	pir C83349 hypothetical protein PA2369 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05757.1 AE004663_3 (AE004663) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-434
SEQ ID n° 6570	PL-1355.1	Contig9 from 812281 to 813291	p	44%	pir D83349 hypothetical protein PA2370 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05758.1 AE004663_4 (AE004663) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-433
SEQ ID n° 6571	PL-1354.1	Contig9 from 813316 to 815322	p	50%	pir G83310 conserved hypothetical protein PA2685 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06073.1 AE004696_7 (AE004696) conserved hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-432
SEQ ID n° 6572	PL-4330.1	Contig9 from 815950 to 816252	p	43%	pir H83542 hypothetical protein PA0824 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04213.1 AE004517_8 (AE004517) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 6573	PL-1352.1	Contig9 from 816266 to 817369	p	44%	pir D83350 hypothetical protein PA2360 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05748.1 AE004662_3 (AE004662) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-430
SEQ ID n° 6574	PL-1350.1	Contig9 from 818043 to 819440	p	40%	pir E82499 hypothetical protein VCA0114 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96028.1 (AE004353) hypothetical protein [Vibrio cholerae]	SEQ ID n-429

TABLEAU II

SEQ ID n° 6575	PL-1349.1	Contig9 from 819440 to 820060	p 29%	pir [F82499 hypothetical protein VCA0115 [imported] - Vibrio cholerae (group 01 strain N16961) gb AAF96029.1 (AE004353) hypothetical protein [Vibrio cholerae] pir [H83437 hypothetical protein PA1669 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05058.1 AE004594_10 (AE004594) hypothetical protein [Pseudomonas aeruginosa] pir [G83635 probable ClpA/B-type chaperone PA0090 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG03480.1 AE004447_13 (AE004447) probable ClpA/B-type chaperone [Pseudomonas aeruginosa]	SEQ ID n-427
SEQ ID n° 6576	PL-1348.1	Contig9 from 820076 to 823585	p 12%		SEQ ID n-426
SEQ ID n° 6577	PL-1347.1	Contig9 from 823578 to 826160	p 61%		
SEQ ID n° 6578	PL-1346.1	Contig9 from 826210 to 827469	p No Hits found	pir [B83182 probable two-component response regulator PA3714 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07101.1 AE004790_6 (AE004790) probable two- component response regulator [Pseudomonas aeruginosa] sp P40330 BVGS_BORPA VIRULENCE SENSOR PROTEIN BVGS PRECURSOR pir [S17946 virulence sensor protein bvgs precursor - Bordetella parapertussis emb CAA37124.1 (X52948) bvgs product, put. sensor protein [Bordetella parapertussis]	SEQ ID n-424
SEQ ID n° 6579	PL-1345.1	Contig9 from 827500 to 828126	p 66%		SEQ ID n-423
SEQ ID n° 6580	PL-1344.1	Contig9 from 828298 to 831741	p 44%		
SEQ ID n° 6581	PL-4326.1	Contig9 from 831886 to 832086	p No Hits found		SEQ ID n-422

#N/A

TABLEAU II

SEQ ID n° 6582	PL-1343.1	Contig9 from 832229 to 833197	p	57%	pir C81839 probable transposase for IS1655 NMA1481 [imported] - Neisseria meningitidis (group B strain MD58, group A strain Z2491) emb CAB84714.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] emb CAB84719.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] SEQ ID n-421
SEQ ID n° 6583	PL-3777.1	Contig9 from 833179 to 833637	p	38%	ref NP_040375.1 entry exclusion protein 2 (exc2) [Plasmid COLE1] gb AB59140.1 (J01566) entry exclusion protein 2 (exc2) [Plasmid COLE1] SEQ ID n-3955
SEQ ID n° 6584	PL-4325.1	Contig9 from 833693 to 833947	p	47%	gb AAD17306.1 (AF121418) putative Phd protein [Francisella tularensis subsp. novicida] #N/A
SEQ ID n° 6585	PL-4324.1	Contig9 from 834218 to 834523	m	51%	gb AAG54353.1 AE005182_2 (AE005182) putative toxin of gyrase inhibiting toxin-antitoxin system [Escherichia coli O157:H7] #N/A
SEQ ID n° 6586	PL-4323.1	Contig9 from 834525 to 834764	m	53%	gb AAG54352.1 AE005182_1 (AE005182) putative antitoxin of gyrase inhibiting toxin- antitoxin system [Escherichia coli O157:H7] #N/A
SEQ ID n° 6587	PL-3776.1	Contig9 from 834852 to 835223	m	No Hits found	SEQ ID n-2954
SEQ ID n° 6588	PL-1342.2	Contig9 from 835518 to 836090	m	No Hits found	SEQ ID n-420
SEQ ID n° 6589	PL-1341.1	Contig9 from 836510 to 837829	m	87%	emb CAA28394.1 (X04691) xylose isomerase (AA 1- 444) [Escherichia coli] SEQ ID n-419

TABLEAU II

SEQ ID n° 6590	PL-1340.1	Contig9 from 838140 to 839321	p	81%	sp P37390 XYLR_ECOLI_XYLOSE OPERON REGULATORY PROTEIN pir S47790 xylose operon regulatory protein - Escherichia coli gb AAB18546.1 (U00039) xylr [Escherichia coli] gb AAC76593.1 (AE000434) putative regulator of xyl operon [Escherichia coli K12] gb AAG58718.1 AE005583_10 (AE005583) putative regulator of xyl operon [Escherichia coli O157:H7]	SEQ ID n-418
SEQ ID n° 6591	PL-1339.1	Contig9 from 839362 to 840804	m	80%	pir H82185 6-phospho-beta-glucosidase VC1558 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94712.1 (AE004233) 6- phospho-beta-glucosidase [Vibrio cholerae] pir T18583 glucosylceramidase (EC 3.2.1.45) precursor - Caenorhabditis elegans emb CAA20283.1 (AL031254) predicted using Genefinder-contains similarity to Pfam domain: PF02055 (O-Glycosyl hydrolase family 30), Score=571.9, E-value=1.3e-168, N=1-cDNA EST yk386f5.3 comes from this gene-cDNA EST yk206c8.5 comes from this gene-cDNA EST yk448c6.5 co> emb CAB02924.1 (Z81058) predicted using Genefinder-contains similarity to Pfam domain: PF02055 (O- Glycosyl hydrolase family 30), Score=571.9, E-value=1.3e-168, N=1-cDNA EST yk386f5.3 comes from this gene-cDNA EST yk206c8.5 comes from this gene-cDNA EST yk448c6.5 comes from this gene-cDNA EST yk448c6.5 comes from this emb CAB77656.1 (AJ390519) hypothetical protein [Candida albicans]	SEQ ID n-416
SEQ ID n° 6592	PL-1338.2	Contig9 from 840843 to 842156	m	49%	emb NP_052450.1 yaca [Plasmid Colib-p9] dbj BAA75089.1 (AB021078) yaca [Plasmid Colib- p9]	SEQ ID n-415
SEQ ID n° 6593	PL-1337.2	Contig9 from 842346 to 843224	p	60%		SEQ ID n-414
SEQ ID n° 6594	PL-4321.1	Contig9 from 843528 to 843806	p	46%		#N/A

TABLEAU II

SEQ ID n° 6595	PL-4319.1	Contig9 from 843803 to 844093	p	52%	ref NP_052451.1 yacB [Plasmid Colib-P9] dbj BAA75090.1 (AB021078) yacB [Plasmid Colib-P9]	#N/A
SEQ ID n° 6596	PL-3775.1	Contig9 from 844312 to 844773	m	37%	pir G70799 hypothetical protein Rv3750c - Mycobacterium tuberculosis (strain H37RV) emb CAA18072.1 (AL022121) hypothetical protein Rv3750c [Mycobacterium tuberculosis]	SEQ ID n-2953
SEQ ID n° 6597	PL-1336.1	Contig9 from 845415 to 846374	p	No Hits found	gb AAC38151.1 (AF034098) lipase [Pseudomonas sp. B11-1]	SEQ ID n-413
SEQ ID n° 6598	PL-1335.1	Contig9 from 846711 to 847631	m	52%	ref NP_053106.1 orf44 [Escherichia coli] dbj BAA84879.1 (AB024946) orf44 [Escherichia coli]	SEQ ID n-412
SEQ ID n° 6599	PL-4317.1	Contig9 from 847961 to 848212	p	81%	sp Q60228 RELX_ECOLI HYPOTHETICAL RELE-LIKE PROTEIN gb AAB61759.1 (M26308) ORF6 [Plasmid IncF]	#N/A
SEQ ID n° 6600	PL-4316.1	Contig9 from 848209 to 848496	p	85%	dbj BAB20938.1 (AB053207) endo-beta-N- acetylglucosaminidase [Flavobacterium sp. SK1022]	#N/A
SEQ ID n° 6601	PL-1334.1	Contig9 from 848652 to 849563	p	22%	ref NP_071207.1 molybdopterine oxidoreductase, molybdopterine binding subunit [Archaeoglobus fulgidus] pir H69547	SEQ ID n-411
SEQ ID n° 6602	PL-1333.2	Contig9 from 849767 to 853213	p	30%	molybdopterine oxidoreductase, molybdopterine binding subunit homolog Archaeoglobus fulgidus gb AAB91274.1 (AE001111) molybdopterine oxidoreductase, molybdopterine binding subunit [Archaeoglobus fulgidus]	SEQ ID n-410
SEQ ID n° 6603	PL-1332.1	Contig9 from 853879 to 854991	p	No Hits found		SEQ ID n-409

TABLEAU II

SEQ ID n° 6604 PL-1331.1	Contig9 from 855248 to 856579	p	85%	pir F83628 beta-alanine--pyruvate transaminase PA0132 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03522.1 AE004451_3 (AE004451) beta-alanine- -pyruvate transaminase [Pseudomonas aeruginosa]	SEQ ID n-408
SEQ ID n° 6605 PL-1330.1	Contig9 from 856700 to 859111	m	43%	gb AAF33136.1 AF196567_12 (AF196567) pdtorfL [Pseudomonas stutzeri] pdb 1B65 A Chain A, Structure Of L- Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold pdb 1B65 B Chain B, Structure Of L- Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold pdb 1B65 C Chain C, Structure Of L- Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold pdb 1B65 D Chain D, Structure Of L- Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold pdb 1B65 E Chain E, Structure Of L- Aminopeptidase D-Ala-EsteraseAMIDASE FROM Ochrobactrum Anthropi, A Prototype For The Serine Aminopeptidases, Reveals A New Variant Among The Ntn Hydrolase Fold	SEQ ID n-407
SEQ ID n° 6606 PL-1329.1	Contig9 from 859477 to 860670	p	62%		
SEQ ID n° 6607 PL-4315.1	Contig9 from 861082 to 861366	m	No Hits found		SEQ ID n-405

#N/A

TABLEAU II

SEQ ID n° 6608	PL-4314.1	Contig9 from 861586 to 861882	m	No Hits found	#N/A
SEQ ID n° 6609	PL-4313.1	Contig9 from 862765 to 862944	m	35%	#N/A
SEQ ID n° 6610	PL-1328.1	Contig9 from 863081 to 863965	p	59%	SEQ ID n-404
SEQ ID n° 6611	PL-4312.1	Contig9 from 864107 to 864397	m	42%	
SEQ ID n° 6612	PL-4311.1	Contig9 from 864497 to 864772	m	79%	#N/A
SEQ ID n° 6613	PL-4310.1	Contig9 from 864783 to 865025	m	81%	#N/A
SEQ ID n° 6614	PL-3774.1	Contig9 from 865147 to 865587	m	47%	SEQ ID n-2952
SEQ ID n° 6615	PL-1327.1	Contig9 from 866058 to 866639	p	48%	SEQ ID n-403

sp|P40819|YHV_SALTY_HYPOTHETICAL_PROTEIN_IN
LIVE 5'REGION

gb|AAC26596.1| (U83995) putative protease
[Porphyromonas gingivalis]

ref|NP_043483.1| orf14 [Bacteriophage HPI]
sp|P51716|YO14_BPH1_HYPOTHETICAL_14.9_KD
PROTEIN_IN_REP-HOL_INTERGENIC_REGION (ORF14)
pir||S69520 hypothetical protein 14 - phage HPI
gb|AAB09199.1| (U24159) orf14 [Bacteriophage
HPI]

ref|NP_047626.1| unknown [Yersinia pestis]
pir||T42908 hypothetical protein Y0075 -
Yersinia pestis plasmid pCD1 gb|AAC69816.1|
(AF074612) unknown [Yersinia pestis]
emb|CAB54885.1| (AL117189) hypothetical protein
YPCD1.08c [Yersinia pestis]

ref|NP_052428.1| unknown [Yersinia
enterocolitica] gb|AAC33681.1| (AF056093)
unknown [Yersinia enterocolitica]
gb|AAD16851.1| (AF102990) unknown [Yersinia
enterocolitica]

pir||S75133 hypothetical protein slr2101 -
Synechocystis sp. (strain PCC 6803)
dbj|BAAL7995.1| (D90910) hypothetical protein
[Synechocystis sp.]

sp|Q10612|YC84_MYCTU_HYPOTHETICAL_18.2_KDA
PROTEIN_RV1284 pir||H70771 hypothetical protein
Rv1284 - Mycobacterium tuberculosis (strain
H37RV) emb|CAA97750.1| (Z73419) hypothetical
protein Rv1284 [Mycobacterium tuberculosis]

TABLEAU II

SEQ ID n° 6616	PL-1326.1	Contig9 from 866734 to 868335	m	73%	pir D70035 permease homolog yveA - Bacillus subtilis emb CAB08050.1 (Z94043) hypothetical protein [Bacillus subtilis] emb CAB15452.1 (Z99121) similar to permease [Bacillus subtilis] SEQ ID n°402
SEQ ID n° 6617	PL-1325.1	Contig9 from 868396 to 869979	m	70%	pir F83368 probable aldehyde dehydrogenase PA2217 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05605.1 AE004648_4 (AE004648) probable aldehyde dehydrogenase [Pseudomonas aeruginosa] SEQ ID n°401 pir D83488 probable dihydrodipicolinate synthetase PA1254 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04643.1 AE004555_3 (AE004555) probable dihydrodipicolinate synthetase [Pseudomonas aeruginosa] pir C83489 probable transcription regulator PA1261 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04650.1 AE004555_10 (AE004555) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n°400
SEQ ID n° 6619	PL-1323.1	Contig9 from 871170 to 871994	m	56%	pir G83487 hypothetical protein PA1268 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04657.1 AE004556_7 (AE004556) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n°399 pir F83487 hypothetical protein PA1267 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04656.1 AE004556_6 (AE004556) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n°398
SEQ ID n° 6621	PL-1321.1	Contig9 from 873207 to 874334	p	63%	ref NP_053432.1 Hypothetical gene [Agrobacterium tumefaciens] dbj BA87817.1 (AB016260) Hypothetical gene [Agrobacterium tumefaciens] SEQ ID n°397
SEQ ID n° 6622	PL-4309.1	Contig9 from 874331 to 874585	p	38%	#N/A

TABLEAU II

SEQ ID n° 6623	PL-1320.1	Contig9 from 874588 to 875880	p	58%	pir B83487 probable oxidoreductase PA1266 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04655.1 AE004556_5 (AE004556) probable oxidoreductase [Pseudomonas aeruginosa]	SEQ ID n-996
SEQ ID n° 6624	PL-1319.1	Contig9 from 876020 to 876997	p	61%	emb CAB90977.1 (AL355832) hypothetical protein SCE22.10 [Streptomyces coelicolor A3(2)]	SEQ ID n-994
SEQ ID n° 6625	PL-1318.1	Contig9 from 877157 to 877927	p	79%	gb AAD43990.1 U59485_17 (U59485) AttM [Agrobacterium tumefaciens]	SEQ ID n-993
SEQ ID n° 6626	PL-1317.1	Contig9 from 878040 to 878987	m	38%	pir S76629 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj BAA10573.1 (D64004) hypothetical protein [Synechocystis sp.] pir T36402 probable monooxygenase - Streptomyces coelicolor emb CAB53314.1 (AL109974) putative monooxygenase [Streptomyces coelicolor A3(2)]	SEQ ID n-992
SEQ ID n° 6628	PL-1315.1	Contig9 from 881099 to 882802	m	61%	emb CAA72201.1 (Y11391) exochitinase [Glossina morsitans s-endosymbiont]	SEQ ID n-990
SEQ ID n° 6629	PL-1314.1	Contig9 from 883203 to 884801	p	47%	emb CAC11387.1 (AL445063) probable histidine ammonia-lyase [Thermoplasma acidophilum]	SEQ ID n-989
SEQ ID n° 6630	PL-1313.1	Contig9 from 885026 to 885775	p	77%	gb AAG56223.1 AE005351_2 (AE005351) putative oxidoreductase [Escherichia coli O157:H7]	SEQ ID n-988
SEQ ID n° 6631	PL-4306.1	Contig9 from 885907 to 886269	p	56%	sp P76170 YNEB_ECOLI HYPOTHETICAL 12.9 KD PROTEIN IN RSPA-SPEG INTERGENIC REGION PRECURSOR pir A64914 hypothetical protein b1583 - Escherichia coli gb AAC74655.1 (AE000254) orf, hypothetical protein [Escherichia coli K12]	#N/A
SEQ ID n° 6632	PL-4305.1	Contig9 from 886285 to 886548	p	60%	gb AAG56573.1 AE005382_7 (AE005382) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A

TABLEAU II

SEQ ID n° 6633	PL-1312.2	Contig9 from 886863 to 888260	P	14%	pir T29511 hypothetical protein C41G11.1 - Caenorhabditis elegans gb AAA85743.1 (U46669) coded for by C. elegans cDNA yk18f9.5 [Caenorhabditis elegans]	SEQ ID n-387
SEQ ID n° 6634	PL-4304.1	Contig9 from 888378 to 888533	m	No Hits found		#N/A
SEQ ID n° 6635	PL-4303.1	Contig9 from 889047 to 889439	P	No Hits found		#N/A
SEQ ID n° 6636	PL-1311.1	Contig9 from 889893 to 890600	m	59%	sp P77201 BID2_ECOLI PUTATIVE DETHIOBIOTIN SYNTHETASE (DETHIOBIOTIN SYNTHASE) (DTB SYNTHETASE) (DTBS)	SEQ ID n-386
SEQ ID n° 6637	PL-1310.1	Contig9 from 890765 to 891976	m	74%	gb AAG56581.1 AE005383_3 (AE005383) putative NAGC-like transcriptional regulator [Escherichia coli O157:H7] sp P77559 YNFL_ECOLI HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN MLC-ASR INTERGENIC REGION pir E64915 probable transcription regulator ynfL - Escherichia coli	SEQ ID n-385
SEQ ID n° 6638	PL-1309.1	Contig9 from 892108 to 893022	m	67%	dbj BAAL5319.1 (D90801) als operon regulatory protein. [Escherichia coli] dbj BAAL5329.1 (D90802) als operon regulatory protein. [Escherichia coli] gb AAC74667.1 (AE000255) putative transcriptional regulator LYSR-type [Escherichia coli K12] sp P43531 YNFM_ECOLI HYPOTHETICAL 45.3 KD PROTEIN IN MLC-ASR INTERGENIC REGION	SEQ ID n-383
SEQ ID n° 6639	PL-1308.1	Contig9 from 893149 to 894423	P	75%	pir F64915 membrane protein ynfM - Escherichia coli dbj BAAL5330.1 (D90802) Bicyclomycin resistance protein (Sulfonamide resistance protein). [Escherichia coli] gb AAC74668.1 (AE000255) putative transport protein [Escherichia coli K12]	SEQ ID n-382

TABLEAU II

SEQ ID n° 6640	PL-1307.1	Contig9 from 894579 to 895595	p	No Hits found		SEQ ID n-381
SEQ ID n° 6641	PL-1306.2	Contig9 from 896502 to 901379	m	42%	emb CAC19493.1 (AJ296651) nematocidal protein 2 [Xenorhabdus bovienii]	SEQ ID n-380
SEQ ID n° 6642	PL-1304.2	Contig9 from 901523 to 902545	m	No Hits found		SEQ ID n-379
SEQ ID n° 6643	PL-3772.1	Contig9 from 902557 to 903117	m	No Hits found		SEQ ID n-2950
SEQ ID n° 6644	PL-4299.1	Contig9 from 903170 to 903415	m	47%	sp O67611 ACP_AQUAE ACYL CARRIER PROTEIN (ACP) pir A70448 acyl carrier protein - Aquifex aeolicus gb AAC07567.1 (AE000752) acyl carrier protein [Aquifex aeolicus]	#N/A
SEQ ID n° 6645	PL-1303.2	Contig9 from 903428 to 904204	m	No Hits found		SEQ ID n-378
SEQ ID n° 6646	PL-1302.1	Contig9 from 904210 to 905475	m	54%	pir B70448 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Aquifex aeolicus gb AAC07574.1 (AE000752) 3-oxoacyl- [acyl-carrier-protein] synthase II [Aquifex aeolicus]	SEQ ID n-377
SEQ ID n° 6647	PL-1301.1	Contig9 from 906606 to 907985	m	43%	gb AAD28497.1 AF061787_4 (AF061787) McjD [Escherichia coli]	SEQ ID n-376
SEQ ID n° 6648	PL-1300.1	Contig9 from 907976 to 908854	m	38%	pir T09914 protein-arginine N-methyltransferase (EC 2.1.1.23) - Arabidopsis emb CAB45311.1 (AL079344) arginine methyltransferase (pam1) [Arabidopsis thaliana] emb CAB79709.1 (AL161575) arginine methyltransferase (pam1) [Arabidopsis thaliana]	SEQ ID n-375
SEQ ID n° 6649	PL-1299.1	Contig9 from 908854 to 909726	m	No Hits found		SEQ ID n-372

TABLEAU II

SEQ ID n° 6650	PL-4297.1	Contig9 from 910114 to 910248	p	No Hits found	#N/A	sp P06202 OPPA_SALTY PERIPLASMIC OLIGOPEPTIDE-BINDING PROTEIN PRECURSOR pir QREBOA oligopeptide-binding protein precursor - Salmonella typhimurium emb CAA29039.1 (X05491) Opp A (AA1-542) [Salmonella typhimurium] emb CAA27785.1 (X04194) precursor polypeptide [Salmonella typhimurium]	SEQ ID n-371
SEQ ID n° 6651	PL-1298.1	Contig9 from 910275 to 911885	p	66%	#N/A	pir C82602 hypothetical protein XF2068 [imported] - Xylella fastidiosa (strain 9a5c) gb AA084867.1 AE004023_3 (AE004023) hypothetical protein [Xylella fastidiosa] ref NP_052451.1 yacB [Plasmid Colib-P9] dbj BAA75090.1 (AB021078) yacB [Plasmid Colib-P9] gb AAG57655.1 AE005484_5 (AE005484) ferredoxin reductase subunit of phenylpropionate dioxygenase [Escherichia coli O157:H7] sp P17295 MPC1_ALCEU METAPYROCATECHASE 1 (CATO2ASE) (CATECHOL 2,3-DIOXYGENASE I) pir S10154 catechol 2,3-dioxygenase (EC 1.13.11.2) I - Alcaligenes eutrophus 1.13.11.2) I - Alcaligenes eutrophus emb CAA36665.1 (X52414) metapyrocatechase (AA 1.313) [Ralstonia eutropha] gb AAG57654.1 AE005484_4 (AE005484) 2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase [Escherichia coli O157:H7]	SEQ ID n-369
SEQ ID n° 6652	PL-4296.1	Contig9 from 912103 to 912192	p	No Hits found	#N/A		
SEQ ID n° 6653	PL-3771.1	Contig9 from 912254 to 912709	p	40%	#N/A		
SEQ ID n° 6654	PL-4294.1	Contig9 from 912706 to 913023	p	51%	#N/A		
SEQ ID n° 6655	PL-1297.1	Contig9 from 913329 to 914513	m	60%	#N/A		
SEQ ID n° 6656	PL-1296.1	Contig9 from 914515 to 915468	m	59%	#N/A		
SEQ ID n° 6657	PL-1295.1	Contig9 from 915458 to 916300	m	68%	#N/A		

TABLEAU II

SEQ ID n° 6658	PL-4293.1	Contig9 from 916300 to 916617	m	79%	sp P77266 HCAC_ECOLI 3-PHENYLPROPIONATE DIOXYGENASE FERREDOXIN SUBUNIT (DIOXYGENIN FERREDOXIN SUBUNIT) pir C65031 biphenyl dioxxygenase (EC 1.14.12.-) Rieske iron-sulfur component b2540 - Escherichia coli (strain K-12) gb AAC75593.1 (AE000340) ferredoxin subunit of phenylpropionate dioxxygenase [Escherichia coli K12] dbj BAA16443.1 (D90884) BIPHENYL DIOXYGENASE SYSTEM FERREDOXIN COMPONENT. [Escherichia coli] emb CAA71950.1 (Y11070) ferredoxin [Escherichia coli] gb AAG57653.1 AE005484_3 (AE005484) ferredoxin subunit of phenylpropionate dioxxygenase [Escherichia coli O157:H7]	#N/A.
SEQ ID n° 6659	PL-3770.1	Contig9 from 916617 to 917159	m	73%	gb AAG57652.1 AE005484_2 (AE005484) small terminal subunit of phenylpropionate dioxxygenase [Escherichia coli O157:H7]	SEQ ID n-2948
SEQ ID n° 6660	PL-1294.1	Contig9 from 917156 to 918517	m	89%	sp Q47139 HCAE_ECOLI 3-PHENYLPROPIONATE DIOXYGENASE ALPHA SUBUNIT (DIOXYGENIN ALPHA SUBUNIT) pir A65031 biphenyl dioxxygenase (EC 1.14.-.-) terminal oxygenase component large chain - Escherichia coli gb AAC75591.1 (AE000340) large terminal subunit of phenylpropionate dioxxygenase [Escherichia coli K12] dbj BAA16441.1 (D90884) BENZENE 1,2-DIOXYGENASE ALPHA SUBUNIT (EC 1.14.12.3). [Escherichia coli] gb AAG57651.1 AE005484_1 (AE005484) large terminal subunit of phenylpropionate dioxxygenase [Escherichia coli O157:H7]	SEQ ID n-367
SEQ ID n° 6661	PL-1293.1	Contig9 from 918654 to 919538	P	66%	gb AAG57650.1 AE005483_9 (AE005483) transcriptional activator of hca cluster [Escherichia coli O157:H7]	SEQ ID n-366

TABLEAU II

SEQ ID n° 6662	PL-1292.1	Contig9 from 919655 to 920554	p	60%	gb AAF81825.1 AF274045_4 (AF274045) 2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase; OhpC [Rhodococcus sp.]	SEQ ID n-365
SEQ ID n° 6663	PL-1291.1	Contig9 from 920624 to 921406	p	64%	gb AAG17135.1 AF190463_8 (AF190463) 2-oxo-4-pentenoate hydratase [Comamonas sp. JS765]	SEQ ID n-364
SEQ ID n° 6664	PL-1290.1	Contig9 from 921756 to 923099	m	47%	gb AAC77368.1 (AF058285) nicotinamidase/pyrazinamidase [Mycobacterium smegmatis]	SEQ ID n-363
SEQ ID n° 6665	PL-1289.1	Contig9 from 923099 to 924484	m	52%	sp Q00538 MMR_BACSU METHYLENOMYCIN A RESISTANCE PROTEIN (MMR PEPTIDE) pir YTB5MA methylenomycin A resistance protein mmr - Bacillus subtilis emb CAA46908.1 (X66121) methylenomycinA resistance protein [Bacillus subtilis] emb CAB15784.1 (Z99123) methylenomycin A resistance protein [Bacillus subtilis]	SEQ ID n-361
SEQ ID n° 6666	PL-1288.1	Contig9 from 924511 to 925773	m	59%	pir B82018 phosphoribosylamine--glycine ligase (EC 6.3.4.13) NMA0238 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB83546.1 (AL162752) phosphoribosylamine--glycine ligase [Neisseria meningitidis Z2491]	SEQ ID n-360
SEQ ID n° 6667	PL-1287.1	Contig9 from 925814 to 927001	m	47%	emb CAC11141.1 (AJ250581) Nixs protein [Streptomyces tendae]	SEQ ID n-359
SEQ ID n° 6668	PL-1286.1	Contig9 from 927010 to 927903	m	35%	ref NP_053211.1 pX02-56 [Bacillus anthracis] gb AAF13661.1 AF188935_59 (AF188935) pX02-56 [Bacillus anthracis]	SEQ ID n-358
SEQ ID n° 6669	PL-4290.1	Contig9 from 927875 to 928111	m	No Hits found		#N/A
SEQ ID n° 6670	PL-3769.1	Contig9 from 928147 to 928587	m	32%	emb CAB95928.1 (AL359989) putative acetyltransferase [Streptomyces coelicolor A3(2)]	SEQ ID n-2946

TABLEAU II

SEQ ID n° 6671	PL-1285.1	Contig9 from 928636 to 929643	m	30%	pir G83493 hypothetical protein PA1213 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04602.1 AE004551_6 (AE004551) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-957
SEQ ID n° 6672	PL-1284.1	Contig9 from 929654 to 930772	m	25%	gb AAD00512.2 (U81376) Paaa [Erwinia herbicola]	SEQ ID n-956
SEQ ID n° 6673	PL-1283.1	Contig9 from 930775 to 934194	m	25%	dbj BAB04638.1 (AP001510) diaminobutyric acid aminotransferase [Bacillus halodurans]	SEQ ID n-955
SEQ ID n° 6674	PL-4289.1	Contig9 from 934849 to 935169	p	59%	gb AAG17135.1 AF190463_8 (AF190463) 2-oxo-4- pentenoate hydratase [Comamonas sp. JS765] sp P42594 YGM_ECOLI HYPOTHETICAL 15.0 KD PROTEIN IN EBGC-UXAA INTERGENIC REGION pir G65096 hypothetical protein YGJM - Escherichia coli (strain K-12) gb AA57883.1 (U18997) ORF f138 [Escherichia coli] gb AAC76117.1 (AE000390) orf, hypothetical protein [Escherichia coli K12]	#N/A
SEQ ID n° 6675	PL-4288.1	Contig9 from 935206 to 935610	p	70%	pir T00236 protein KfrAs - Escherichia coli plasmid pO157	#N/A
SEQ ID n° 6676	PL-4287.1	Contig9 from 935697 to 935867	m	41%	gb AAF74779.1 AF265211_4 (AF265211) indigoldine synthesis protein IdgA [Pectobacterium chrysanthemi]	SEQ ID n-954
SEQ ID n° 6677	PL-1282.1	Contig9 from 935908 to 936864	m	72%	emb CAB87990.1 (AJ277403) indigoldine synthase [Erwinia chrysanthemi]	SEQ ID n-953
SEQ ID n° 6678	PL-1281.1	Contig9 from 936951 to 940805	m	64%	emb CAB45045.1 (AL078635) hypothetical protein [Amycolatopsis orientalis]	SEQ ID n-952
SEQ ID n° 6679	PL-1280.1	Contig9 from 941134 to 942312	m	18%	gb AAK05853.1 AE006405_7 (AE006405) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis]	#N/A
SEQ ID n° 6680	PL-4286.1	Contig9 from 942328 to 942765	m	51%		

TABLEAU II

SEQ ID n° 6681	PL-3768.1	Contig9 from 942765 to 943241	m	42%	gb AAK05853.1 AE006405_7 (AE006405) UNKNOWN PROTEIN [Lactococcus lactis subsp. lactis]	SEQ ID n-2945
SEQ ID n° 6682	PL-1279.1	Contig9 from 943238 to 943906	m	56%	gb AAF74780.1 AF265211_5 (AF265211) indigoidine synthesis protein IdgB [Pectobacterium chrysanthemi]	SEQ ID n-350
SEQ ID n° 6683	PL-4285.1	Contig9 from 943947 to 944171	m	59%	gb AAG56310.1 AE005360_2 (AE005360) ydcE gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6684	PL-1278.1	Contig9 from 944258 to 944914	m	66%	gb AAG48136.1 (AF322179) nikkomycin biosynthesis protein SanR [Streptomyces ansochromogenes]	SEQ ID n-349
SEQ ID n° 6685	PL-1277.1	Contig9 from 945430 to 946185	p	91%	gb AAF73870.1 AF220669_2 (AF220669) fumarate nitrate reduction regulatory protein [Klebsiella pneumoniae]	SEQ ID n-348
SEQ ID n° 6686	PL-1276.1	Contig9 from 946321 to 947265	p	80%	sp P03807 YDAA_ECOLI 35.6 KDA PROTEIN IN TPX-FNR INTERGENIC REGION pir QCECX membrane protein ydaA - Escherichia coli dbj BAAL4926.1 (D90771) ORF_ID:0261#5-similar to [SwissProt Accession Number P44195] [Escherichia coli] dbj BAA14936.1 (D90772) ORF_ID:0261#5-similar to [SwissProt Accession Number P44195] [Escherichia coli] gb AAC74415.1 (AE000231) orf, hypothetical protein [Escherichia coli K12] gb AAG56467.1 AE005373_1 (AE005373) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-347
SEQ ID n° 6687	PL-1275.1	Contig9 from 947323 to 948288	m	76%	gb AAA87858.2 (U40842) urease accessory protein [Yersinia pseudotuberculosis]	SEQ ID n-346
SEQ ID n° 6688	PL-1274.1	Contig9 from 948285 to 948920	m	91%	sp P42871 UREG_YEREN UREASE ACCESSORY PROTEIN UREG gb AAA50999.1 (L24101) urease [Yersinia enterocolitica]	SEQ ID n-345
SEQ ID n° 6689	PL-1273.1	Contig9 from 948973 to 949659	m	72%	gb AAA87856.2 (U40842) urease accessory protein [Yersinia pseudotuberculosis]	SEQ ID n-344

TABLEAU II

SEQ ID n° 6690	PL-1272.1	Contig9 from 949656 to 950252	m	68%	gb AAA87855.2 (U40842) urease accessory protein [Yersinia pseudotuberculosis]	SEQ ID n-343
SEQ ID n° 6691	PL-1271.1	Contig9 from 950327 to 952042	m	91%	sp P31494 URE1_YEREN_UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE) gb AAA50996.1 (L24101) urease alpha subunit [Yersinia enterocolitica]	SEQ ID n-342
SEQ ID n° 6692	PL-4283.1	Contig9 from 952110 to 952499	m	75%	sp P52314 URE2_YERPS_UREASE BETA SUBUNIT (UREA AMIDOHYDROLASE) gb AAA87853.1 (U40842) urease beta subunit [Yersinia pseudotuberculosis] gb AAC78633.1 (AF095636) urease beta subunit UreB [Yersinia pestis]	#N/A
SEQ ID n° 6693	PL-4282.1	Contig9 from 952591 to 952893	m	74%	sp Q9ZFS0 URE3_YERPE_UREASE GAMMA SUBUNIT (UREA AMIDOHYDROLASE) sp P52315 URE3_YERPS_UREASE GAMMA SUBUNIT (UREA AMIDOHYDROLASE) emb CAA79314.1 (Z18865) YeuA [Yersinia enterocolitica] gb AAC78632.1 (AF095636) urease gamma subunit UreA [Yersinia pestis] gb AAA87852.2 (U40842) urease gamma subunit [Yersinia pseudotuberculosis]	#N/A
SEQ ID n° 6694	PL-1270.1	Contig9 from 953386 to 954411	p	78%	gb AAG31202.1 AF020810_3 (AF020810) NxiA [Salmonella enterica]	SEQ ID n-341
SEQ ID n° 6695	PL-4279.1	Contig9 from 954803 to 955099	p	53%	pir A82603 hypothetical protein XF2074 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84873.1 AE004023_9 (AE004023) hypothetical protein [Xylella fastidiosa]	#N/A

TABLEAU II

SEQ ID n° 6696 PL-1269.1	Contig9 from 955228 to 956616	m	94%	sp P07002 PNTB_ECOLI_NAD(P) TRANSYDROGENASE SUBUNIT BETA (PYRIDINE NUCLEOTIDE TRANSYDROGENASE SUBUNIT BETA) (NICOTINAMIDE NUCLEOTIDE TRANSYDROGENASE SUBUNIT BETA) pir DEECXB NAD(P)+ transhydrogenase (B- specific) (EC 1.6.1.1) beta chain - Escherichia coli emb CAA46885.1 (X66086) pyridine nucleotide transhydrogenase [Escherichia coli] dbj BAA15336.1 (D90802) NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) b chain [Escherichia coli] dbj BAA15341.1 (D90803) NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) b chain [Escherichia coli] gb AAC74674.1 (AE000255) pyridine nucleotide transhydrogenase, beta subunit [Escherichia coli K12] emb CAB37090.1 (X04195) NAD(P)(+) transhydrogenase subunit beta [Escherichia coli] gb AAG56589.1 AE005383_11 (AE005383) pyridine nucleotide transhydrogenase, beta subunit [Escherichia coli 0157:H7]
				SEQ ID n-339

TABLEAU II

SEQ ID n° 6697	PL-1268.1	Contig9 from 956627 to 958156	m	89%	sp P07001 PNTA_ECOLI_NAD(P) TRANSHYDROGENASE SUBUNIT ALPHA (PYRIDINE NUCLEOTIDE) TRANSHYDROGENASE SUBUNIT ALPHA (NICOTINAMIDE NUCLEOTIDE) TRANSHYDROGENASE SUBUNIT ALPHA) pir DECKA_NAD(P)+ transhydrogenase (B- specific) (EC 1.6.1.1) alpha chain - Escherichia coli emb CAA46884.1 (X66086) pyridine nucleotide transhydrogenase [Escherichia coli] dbj BAA15342.1 (D90803) NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) a chain [Escherichia coli] dbj BAA15352.1 (D90804) NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) a chain [Escherichia coli] gb AAC74675.1 (AE000255) pyridine nucleotide transhydrogenase, alpha subunit [Escherichia coli K12] emb CAB37089.1 (X04195) NAD(P)(+) transhydrogenase subunit alpha [Escherichia coli]	SEQ ID n-938
SEQ ID n° 6698	PL-1267.1	Contig9 from 958680 to 959633	p	69%	gb AAG56591.1 AE005384_1 (AE005384) orf, hypothetical protein [Escherichia coli O157:H7] pir E82128 acyl carrier protein VC2020 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95168.1 (AE004276) acyl carrier protein [Vibrio cholerae] sp O67185 FABH_AQUAE_3-OXOACYL-[ACYL-CARRIER- PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) pir F70394 3-oxoacyl- [acyl-carrier-protein] synthase III - Aquifex aeolicus gb AAC07144.1 (AE000723) 3-oxoacyl- [acyl-carrier-protein] synthase III [Aquifex aeolicus]	SEQ ID n-937
SEQ ID n° 6699	PL-4277.1	Contig9 from 959708 to 959950	m	65%		#N/A
SEQ ID n° 6700	PL-1266.2	Contig9 from 960030 to 961178	m	37%		
SEQ ID n° 6701	PL-1265.2	Contig9 from 961179 to 962126	m	No Hits found		SEQ ID n-936
						SEQ ID n-935

TABLEAU II

SEQ ID n° 6702	PL-1264.2	Contig9 from 963193 to 964584	p	83%	gb AAG56592.1 AE005384.2 (AE005384) putative arginine/ornithine antiporter [Escherichia coli O157:H7]	SEQ ID n-934
SEQ ID n° 6703	PL-4273.1	Contig9 from 964739 to 964966	m	No Hits found		#N/A
SEQ ID n° 6704	PL-1263.2	Contig9 from 964973 to 965809	m	19%	emb CAB56657.1 (AL121596) putative hydrolase [Streptomyces coelicolor A3(2)]	SEQ ID n-933
SEQ ID n° 6705	PL-3765.1	Contig9 from 966612 to 967142	p	59%	gb AAG58930.1 AE005604.7 (AE005604) putative major fimbrial subunit [Escherichia coli O157:H7]	SEQ ID n-2944
SEQ ID n° 6706	PL-2808.1	Contig9 from 967257 to 967931	p	63%	gb AAG58276.1 AE005543.6 (AE005543) putative chaperone [Escherichia coli O157:H7]	SEQ ID n-2019
SEQ ID n° 6707	PL-2809.1	Contig9 from 967969 to 970509	p	59%	sp P43662 LPFC_SALTY OUTER MEMBRANE USHER PROTEIN LPFC PRECURSOR pir C56271 outer membrane usher protein lpfc precursor - Salmonella typhimurium gb AAA73968.1 (U18559) lpfc gene product [Salmonella typhimurium]	SEQ ID n-2020
SEQ ID n° 6708	PL-2810.1	Contig9 from 970529 to 971521	p	41%	sp P21648 MRKD_KLEPN FIMBRIA ADHESIN PROTEIN PRECURSOR pir B32801 fimbrial adhesin precursor, type 3 - Klebsiella pneumoniae gb AAA25096.1 (M55912) mrkd [Klebsiella pneumoniae] gb AAA25098.1 (M24536) fimbrial adhesin [Klebsiella pneumoniae]	SEQ ID n-2022
SEQ ID n° 6709	PL-4270.1	Contig9 from 971636 to 971956	m	No Hits found		#N/A
SEQ ID n° 6710	PL-4269.1	Contig9 from 971956 to 972204	m	No Hits found		#N/A
SEQ ID n° 6711	PL-4268.1	Contig9 from 972616 to 972876	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6712	PL-2812.1	Contig9 from 973067 to 973810	m	32%	gb AAFL9774.1 AF128451_1 (AF128451) repeat motif protein bdrA8 [Borrelia turicatae]	SEQ ID n-2024
SEQ ID n° 6713	PL-3764.1	Contig9 from 973923 to 974375	m	No Hits found		SEQ ID n-2943
SEQ ID n° 6714	PL-2813.1	Contig9 from 974544 to 978287	m	89%	gb AAG56366.1 AE005364_11 (AE005364) helicase, ATP-dependent [Escherichia coli O157:H7] sp P41407 ACPD_ECOLI ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE) pir G64892 [acyl-carrier-protein] phosphodiesterase (EC 3.1.4.14) acpD - Escherichia coli dbj BAAL5024.1 (D90779) Acyl carrier protein phosphodiesterase (ACP phosphodiesterase) (fragment). [Escherichia coli] dbj BAAL5028.1 (D90780) Acyl carrier protein phosphodiesterase (ACP phosphodiesterase) (fragment). [Escherichia coli] gb AAC74494.1 (AE000238) acyl carrier protein phosphodiesterase [Escherichia coli K12]	SEQ ID n-2025
SEQ ID n° 6715	PL-2814.1	Contig9 from 978578 to 979180	p	80%		SEQ ID n-2026
SEQ ID n° 6716	PL-4267.1	Contig9 from 979248 to 979574	m	71%	gb AAG56377.1 AE005366_3 (AE005366) ydbL gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6717	PL-4266.1	Contig9 from 979587 to 979784	m	66%	sp P76075 YNBE_ECOLI HYPOTHETICAL 6.8 KD PROTEIN IN LDHA-FEAR INTERGENIC REGION pir A64889 ynbE protein precursor - Escherichia coli gb AAC74464.1 (AE000235) orf, hypothetical protein [Escherichia coli K12]	#N/A

TABLEAU II

SEQ ID n° 6718	PL-2815.2	Contig9 from 979781 to 982408	m	62%	sp P52645 YDBH_ECOLI_HYPOTHETICAL_96.8_KDA PROTEIN IN LDHA-TYNA INTERGENIC REGION pir H64888 membrane protein ydbH - Escherichia coli dbj BAA14991.1 (D90776) ORF_ID:0265#2; similar to [SwissProt Accession Number P52645] [Escherichia coli] gb AAC74463.1 (AE000235) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-2027
SEQ ID n° 6719	PL-2442.2	Contig9 from 982775 to 983779	p	75%	gb AAG56380.1 AE005366_6 (AE005366) fermentative D-lactate dehydrogenase, NAD-dependent [Escherichia coli O157:H7] SEQ ID n-1622
SEQ ID n° 6720	PL-4265.1	Contig9 from 983801 to 984214	p	60%	sp P52644 HSLJ_ECOLI_HEAT_SHOCK_PROTEIN_HSLJ pir F64888 heat shock protein precursor hslJ - Escherichia coli dbj BAA14984.1 (D90775) Heat shock protein HslJ. [Escherichia coli] dbj BAA14989.1 (D90776) Heat shock protein HslJ. [Escherichia coli] gb AAC74461.1 (AE000235) heat shock protein hslJ [Escherichia coli K12] #N/A
SEQ ID n° 6721	PL-2441.1	Contig9 from 984538 to 985158	p	No Hits found	SEQ ID n-1621
SEQ ID n° 6722	PL-2440.1	Contig9 from 985352 to 985993	m	No Hits found	SEQ ID n-2620
SEQ ID n° 6723	PL-4264.1	Contig9 from 986299 to 986730	m	85%	#N/A
SEQ ID n° 6724	PL-2439.1	Contig9 from 986755 to 987411	m	80%	sp P76005 YCGN_ECOLI_HYPOTHETICAL_17.9_KD PROTEIN IN MINC-SHEA INTERGENIC REGION sp P76004 YCGM_ECOLI_PROTEIN_YCGM_pir A64864 probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase b1180 - Escherichia coli gb AAC74264.1 (AE000216) putative isomerase [Escherichia coli K12] dbj BAA36014.1 (D90751) ZK688.3 protein [Escherichia coli] dbj BAA36027.1 (D90752) ZK688.3 protein [Escherichia coli] SEQ ID n-1618

TABLEAU II

SEQ ID n°	Contig9 from	p	No Hits found	#N/A
6725 PL-4263.2	987694 to 987798			
				sp P76003 YCGL_ECOLI PROTEIN YCGL pir H64863 ycgl protein - Escherichia coli gb AAC74263.1 (AE000216) orf, hypothetical protein [Escherichia coli K12] dbj BAA36013.1 (D90751) Hypothetical protein HI1446 [Escherichia coli] dbj BAA36026.1 (D90752) Hypothetical protein HI1446 [Escherichia coli] gb AAG56030.1 AE005335_3 (AE005335) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG56027.1 AE005334_14 (AE005334) cell division inhibitor, inhibitsftsZ ring formation [Escherichia coli O157:H7]
6726 PL-4262.1	987763 to 988059	m	66%	
6727 PL-2438.1	988180 to 988863	p	78%	
				sp P18197 MIND_ECOLI SEPTUM SITE-DETERMINING PROTEIN MIND (CELL DIVISION INHIBITOR MIND) pir CCECID cell division inhibitor mind - Escherichia coli gb AAB59062.1 (J03153) MIND protein [Escherichia coli] dbj BAA36009.1 (D90751) Cell division inhibitor MIND. [Escherichia coli] dbj BAA36022.1 (D90752) Cell division inhibitor MIND. [Escherichia coli] gb AAC74259.1 (AE000216) cell division inhibitor, a membrane ATPase, activates mind [Escherichia coli K12] gb AAG56026.1 AE005334_13 (AE005334) cell division inhibitor, a membrane ATPase, activates mind [Escherichia coli O157:H7]
6728 PL-2437.1	988887 to 989699	p	90%	

SEQ ID n-1616

TABLEAU II

SEQ ID n° 6729 PL-4261.1	Contig9 from 989703 to 989972	p	85%	sp P18198 MINE_ECOLI_CELL_DIVISION_TOPOLOGICAL SPECIFICITY_FACTOR_pir CECTF cell division topological specificity factor - Escherichia coli gb AAB59063.1 (J03153) MinB protein [Escherichia coli] dbj BAA36008.1 (D90751) Cell division topological specificity factor. [Escherichia coli] dbj BAA36021.1 (D90752) Cell division topological specificity factor. [Escherichia coli] gb AAC74258.1 (AE000216) cell division topological specificity factor, reverses MinC inhibition of ftsZ ring formation [Escherichia coli K12] gb AAG56025.1 AE005334_12 (AE005334) cell division topological specificity factor, reverses MinC inhibition of ftsZ ring formation [Escherichia coli O157:H7] sp P09155 RND_ECOLI_RIBONUCLEASE_D (RNASE D) pir NRECD ribonuclease III (EC 3.1.26.3) rnd - Escherichia coli emb CAA30098.1 (X07055) ribonuclease D (AA 1-375) (start codon uug) [Escherichia coli] dbj BAA15599.1 (D90823) Ribonuclease D (EC 3.1.13.-) [Escherichia coli] dbj BAA15608.1 (D90824) Ribonuclease D (EC 3.1.13.-) [Escherichia coli] gb AAC74874.1 (AE000274) RNase D, processes tRNA precursor [Escherichia coli K12] prf 1410308A ribonuclease D [Escherichia coli] gb AAG56794.1 AE005403_5 (AE005403) acyl-CoA synthetase, long-chain-fatty-acid--CoA ligase [Escherichia coli O157:H7]	#N/A
				SEQ ID n-2615	
SEQ ID n° 6730 PL-2436.1	Contig9 from 990113 to 991240	m	77%		#N/A
SEQ ID n° 6731 PL-2435.1	Contig9 from 991336 to 993018	m	85%		#N/A
SEQ ID n° 6732 PL-4258.1	Contig9 from 993473 to 993598	p	No Hits found		#N/A
SEQ ID n° 6733 PL-4257.1	Contig9 from 993689 to 993808	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6734	PL-2434.1	Contig9 from 993885 to 994463	m	61%	dbj BAA15610.1 (D90824) Outer membrane protein SLP precursor. [Escherichia coli] dbj BAA15615.1 (D90825) Outer membrane protein SLP precursor. [Escherichia coli] gb AAC74876.1 (AE000275) putative outer membrane protein [Escherichia coli K12]	SEQ ID n-3613
SEQ ID n° 6735	PL-2433.1	Contig9 from 994547 to 995242	m	78%	gb AAG56796.1 AE005403_7 (AE005403) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-3612
SEQ ID n° 6736	PL-4256.1	Contig9 from 995475 to 995792	m	72%	pir A81032 helix-turn-helix family protein NMB1891 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF42225.1 (AE002538) helix-turn-helix family protein [Neisseria meningitidis MC58]	#N/A
SEQ ID n° 6737	PL-4255.1	Contig9 from 995785 to 996159	m	69%	pir C81975 hypothetical protein NMA0565 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB83857.1 (AL162753) hypothetical protein NMA0565 [Neisseria meningitidis Z2491]	#N/A
SEQ ID n° 6738	PL-2432.2	Contig9 from 996426 to 998348	m	85%	gb AAG56797.1 AE005403_8 (AE005403) putative enzyme [Escherichia coli O157:H7]	SEQ ID n-3611
SEQ ID n° 6739	PL-4254.1	Contig9 from 998449 to 998793	p	70%	gb AAG56798.1 AE005404_1 (AE005404) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6740	PL-4253.1	Contig9 from 999098 to 999430	p	No Hits found		#N/A
SEQ ID n° 6741	PL-3763.1	Contig9 from 999459 to 999920	p	No Hits found		SEQ ID n-2942
SEQ ID n° 6742	PL-4252.1	Contig9 from 1000287 to 1000523	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6743	PL-4251.1	Contig9 from 1000677 to 1001006	m	80%	sp P77670 YDGE_ECOLI HYPOTHETICAL 11.7 KDA PROTEIN IN ASR-PNTB INTERGENIC REGION pir A64916 probable membrane protein b1599 - Escherichia coli dbj BAAL5333.1 (D90802) Putative ethidium bromide resistance protein (E1 protein). [Escherichia coli] dbj BAAL5338.1 (D90803) Putative ethidium bromide resistance protein (E1 protein). [Escherichia coli] gb AAC74671.1 (AE000255) possible chaperone [Escherichia coli K12] gb AAG56586.1 AE005383_8 (AE005383) possible chaperone [Escherichia coli O157:H7] sp P77412 YDGE_ECOLI HYPOTHETICAL 13.1 KDA PROTEIN IN ASR-PNTB INTERGENIC REGION pir B64916 probable membrane protein b1600 - Escherichia coli dbj BAAL5334.1 (D90802) Putative ethidium bromide resistance protein (E1 protein). [Escherichia coli]	#N/A
SEQ ID n° 6744	PL-3762.1	Contig9 from 1001011 to 1001427	m	56%	dbj BAAL5339.1 (D90803) Putative ethidium bromide resistance protein (E1 protein). [Escherichia coli] gb AAC74672.1 (AE000255) possible chaperone [Escherichia coli K12] gb AAG56587.1 AE005383_9 (AE005383) possible chaperone [Escherichia coli O157:H7] sp P37986 G6PD_ERWCH GLUCOSE-6-PHOSPHATE 1- DEHYDROGENASE (G6PD) pir S37053 glucose-6- phosphate 1-dehydrogenase (EC 1.1.1.49) - Erwinia chrysanthemi emb CAA52858.1 (X74866) glucose-6-phosphate 1-dehydrogenase [Erwinia chrysanthemi]	SEQ ID n° 2941
SEQ ID n° 6745	PL-2431.1	Contig9 from 1001926 to 1003401	m	87%	gb AAG56843.1 AE005408_1 (AE005408) orf, hypothetical protein [Escherichia coli O157:H7] pir S18689 Sc/Svp protein - Escherichia coli plasmid p15B emb CAA44052.1 (X62121) DNA inversion product [Escherichia coli]	SEQ ID n° 1607
SEQ ID n° 6746	PL-2429.1	Contig9 from 1003746 to 1004606	p	87%		SEQ ID n° 1610
SEQ ID n° 6747	PL-2428.1	Contig9 from 1005079 to 1005981	p	41%		SEQ ID n° 1606

TABLEAU II

SEQ ID n°	Contig9 from	p	17%	gb	SEQ ID n-1605
6748	PL-2427.1	p	17%	gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	
6749	PL-4249.1	p	No Hits found		#N/A
6750	PL-2426.1	p	91%	sp P21599 KPY2_ECOLI PYRUVATE KINASE II (PK-2) pir S29790 pyruvate kinase (EC 2.7.1.40) A - Escherichia coli gb AAA24473.1 (M63703) pyruvate kinase type II [Escherichia coli] dbj BAA15662.1 (D90828) pyruvate kinase (EC 2.7.1.40) [Escherichia coli] gb AAC74924.1 (AE000279) pyruvate kinase II, glucose stimulated [Escherichia coli K12] K12] gb AAG56845.1 AE005408_3 (AE005408) suppressor of htrB, heat shock protein [Escherichia coli O157:H7]	SEQ ID n-1604
6751	PL-2425.1	m	68%	sp P24204 YEBA_ECOLI HYPOTHETICAL 46.7 KD PROTEIN IN MSBB-RUVB INTERGENIC REGION (ORFU) pir H64947 membrane protein yeba - Escherichia coli dbj BAA15664.1 (D90828) lysostaphin precursor (EC 3.5.1.-). [Escherichia coli] gb AAC74926.1 (AE000279) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-1603
6752	PL-2424.1	m	72%	gb AAG56847.1 AE005408_5 (AE005408) putative adhesin [Escherichia coli O157:H7]	SEQ ID n-1602
6753	PL-2423.1	m	71%	sp P52648 ZNUC_ECOLI HIGH-AFFINITY ZINC UPTAKE SYSTEM ATP-BINDING PROTEIN ZNUC pir B64948 probable ABC transport system ATP-binding protein yebM - Escherichia coli dbj BAA15666.1 (D90828) sulfate transport ATP-binding protein CysA. [Escherichia coli] gb AAC74928.1 (AE000280) putative ATP-binding component of a transport system [Escherichia coli K12]	SEQ ID n-1601
6754	PL-2422.1	p	75%		SEQ ID n-1600

TABLEAU II

SEQ ID n° 6755 PL-2421.1	Contig9 from 1013890 to 1014675	p	90%	sp P39832 ZNUB_ECOLI HIGH-AFFINITY ZINC UPTAKE SYSTEM MEMBRANE PROTEIN ZNUB pir C64948 probable membrane protein yebi - Escherichia coli dbj BAA15667.1 (D90828)
				ORF_ID:0336gap#12; similar to [SwissProt Accession Number P39832] [Escherichia coli] dbj BAA15670.1 (D90829)
SEQ ID n° 6756 PL-2420.1	Contig9 from 1014889 to 1015896	m	89%	ORF_ID:0336gap#12-similar to [SwissProt Accession Number P39832] [Escherichia coli] gb AAC74929.1 (AE000280) orf, hypothetical protein [Escherichia coli K12] sp P08577 RUVB_ECOLI HOLLIDAY JUNCTION DNA HELICASE RUVB pir BVECVB DNA-binding protein ruvB - Escherichia coli emb CAA30120.1 (X07091) ruvB gene product (AA 1 - 336) [Escherichia coli] gb AAA24613.1 (M21298) ruvB protein [Escherichia coli] dbj BAA15671.1 (D90829) Holliday junction DNA helicase RuvB. [Escherichia coli] gb AAC74930.1 (AE000280) Holliday junction helicase subunit A; branch migration; repair [Escherichia coli K12] gb AAG56850.1 AE005408_8 (AE005408) Holliday junction helicase subunit A; branch migration; repair [Escherichia coli O157:H7]
				SEQ ID n°1598

TABLEAU II

SEQ ID n° 6757	PL-2419.1	Contig9 from 1015913 to 1016530	m 85%	sp P08576 RUVA_ECOLI HOLLIDAY JUNCTION DNA HELICASE RUVA pir BVECRV ruva protein - Escherichia coli pdb 1C7Y A Chain A, E.Coli Ruva-Holliday Junction Complex pdb 1HJP Holliday Junction Binding Protein Ruva From E. Coli pdb 1BDX A Chain A, E. Coli Ruva With Bound Dna Holliday Junction, Alpha Carbons And Phosphate Atoms Only pdb 1BDX B Chain B, E. Coli Ruva With Bound Dna Holliday Junction, Alpha Carbons And Phosphate Atoms Only pdb 1BDX C Chain C, E. Coli Ruva With Bound Dna Holliday Junction, Alpha Carbons And Phosphate Atoms Only pdb 1BDX D Chain D, E. Coli Ruva With Bound Dna Holliday Junction, Alpha Carbons And Phosphate Atoms Only gb AA24612.1 (M21298) ruva protein (gtg start) [Escherichia coli] dbj BA15672.1 (D90829) Ruva protein [Escherichia coli] gb AAC74931.1 (AE000280) Holliday junction helicase subunit B; branch migration; repair [Escherichia coli K12] gb AAG56851.1 AE005408_9 (AE005408) Holliday junction helicase subunit B; branch migration;
				SEQ ID n°2596

TABLEAU II

SEQ ID n° 6758 PL-3761.1	Contig9 from 1016617 to 1017138	m 88%	sp P24239 RUV_C_ECOLI_CROSSOVER_JUNCTION ENDODEOXYRIBONUCLEASE RUV_C (HOLLIDAY JUNCTION NUCLEASE RUV_C) (HOLLIDAY JUNCTION RESOLVASE RUV_C) pir D38113 crossover junction endodeoxyribonuclease (EC 3.1.22.4) ruvc - Escherichia coli emb CAA42128.1 (X59551) ruvc [Escherichia coli] dbj BAA01032.1 (D10165) RUV_C [Escherichia coli] dbj BAA15674.1 (D90829) DNA repair protein ruvc [Escherichia coli] gb AAC74933.1 (AE000280) Holliday junction nuclease; resolution of structures; repair [Escherichia coli K12] gb AAG56853.1 AE005408_11 (AE005408) Holliday junction nuclease; resolution of structures; repair [Escherichia coli O157:H7]	SEQ ID n-2940
			gb AAG56854.1 AE005408_12 (AE005408) orf, hypothetical protein [Escherichia coli O157:H7] emb CAA42125.1 (X59551) alternative [Escherichia coli] dbj BAA01030.1 (D10165) Orf17 [Escherichia coli]	SEQ ID n-2595
			sp P21889 SYD_ECOLI_ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) pir [SYECD aspartate--trna ligase (EC 6.1.1.12) - Escherichia coli pdb LEQR A Chain A, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR B Chain B, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR C Chain C, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli emb CAA37856.1 (X53863) aspartate-trna ligase [Escherichia coli] dbj BAA15677.1 (D90829) Aspartate--trna ligase (EC 6.1.1.12) [Escherichia coli] gb AAC74936.1 (AE000280) aspartate trna synthetase [Escherichia coli K12]	SEQ ID n-3594
SEQ ID n° 6759 PL-2418.1	Contig9 from 1017370 to 1018113	m 88%	gb AAG56854.1 AE005408_12 (AE005408) orf, hypothetical protein [Escherichia coli O157:H7] emb CAA42125.1 (X59551) alternative [Escherichia coli] dbj BAA01030.1 (D10165) Orf17 [Escherichia coli]	SEQ ID n-2940
			sp P21889 SYD_ECOLI_ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) pir [SYECD aspartate--trna ligase (EC 6.1.1.12) - Escherichia coli pdb LEQR A Chain A, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR B Chain B, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR C Chain C, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli emb CAA37856.1 (X53863) aspartate-trna ligase [Escherichia coli] dbj BAA15677.1 (D90829) Aspartate--trna ligase (EC 6.1.1.12) [Escherichia coli] gb AAC74936.1 (AE000280) aspartate trna synthetase [Escherichia coli K12]	SEQ ID n-3594
			sp P21889 SYD_ECOLI_ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) pir [SYECD aspartate--trna ligase (EC 6.1.1.12) - Escherichia coli pdb LEQR A Chain A, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR B Chain B, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR C Chain C, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli emb CAA37856.1 (X53863) aspartate-trna ligase [Escherichia coli] dbj BAA15677.1 (D90829) Aspartate--trna ligase (EC 6.1.1.12) [Escherichia coli] gb AAC74936.1 (AE000280) aspartate trna synthetase [Escherichia coli K12]	SEQ ID n-3594
SEQ ID n° 6760 PL-4244.1	Contig9 from 1018143 to 1018580	m 80%	gb AAG56854.1 AE005408_12 (AE005408) orf, hypothetical protein [Escherichia coli O157:H7] emb CAA42125.1 (X59551) alternative [Escherichia coli] dbj BAA01030.1 (D10165) Orf17 [Escherichia coli]	SEQ ID n-2940
			sp P21889 SYD_ECOLI_ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) pir [SYECD aspartate--trna ligase (EC 6.1.1.12) - Escherichia coli pdb LEQR A Chain A, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR B Chain B, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR C Chain C, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli emb CAA37856.1 (X53863) aspartate-trna ligase [Escherichia coli] dbj BAA15677.1 (D90829) Aspartate--trna ligase (EC 6.1.1.12) [Escherichia coli] gb AAC74936.1 (AE000280) aspartate trna synthetase [Escherichia coli K12]	SEQ ID n-3594
			sp P21889 SYD_ECOLI_ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) pir [SYECD aspartate--trna ligase (EC 6.1.1.12) - Escherichia coli pdb LEQR A Chain A, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR B Chain B, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR C Chain C, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli emb CAA37856.1 (X53863) aspartate-trna ligase [Escherichia coli] dbj BAA15677.1 (D90829) Aspartate--trna ligase (EC 6.1.1.12) [Escherichia coli] gb AAC74936.1 (AE000280) aspartate trna synthetase [Escherichia coli K12]	SEQ ID n-3594
SEQ ID n° 6761 PL-2417.1	Contig9 from 1018580 to 1020352	m 84%	gb AAG56854.1 AE005408_12 (AE005408) orf, hypothetical protein [Escherichia coli O157:H7] emb CAA42125.1 (X59551) alternative [Escherichia coli] dbj BAA01030.1 (D10165) Orf17 [Escherichia coli]	SEQ ID n-2940
			sp P21889 SYD_ECOLI_ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) pir [SYECD aspartate--trna ligase (EC 6.1.1.12) - Escherichia coli pdb LEQR A Chain A, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR B Chain B, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR C Chain C, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli emb CAA37856.1 (X53863) aspartate-trna ligase [Escherichia coli] dbj BAA15677.1 (D90829) Aspartate--trna ligase (EC 6.1.1.12) [Escherichia coli] gb AAC74936.1 (AE000280) aspartate trna synthetase [Escherichia coli K12]	SEQ ID n-3594
			sp P21889 SYD_ECOLI_ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) pir [SYECD aspartate--trna ligase (EC 6.1.1.12) - Escherichia coli pdb LEQR A Chain A, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR B Chain B, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli pdb LEQR C Chain C, Crystal Structure Of Free Aspartyl-Trna Synthetase From Escherichia Coli emb CAA37856.1 (X53863) aspartate-trna ligase [Escherichia coli] dbj BAA15677.1 (D90829) Aspartate--trna ligase (EC 6.1.1.12) [Escherichia coli] gb AAC74936.1 (AE000280) aspartate trna synthetase [Escherichia coli K12]	SEQ ID n-3594

TABLEAU II

SEQ ID n° 6762	PL-4243.1	Contig9 from 1020629 to 1021024	p	83%	sp P76289 YECN_ECOLI_HYPOTHETICAL_15.2_KD PROTEIN IN ASPS-BISZ INTERGENIC REGION	#N/A
SEQ ID n° 6763	PL-4242.1	Contig9 from 1021151 to 1021441	m	76%	gb AAC84004.1 (AF072126) stability protein StbE [Morganella morganii]	#N/A
SEQ ID n° 6764	PL-4241.1	Contig9 from 1021431 to 1021682	m	77%	gb AAC84003.1 (AF072126) stability protein StbD [Morganella morganii]	#N/A
SEQ ID n° 6765	PL-2415.1	Contig9 from 1021955 to 1022713	p	78%	gb AAG56860.1 AE005409_5 (AE005409) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n° 2592
SEQ ID n° 6766	PL-2414.1	Contig9 from 1022710 to 1023681	p	86%	gb AAG56861.1 AE005409_6 (AE005409) putative enzyme [Escherichia coli O157:H7]	SEQ ID n° 2591
SEQ ID n° 6767	PL-2413.2	Contig9 from 1023857 to 1024603	m	67%	sp P46719 CUTC_ECOLI_COPPER_HOMEOSTASIS_PROTEIN CUTC dbj BAAL5684.1 (D90829) Copper homeostasis protein CUTC. [Escherichia coli] dbj BAAL5691.1 (D90830) Copper homeostasis protein CUTC. [Escherichia coli]	SEQ ID n° 2590
SEQ ID n° 6768	PL-4240.1	Contig9 from 1024741 to 1024908	m	46%	gb AAG56865.1 AE005410_1 (AE005410) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6769	PL-4239.1	Contig9 from 1024954 to 1025289	p	63%	pir D82455 hypothetical protein VCA0468 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96372.1 (AE004379) hypothetical protein [Vibrio cholerae] pir E82455 conserved hypothetical protein VCA0469 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96373.1 (AE004379) conserved hypothetical protein [Vibrio cholerae]	#N/A
SEQ ID n° 6770	PL-4238.1	Contig9 from 1025290 to 1025604	p	68%		#N/A
SEQ ID n° 6771	PL-2412.1	Contig9 from 1025620 to 1026183	m	61%	sp P52007 YECM_ECOLI_PROTEIN_YECM	SEQ ID n° 2589

TABLEAU II

SEQ ID n° 6772	PL-3759.1	Contig9 from 1027152 to 1027520	p	37%	gb AAD19708.1 (AF123694) galactophilic lectin PA-I [Pseudomonas aeruginosa]	SEQ ID n-2938
SEQ ID n° 6773	PL-3758.1	Contig9 from 1027834 to 1028412	m	82%	sp P37904 YCEI_ECOLI PROTEIN YCEI PRECURSOR pir E64848 ycei protein precursor - Escherichia coli gb AAC74140.1 (AE000207) orf, hypothetical protein [Escherichia coli K12] dbj BAA35854.1 (D90742) 18.7 kd protein in htrB 5'region precursor. [Escherichia coli] dbj BAA35865.1 (D90743) 18.7 kd protein in htrB 5'region precursor. [Escherichia coli] gb AAG55802.1 AE005316_7 (AE005316) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2937
SEQ ID n° 6774	PL-2411.1	Contig9 from 1028439 to 1028993	m	63%	gb AAG55803.1 AE005316_8 (AE005316) putative cytochrome [Escherichia coli O157:H7]	SEQ ID n-2588
SEQ ID n° 6775	PL-2410.1	Contig9 from 1029597 to 1030334	p	63%	gb AAK02181.1 (AE006045) unknown [Pasteurella multocida]	SEQ ID n-2587
SEQ ID n° 6776	PL-2409.1	Contig9 from 1030689 to 1032419	p	89%	sp P11875 SYR_ECOLI ARGINYL-TRNA SYNTHETASE (ARGININE--TRNA LIGASE) (ARGRS) pir SYECRT arginine--trna ligase (EC 6.1.1.19) [validated] Escherichia coli emb CAA33384.1 (X15320) arginyl-trna-synthetase (AA 1-577) [Escherichia coli] dbj BAA15686.1 (D90829) Arginine--trna ligase (EC 6.1.1.19) [Escherichia coli] dbj BAA15693.1 (D90830) Arginine--trna ligase (EC 6.1.1.19) [Escherichia coli] gb AAC74946.1 (AE000281) arginine trna synthetase [Escherichia coli K12]	SEQ ID n-2585
SEQ ID n° 6777	PL-2408.1	Contig9 from 1032784 to 1034319	m	88%	sp P37169 MVIN_SALTY VIRULENCE FACTOR MVIN pir S40271 virulence factor mvin - Salmonella typhimurium emb CAA81134.1 (Z26133) mvIB [Salmonella typhimurium] dbj BAA04980.1 (D25292) ORF2 [Salmonella typhimurium]	SEQ ID n-2584

TABLEAU II

SEQ ID n°	Contig9 from	p	No Hits found	#N/A	#N/A
SEQ ID n° 6778 PL-4234.1	Contig9 from 1035125 to 1035328	p	No Hits found		
SEQ ID n° 6779 PL-4233.1	Contig9 from 1035353 to 1035583	p	No Hits found		
SEQ ID n° 6780 PL-3757.1	Contig9 from 1035716 to 1036300	m	80%		sp P09454 RIMJ_ECOLI RIBOSOMAL-PROTEIN-ALANINE ACETYLTRANSFERASE (ACETYLATING ENZYME FOR N-TERMINAL OF RIBOSOMAL PROTEIN S5) pir S01084 ribosomal-protein-alanine N-acetyltransferase (EC 2.3.1.128) rimJ - Escherichia coli emb CAA29490.1 (X06118) S5 (AA 1-124) [Escherichia coli] gb AA24549.1 (M99278) acetylase [Escherichia coli] dbj BAA35874.1 (D90743) Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128) (acetylating enzyme for N-terminal of ribosomal protein S5). [Escherichia coli] gb AAC74150.1 (AE000207) acetylation of N- terminal alanine of 30S ribosomal subunit protein S5 [Escherichia coli K12] gb AAG55812.1 AE005317.1 (AE005317) acetylation of N-terminal alanine of 30S ribosomal subunit protein S5 [Escherichia coli O157:H7] pir P64849 probable permease b1065 - Escherichia coli gb AAC74149.1 (AE000207) orf, hypothetical protein [Escherichia coli K12] dbj BAA35873.1 (D90743) Hypothetical 44.7 kd protein in glnQ-ansR intergenic region. [Escherichia coli] gb AAG55809.1 AE005316.14 (AE005316) orf, hypothetical protein [Escherichia coli O157:H7]
SEQ ID n° 6781 PL-2407.1	Contig9 from 1036489 to 1037694	p	85%		SEQ ID n-2936
SEQ ID n° 6782 PL-2406.1	Contig9 from 1037732 to 1038295	p	66%		SEQ ID n-1583 SEQ ID n-1582

TABLEAU II

SEQ ID n° 6783	PL-2405.1	Contig9 from 1038486 to 1039025	m	68%	sp P75915 YCDY_ECOLI HYPOTHETICAL 20.7 KDA PROTEIN IN PHOH-CSGG INTERGENIC REGION pir H64845 ycdy protein - Escherichia coli gb AAC74119.1 (AE000205) putative oxidoreductase component [Escherichia coli K12] dbj BA35816.1 (D90740) Hypothetical protein HI1543 [Escherichia coli] dbj BA35825.1 (D90741) Hypothetical protein HI1543 [Escherichia coli] sp P75913 YCDW_ECOLI PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN PHOH-CSGG INTERGENIC REGION pir F64845 probable 2-hydroxyacid dehydrogenase ycdW - Escherichia coli gb AAC74117.1 (AE000205) putative dehydrogenase [Escherichia coli K12] SEQ ID n-1581
SEQ ID n° 6784	PL-2404.1	Contig9 from 1039098 to 1040039	m	68%	sp P76125 YDDM_ECOLI HYPOTHETICAL 13.3 KD PROTEIN IN FDNI-ADHP INTERGENIC REGION pir H64900 hypothetical protein bi477 - Escherichia coli gb AAD13441.1 (AE000244) orf, hypothetical protein [Escherichia coli K12] sp P44217 YE92_HAETIN HYPOTHETICAL PROTEIN HI1492 PRECURSOR pir B64032 hypothetical protein HI1492 - Haemophilus influenzae (strain Rd KW20) gb AAC23144.1 (U32826) H. influenzae predicted coding region HI1492 [Haemophilus influenzae Rd] SEQ ID n-1579
SEQ ID n° 6785	PL-2403.1	Contig9 from 1041234 to 1041815	m	39%	gb AAA27621.1 (M90093) luxE [Xenorhabdus luminescens] gb AAG09983.1 AF251497_1 (AF251497) LuxE [cloning vector HKBS1] pir C35411 alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) beta chain - Xenorhabdus luminescens gb AAA27627.1 (M55977) luciferase beta subunit [Xenorhabdus luminescens] SEQ ID n-1578
SEQ ID n° 6786	PL-2402.1	Contig9 from 1041984 to 1043096	m	94%	gb AAA27621.1 (M90093) luxE [Xenorhabdus luminescens] gb AAG09983.1 AF251497_1 (AF251497) LuxE [cloning vector HKBS1] pir C35411 alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) beta chain - Xenorhabdus luminescens gb AAA27627.1 (M55977) luciferase beta subunit [Xenorhabdus luminescens] SEQ ID n-1577
SEQ ID n° 6787	PL-2402.1	Contig9 from 1041984 to 1043096	m	94%	gb AAA27621.1 (M90093) luxE [Xenorhabdus luminescens] gb AAG09983.1 AF251497_1 (AF251497) LuxE [cloning vector HKBS1] pir C35411 alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) beta chain - Xenorhabdus luminescens gb AAA27627.1 (M55977) luciferase beta subunit [Xenorhabdus luminescens] SEQ ID n-1578
SEQ ID n° 6788	PL-2401.1	Contig9 from 1043158 to 1044132	m	92%	gb AAA27621.1 (M90093) luxE [Xenorhabdus luminescens] gb AAG09983.1 AF251497_1 (AF251497) LuxE [cloning vector HKBS1] pir C35411 alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) beta chain - Xenorhabdus luminescens gb AAA27627.1 (M55977) luciferase beta subunit [Xenorhabdus luminescens] SEQ ID n-1577

TABLEAU II

SEQ ID n° 6789	PL-2400.1	Contig9 from 1044150 to 1045229	m	97%	sp P19839 LXA1_PHOLU_ALKANAL_MONOOXYGENASE_ALPHA CHAIN (BACTERIAL_LUCIFERASE_ALPHA CHAIN) pir B35411 alkanal monooxygenase (FMN- linked) (EC 1.14.14.3) alpha chain - Xenorhabdus luminescens gb AA27619.1 (M90093) luciferase [Xenorhabdus luminescens] gb AA27623.1 (M57416) luciferase alpha subunit [Xenorhabdus luminescens] gb AA27626.1 (M55977) luciferase alpha subunit [Xenorhabdus luminescens] gb AAG09985.1 AF251497_3 (AF251497) luciferase [cloning vector HKBS1]	SEQ ID n-1576
SEQ ID n° 6790	PL-2399.1	Contig9 from 1045406 to 1046329	m	95%	pir D39853 acyltransferase (EC 2.3.1.-) LuxD - Xenorhabdus luminescens gb AA27617.1 (M90093) fatty acid reductase [Xenorhabdus luminescens] gb AAG09987.1 AF251497_5 (AF251497) fatty acid reductase [cloning vector HKBS1]	SEQ ID n-1573
SEQ ID n° 6791	PL-2398.1	Contig9 from 1046342 to 1047784	m	96%		SEQ ID n-1572
SEQ ID n° 6792	PL-4229.1	Contig9 from 1048324 to 1048599	m	No Hits found		#N/A
SEQ ID n° 6793	PL-4227.1	Contig9 from 1048761 to 1049045	m	No Hits found		#N/A
SEQ ID n° 6794	PL-2397.1	Contig9 from 1049367 to 1051118	m	50%	sp P74178 YB78_SYNY3_HYPOTHETICAL_69.1_KD PROTEIN_SLL1178 pir S75808 modulation protein Synecocystis sp. (strain PCC 6803) dbj BAAL8267.1 (D90913) modulation protein [Synecocystis sp.]	SEQ ID n-1571
SEQ ID n° 6795	PL-2396.1	Contig9 from 1051713 to 1052405	m	48%	gb AAG34189.1 AF321122_8 (AF321122) Sim-nJ2 [Streptomyces antibioticus]	SEQ ID n-1570

TABLEAU II

SEQ ID n° 6796 PL-2395.1	Contig9 from 1053177 to 1054877	P	79%	sp P40877 YCHM_ECOLI HYPOTHETICAL 58.4 KDA PROTEIN IN PTH-PRSA INTERGENIC REGION pir C64867 probable sulfate transport protein ychm - Escherichia coli gb AAC74290.1 (AE000219) orf, hypothetical protein [Escherichia coli K12] dbj BAA36064.1 (D90756) Hypothetical protein in pth-prsa intergenic region . [Escherichia coli] gb AAG56064.1 AE005338_4 (AE005338) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2569 sp P17579 KDSA_ECOLI 2-DEHYDRO-3- DEOXYPHOSPHOCTONATE ALDOLASE (PHOSPHO-2-DEHYDRO-3-DEOXYOCTONATE ALDOLASE) (3-DEOXY-D-MANNO-OCTULOSONIC ACID 8-PHOSPHATE SYNTHETASE) (KDO-8-PHOSPHATE SYNTHETASE) (KDO 8- P SYNTHASE) pir I83573 3-deoxy-D- manno-octulosonic acid 8-phosphate synthetase - Escherichia coli pir SVECOL 2-dehydro-3- deoxyphosphoactonate aldolase (EC 4.1.2.16) - Escherichia coli pdb 1D9E A Chain A, Structure Of E. Coli Kdo8p Synthase pdb 1D9E B Chain B, Structure Of E. Coli Kdo8p Synthase pdb 1D9E C Chain C, Structure Of E. Coli Kdo8p Synthase pdb 1D9E D Chain D, Structure Of E. Coli Kdo8p Synthase pdb 1GGO A Chain A, Crystal Structure Analysis Of Kdo8p Synthase At 3.0 A gb AAC43441.1 (U18555) 3-deoxy-D-manno- octulosonic acid 8-phosphate synthetase [Escherichia coli] dbj BAA36073.1 (D90756) 3- deoxy-D-manno-octulosonic acid 8-phosphate synthetase [Escherichia coli] dbj BAA36083.1 (D90757) 3-deoxy-D-manno-
				SEQ ID n-2568
SEQ ID n° 6797 PL-2394.1	Contig9 from 1054993 to 1055847	m	90%	

TABLEAU II

SEQ ID n° 6798	PL-2393.1	Contig9 from 1056003 to 1056812	m	74%	sp P20101 YCHA_ECOLI_HYPOTHETICAL_30.8_KDA PROTEIN IN HEMK-KDSA INTERGENIC REGION pir I83572 ycha protein - Escherichia coli gb AAC43440.1 (U18555) orf1 gene product [Escherichia coli] gb AAC74298.1 (AE000219) orf, hypothetical protein [Escherichia coli K12] dbj BAA36072.1 (D90756) Hypothetical protein 1 (ksdA 3' region) [Escherichia coli] dbj BAA36082.1 (D90757) Hypothetical protein 1 (ksdA 3' region) [Escherichia coli] gb AAG56072.1 AE005338_12 (AE005338) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3567 gb AAG56070.1 AE005338_10 (AE005338) possible protoporphyrinogen oxidase [Escherichia coli O157:H7] SEQ ID n-3566
SEQ ID n° 6799	PL-2392.1	Contig9 from 1056796 to 1057644	m	73%	sp P07011 RF1_ECOLI_PPTIDE_CHAIN_RELEASE_FACTOR 1 (RF-1) pir FCECR1 translation releasing factor RF-1 - Escherichia coli dbj BAA36069.1 (D90756) Peptide chain release factor 1 (rf-1). [Escherichia coli] dbj BAA36079.1 (D90757) Peptide chain release factor 1 (rf-1). [Escherichia coli] gb AAC74295.1 (AE000219) peptide chain release factor RF-1 [Escherichia coli K12] SEQ ID n-3565
SEQ ID n° 6800	PL-2391.1	Contig9 from 1057644 to 1058726	m	92%	gb ANG56068.1 AE005338_8 (AE005338) enzyme in alternate path of synthesis of 5- aminolevulinate [Escherichia coli O157:H7] SEQ ID n-3564
SEQ ID n° 6801	PL-2390.1	Contig9 from 1058758 to 1060020	m	85%	

TABLEAU II

SEQ ID n° 6802 PL-2389.1	Contig9 from 1061024 to 1061024	p 68*	sp P24208 LOLB_ECOLI OUTER-MEMBRANE LIPOPROTEIN	SEQ ID n-1562
			LOLB PRECURSOR pir A47706 5-aminolevulinate synthase (EC 2.3.1.37) hemM - Escherichia coli gb AA24433.1 (M77237) ORF1 [Escherichia coli] dbj BAA36067.1 (D90756) 22k hypothetical protein (3' of hemA) [Escherichia coli] gb AAC74293.1 (AE000219) an enzyme in main pathway of synthesis of 5- aminolevulinate, possibly glutamyl-tRNA dehydrogenase [Escherichia coli K12] gb AAG56067.1 AE005338_7 (AE005338) an enzyme in main pathway of synthesis of 5- aminolevulinate, possibly glutamyl-tRNA dehydrogenase [Escherichia coli O157:H7]	
SEQ ID n° 6803 PL-2388.1	Contig9 from 1061024 to 1061899	p 75*	sp P24209 ISPE_ECOLI 4-DIPHOSPHOCYTIDYL-2-C- METHYL-D-ERYTHRITOL KINASE (CMK) (4- (CYTIDINE-5'-DIPHOSPHO)-2-C-METHYL-D-ERYTHRITOL KINASE) pir B47706 ychB protein - Escherichia coli gb AA24434.1 (M77237) ORF2 [Escherichia coli] gb AAC43434.1 (U18555) orfY gene product [Escherichia coli] gb AAC74292.1 (AE000219) orf, hypothetical protein [Escherichia coli K12] dbj BAA36066.1 (D90756) 31k hypothetical protein (5' of prs) [Escherichia coli] gb AAF13867.1 (AF179284) isopentenyl monophosphate kinase [Escherichia coli] emb CAB64963.1 (AJ249325) isopentenyl monophosphate kinase [Escherichia coli] gb AAF29530.1 AF216300_1 (AF216300) 4- diphosphocytidyl-2C-methyl-D-erythritol kinase [Escherichia coli] dbj BAA94247.1 (AB037116) 4- (cytidine-5'-diphospho)-2-C-methyl-D-erythrito 1 kinase [Escherichia coli]	SEQ ID n-1561

TABLEAU II

SEQ ID n° 6804	PL-2387.1	Contig9 from 1061963 to 1062910	p	91%	sp P08330 KPRS_ECOLI RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE) pir [KIECRY ribose-phosphate pyrophosphokinase (EC 2.7.6.1) [validated] - Escherichia coli gb AAC74291.1 (AE000219) phosphoribosylpyrophosphate synthetase [Escherichia coli K12] dbj BAA36065.1 (D90756) Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) (phosphoribosyl pyrophosphate synthetase). [Escherichia coli] sp P31807 YCHH_ECOLI HYPOTHETICAL 10.5 KDA PROTEIN IN PTH-PRS INTERGENIC REGION (ORF-2) pir [B64867 probable membrane protein ychH - Escherichia coli emb CAA43947.1 (X61941) ORF-2 [Escherichia coli] gb AAC74289.1 (AE000219) orf, hypothetical protein [Escherichia coli K12] dbj BAA36063.1 (D90756) Hypothetical 10.5 kd protein in pth-prs intergenic region (orf-2). [Escherichia coli] gb AAG56063.1 AE005338_3 (AE005338) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-1560
SEQ ID n° 6805	PL-4225.1	Contig9 from 1063006 to 1063281	m	70%	gb AAG57041.1 AE005423_3 (AE005423) putative invasin [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6806	PL-2386.1	Contig9 from 1063761 to 1064729	m	32%		SEQ ID n-1559
SEQ ID n° 6807	PL-2385.2	Contig9 from 1064844 to 1066169	m	No Hits found		SEQ ID n-1558
SEQ ID n° 6808	PL-2383.1	Contig9 from 1066936 to 1068534	m	No Hits found		SEQ ID n-1557
SEQ ID n° 6809	PL-2382.1	Contig9 from 1068874 to 1070376	m	No Hits found		SEQ ID n-1556

TABLEAU II

SEQ ID n° 6810	PL-2381.1	Contig9 from 1070759 to 1072261	m	No Hits found	SEQ ID n-2555
SEQ ID n° 6811	PL-2380.2	Contig9 from 1072846 to 1074348	m	No Hits found	SEQ ID n-2554
SEQ ID n° 6812	PL-2379.1	Contig9 from 1075148 to 1080235	m	35%	SEQ ID n-2552
SEQ ID n° 6813	PL-2378.1	Contig9 from 1080732 to 1082672	m	8%	SEQ ID n-2551
SEQ ID n° 6814	PL-3756.1	Contig9 from 1083076 to 1083666	p	84%	SEQ ID n-2935
SEQ ID n° 6815	PL-2377.1	Contig9 from 1083808 to 1084899	p	95%	SEQ ID n-2550
SEQ ID n° 6816	PL-2376.1	Contig9 from 1085050 to 1086747	m	44%	SEQ ID n-2549
SEQ ID n° 6817	PL-4221.1	Contig9 from 1087244 to 1087543	m	No Hits found	#N/A
SEQ ID n° 6818	PL-4220.1	Contig9 from 1088131 to 1088352	p	No Hits found	#N/A

gb|AAG54632.1|AE005207_7 (AE005207) putative
adhesin [Escherichia coli O157:H7]
ref|NP_050653.1| s [Bacteriophage Mu]
sp|Q9TIV0|VPS BPMU TAIL FIBER PROTEIN (GPS)
gb|AAF01127.1|AF083977_46 (AF083977) S
[Bacteriophage Mu]
sp|Q60001|PTH_SALTI PEPTIDYL-TRNA HYDROLASE
(PTH) gb|AAB06185.1| (U31571) peptidyl-trna
hydrolase [Salmonella typhi]
sp|P31216|YCHF_ECOLI PROBABLE GTP-BINDING
PROTEIN IN TREA-PTH INTERGENIC REGION (ORF-3)
pir||H64866 probable GTP-binding protein ychF -
Escherichia coli gb|AAC74287.1| (AE000219)
putative GTP-binding protein [Escherichia coli
K12] dbj|BAA36061.1| (D90756) Probable GTP-
binding protein in pth 3'region (orf-3) .
[Escherichia coli]
pir||B75371 ABC transporter, ATP-binding
protein, EF-3 family - Deinococcus
radiodurans (strain R1)
gb|AAF11195.1|AE002007_1 (AE002007) ABC
transporter, ATP-binding protein, EF-3 family
[Deinococcus radiodurans]

TABLEAU II

SEQ ID n° 6819	PL-4219.1	Contig9 from 1088349 to 1088783	p	No Hits found		#N/A
SEQ ID n° 6820	PL-2375.2	Contig9 from 1088852 to 1090063	m	12%	ref NP_050653.1 S [Bacteriophage Mu] sp Q9T1V0 VPS_BPMU TAIL FIBER PROTEIN (GPS) gb AAE01127.1 AF083977_46 (AF083977) S [Bacteriophage Mu]	SEQ ID n-2348
SEQ ID n° 6821	PL-3102.2	Contig9 from 1090903 to 1091709	p	No Hits found		SEQ ID n-2343
SEQ ID n° 6822	PL-3103.2	Contig9 from 1091805 to 1092830	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-2344
SEQ ID n° 6823	PL-3104.1	Contig9 from 1093584 to 1094426	p	No Hits found		SEQ ID n-2345
SEQ ID n° 6824	PL-4217.1	Contig9 from 1094623 to 1094823	m	56%	sp P18355 YPFU_ECOLI HYPOTHETICAL 8.5 KDA PROTEIN IN TRAD-TRAI INTERGENIC REGION pir Q4ECTI hypothetical 8.5K protein (trad-trai intergenic region) - Escherichia coli plasmid F	#N/A
SEQ ID n° 6825	PL-3105.1	Contig9 from 1094861 to 1096285	m	78%	pir T46999 hypothetical protein [imported] - Yersinia pestis emb CAA21342.1 (AL031866) ORF19, len: 473 aa, similar to tyrosine aminotransferase, highly similar to E. coli D90784_2, FastA scores opt:1842, E(): 0 [Yersinia pestis]	SEQ ID n-2346

TABLEAU II

SEQ ID n° 6826 PL-3106.1	Contig9 from 1096414 to 1097751	p 85%	pir T47273 cyanide insensitive terminal oxidase chain cioA [imported] - Pseudomonas aeruginosa pir G83155 cyanide insensitive terminal oxidase PA3930 [imported] - Pseudomonas aeruginosa (strain PAO1) emb CAA71555.1 (Y10528) cyanide insensitive terminal oxidase [Pseudomonas aeruginosa] gb AAG07317.1 AE004810_9 (AE004810) cyanide insensitive terminal oxidase [Pseudomonas aeruginosa] SEQ ID n-2347
			pir T47274 cyanide insensitive terminal oxidase chain cioB [imported] - Pseudomonas aeruginosa pir F83155 cyanide insensitive terminal oxidase PA3929 [imported] - Pseudomonas aeruginosa (strain PAO1) emb CAA71556.1 (Y10528) cyanide insensitive terminal oxidase [Pseudomonas aeruginosa] gb AAG07316.1 AE004810_8 (AE004810) cyanide insensitive terminal oxidase [Pseudomonas aeruginosa] SEQ ID n-2348
SEQ ID n° 6827 PL-3107.1	Contig9 from 1097741 to 1098748	p 79%	pir T47000 nitrate/nitrite sensor protein (EC 2.7.3.-) [similarity] - Yersinia pestis emb CAA21343.1 (AL031866) ORF20, len: 593 aa, probable nitrate/nitrite sensor protein, highly similar to many, e.g. E. coli P10956, 47.9% identity in 595 aa overlap Fasta scores: opt: 1801, E():0, and PSNAPXL_2 Pseudomonas aeruginosa narX, 33.1% identity in 596 aa ove>
			SEQ ID n-2349

TABLEAU II

SEQ ID n° 6829	PL-3109.1	Contig9 from 1100323 to 1101156	P	50%	sp Q56646 VIUB_VIBCH VIBRIOBACTIN UTILIZATION PROTEIN VIUB pir C82104 vibriobactin utilization protein Viub VC2210 [imported] - Vibrio cholerae (group O1 strain N15961) gb AAB86829.1 (AF030977) Viub protein [Vibrio cholerae] gb AAF95354.1 (AE004293) vibriobactin utilization protein Viub [Vibrio cholerae]	SEQ ID n-2350
SEQ ID n° 6830	PL-3110.1	Contig9 from 1101591 to 1102379	m	86%	sp P31544 PHO ECOLI PHO PROTEIN (PHOSPHATE STARVATION-INDUCIBLE PROTEIN PSIH) pir B47065 phosphate starvation-inducible protein psih - Escherichia coli dbj BAA01230.1 (D10391) PhoH protein [Escherichia coli] dbj BAA35801.1 (D90739) PhoH protein (phosphate starvation- inducible protein PsiH). [Escherichia coli] gb AAC74105.1 (AE000204) PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation [Escherichia coli K12]	SEQ ID n-2352
SEQ ID n° 6831	PL-4214.1	Contig9 from 1102707 to 1102856	m	No Hits found		#N/A
SEQ ID n° 6832	PL-3111.3	Contig9 from 1103031 to 1104029	m	43%	dbj BAB37244.1 (AP002563) DNA-specific endonuclease I [Escherichia coli O157:H7]	#N/A
SEQ ID n° 6833	PL-3112.1	Contig9 from 1104263 to 1105549	m	14%	gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-2354
SEQ ID n° 6834	PL-3113.1	Contig9 from 1105787 to 1106413	m	55%	sp Q47427 TFAB_ECOLI TAIL FIBER ASSEMBLY PROTEIN HOMOLOG pir s18684 gene T protein - Escherichia coli plasmid p15B emb CAA44047.1 (X62121) T [Escherichia coli]	SEQ ID n-2355
SEQ ID n° 6835	PL-3114.1	Contig9 from 1106435 to 1107154	m	39%	pir s18689 Sc/svp protein - Escherichia coli plasmid p15B emb CAA44052.1 (X62121) DNA inversion product [Escherichia coli]	SEQ ID n-2356

TABLEAU II

SEQ ID n° 6836	PL-3115.1	Contig9 from 1107537 to 1108232	m	85%	gb AAG55257.1 AE005269_1 (AE005269) transmembrane water channel; aquaporin 2 [Escherichia coli O157:H7]	SEQ ID n-2357
SEQ ID n° 6837	PL-3754.1	Contig9 from 1108724 to 1109161	m	53%	gb AAG54942.1 AE005240_8 (AE005240) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2934
SEQ ID n° 6838	PL-4211.1	Contig9 from 1109340 to 1109678	m	53%	pir G82351 hypothetical protein VC0198 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93374.1 (AE004110) hypothetical protein [Vibrio cholerae]	#N/A
SEQ ID n° 6839	PL-3753.1	Contig9 from 1109939 to 1110367	m	63%	gb AAG54942.1 AE005240_8 (AE005240) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2933
SEQ ID n° 6840	PL-4210.1	Contig9 from 1110727 to 1110951	m	40%	sp P46120 YECF_ECOLI HYPOTHETICAL 8.2 KD PROTEIN IN UVRY-SDIA INTERGENIC REGION pir H64954 yecF protein - Escherichia coli dbj BAAL5735.1 (D90832) ORF ID:0341#12; similar to [SwissProt Accession Number P46120] [Escherichia coli] gb AAC74982.1 (AE000284) orf, hypothetical protein [Escherichia coli K12]	#N/A
SEQ ID n° 6841	PL-3116.1	Contig9 from 1111386 to 1112051	p	85%	emb CAA64809.1 (X95564) expA [Erwinia carotovora]	SEQ ID n-2358
SEQ ID n° 6842	PL-3117.1	Contig9 from 1112035 to 1113867	p	90%	dbj BAAL5733.1 (D90832) Excinuclease ABC subunit C. [Escherichia coli]	SEQ ID n-2359

TABLEAU II

SEQ ID n° 6843	PL-3752.1	Contig9 from 1113925 to 1114473	p 80%	sp P06978 PGSA_ECOLI_CDP-DIACYLGLYCEROL-- GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE) (PGP SYNTHASE) pir XNECPG CDPdiacylglycerol-- glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) - Escherichia coli gb AA98754.1 (M12299) phosphatidylglycerophosphate synthase [Escherichia coli] gb AAC74979.1 (AE000284) phosphatidylglycerophosphate synthetase = CDP-1,2-diacyl-sn-glycero-3-phosphate phosphatidyl transferase [Escherichia coli K12] gb AAG56927.1 AE005414_4 (AE005414) phosphatidylglycerophosphate synthetase = CDP-1,2-diacyl-sn-glycero-3-phosphate phosphatidyl transferase [Escherichia coli O157:H7]	SEQ ID n-2932
SEQ ID n° 6844	PL-4207.1	Contig9 from 1114710 to 1114874	p 31%	gb AAK02985.1 (AE006129) unknown [Pasteurella multocida]	#N/A
SEQ ID n° 6845	PL-4205.1	Contig9 from 1115193 to 1115465	p No Hits found		#N/A
SEQ ID n° 6846	PL-3118.1	Contig9 from 1115899 to 1116648	m 51%	pir S18690 Sc/SvQ protein - Escherichia coli plasmid p15B emb CAA44053.1 (X62121) DNA inversion product [Escherichia coli] gb AAG56009.1 AE005333_6 (AE005333) putative tail fiber protein of prophage CP-933X [Escherichia coli O157:H7]	SEQ ID n-2360
SEQ ID n° 6847	PL-3119.1	Contig9 from 1116703 to 1118184	m 22%	pir S18690 Sc/SvQ protein - Escherichia coli plasmid p15B emb CAA44053.1 (X62121) DNA inversion product [Escherichia coli] gb AAG56916.1 AE005413_10 (AE005413) putative serine acetyltransferase of prophage CP-933T [Escherichia coli O157:H7]	SEQ ID n-2361
SEQ ID n° 6848	PL-3120.1	Contig9 from 1118978 to 1119895	m 31%		SEQ ID n-2363
SEQ ID n° 6849	PL-3751.1	Contig9 from 1120502 to 1121098	p 47%		SEQ ID n-2931

TABLEAU II

SEQ ID n° 6850 PL-3121.1	Contig9 from 1121134 to 1122042	p	52%	gb AAD37764.1 AF146532.4 (AF146532) putative glycosyltransferase [Klebsiella pneumoniae] pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-2364
SEQ ID n° 6851 PL-3122.1	Contig9 from 1123092 to 1123766	p	41%		SEQ ID n-2365
SEQ ID n° 6852 PL-7020.1	Contig9 from 1123939 to 1124055	p	No Hits found		#N/A
SEQ ID n° 6853 PL-3123.2	Contig9 from 1124515 to 1125141	p	43%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-2366
SEQ ID n° 6854 PL-4200.1	Contig9 from 1125457 to 1125744	m	42%	dbj BAA93674.1 (AB027193) Usp [Escherichia coli]	#N/A
SEQ ID n° 6855 PL-3124.2	Contig9 from 1126572 to 1127264	p	39%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 6856 PL-3125.2	Contig9 from 1127320 to 1127997	p	40%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 6857 PL-4198.1	Contig9 from 1128027 to 1128173	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6858	PL-3750.1	Contig9 from 1128158 to 1128838	p 41%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-2930
SEQ ID n° 6859	PL-3749.1	Contig9 from 1128865 to 1129545	p 39%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-2928
SEQ ID n° 6860	PL-4197.1	Contig9 from 1129706 to 1130386	p 39%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] #N/A
SEQ ID n° 6861	PL-3203.2	Contig9 from 1130547 to 1131227	p 41%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] #N/A
SEQ ID n° 6862	PL-3209.2	Contig9 from 1131498 to 1132181	p 38%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] #N/A
SEQ ID n° 6863	PL-3208.1	Contig9 from 1132442 to 1133122	p 39%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-2450

TABLEAU II

SEQ ID n° 6864	PL-3207.1	Contig9 from 1133153 to 1133833	p 42%	pir B82381 transcription regulator LuxR family VCA1078 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96971.1 (AE004433) transcriptional regulator, LuxR family [Vibrio cholerae]	SEQ ID n-2459
SEQ ID n° 6865	PL-3206.1	Contig9 from 1133863 to 1134543	p 38%	pir B82381 transcription regulator LuxR family VCA1078 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96971.1 (AE004433) transcriptional regulator, LuxR family [Vibrio cholerae]	SEQ ID n-2458
SEQ ID n° 6866	PL-3205.1	Contig9 from 1134574 to 1135254	p 39%	pir C83477 probable transcription regulator PA1347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AB004564_5 (AB004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-2457
SEQ ID n° 6867	PL-3204.2	Contig9 from 1135284 to 1135907	p 39%	pir B82381 transcription regulator LuxR family VCA1078 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96971.1 (AE004433) transcriptional regulator, LuxR family [Vibrio cholerae]	#N/A
SEQ ID n° 6868	PL-4195.1	Contig9 from 1136257 to 1136937	p 41%	pir C83477 probable transcription regulator PA1347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AB004564_5 (AB004564) probable transcriptional regulator [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 6869	PL-2152.2	Contig9 from 1136965 to 1137636	p 42%	pir C83477 probable transcription regulator PA1347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AB004564_5 (AB004564) probable transcriptional regulator [Pseudomonas aeruginosa]	#N/A

TABLEAU II

SEQ ID n° 6870	PL-2153.1	Contig9 from 1137784 to 1138479	P	43%	pir C83477 probable transcription regulator PA1347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564.5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-1305
SEQ ID n° 6871	PL-2154.1	Contig9 from 1138766 to 1139902	m	73%	sp P45545 YHFS_ECOLI_HYPOTHETICAL 38.6 KD PROTEIN IN CYSG-TRPS INTERGENIC REGION (F361) pir C65132 hypothetical 38.6 kD protein in cysg- trps intergenic region - Escherichia coli (strain K-12) gb AAA58173.1 (U18997) ORF_f361 [Escherichia coli] gb AAC76401.1 (AE000413) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-1306
SEQ ID n° 6872	PL-2155.1	Contig9 from 1139950 to 1141284	m	64%	dbj BAB04308.1 (AP001509) BH0589-unknown conserved protein in others [Bacillus halodurans] SEQ ID n-1307
SEQ ID n° 6873	PL-4194.1	Contig9 from 1141322 to 1141681	m	65%	dbj BAB04307.1 (AP001509) BH0588-unknown conserved protein in others [Bacillus halodurans] #N/A
SEQ ID n° 6874	PL-2156.1	Contig9 from 1141693 to 1142583	m	71%	pdb 1BF6 B Chain B, Phosphotriesterase Homology Protein From Escherichia Coli pdb 1BF6 A Chain A, Phosphotriesterase Homology Protein From Escherichia Coli SEQ ID n-1308
SEQ ID n° 6875	PL-2157.1	Contig9 from 1142627 to 1143805	m	73%	sp P45550 YHFX_ECOLI_HYPOTHETICAL 44.3 KD PROTEIN IN CYSG-TRPS INTERGENIC REGION (F387) pir H65132 hypothetical 44.3 kD protein in cysg- trps intergenic region - Escherichia coli (strain K-12) gb AAA58178.1 (U18997) ORF_f387 [Escherichia coli] gb AAC76406.1 (AE000413) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-1309
SEQ ID n° 6876	PL-4193.1	Contig9 from 1143922 to 1144278	m	70%	sp P45551 YHFX_ECOLI_HYPOTHETICAL 13.5 KD PROTEIN IN CYSG-TRPS INTERGENIC REGION #N/A

TABLEAU II

SEQ ID n° 6877	PL-2158.1	Contig9 from 1144302 to 1145207	m 72%	sp P45552 YHFZ_ECOLI HYPOTHETICAL 30.3 KD PROTEIN IN CYSQ-TRPS INTERGENIC REGION SEQ ID n-2310
SEQ ID n° 6878	PL-2159.1	Contig9 from 1145360 to 1147030	m 81%	sp P20966 PTFB_ECOLI PTS SYSTEM, FRUCTOSE- SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-FRU) pir A34962 phosphotransferase system enzyme II (EC 2.7.1.69), fructose-specific - Escherichia coli gb AAA60524.1 (U00007) fructose-specific IIBC component [Escherichia coli] gb AAA62624.1 (M23196) enzyme II-fru [Escherichia coli] gb AAC75228.1 (AE000306) PTS system, fructose-specific transport protein [Escherichia coli K12] prf 2014253BN fruA gene [Escherichia coli] SEQ ID n-2311

SEQ ID n°	Accession	Contig9 from	Length	Gene	Function
6879	PL-2160.1	1147100 to 1148227	74%	sp P24217 PTFA_ECOLI PTS SYSTEM, FRUCTOSE-SPECIFIC IIA/FPR COMPONENT (EIIA-FRU) (FRUCTOSE-PERMEASE IIA/FPR COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A/FPR COMPONENT) (PHOSPHOTRANSFERASE FPR PROTEIN) (PSEUDO-HPR) (EIII-FRU)	TRANSFER PROTEIN pir I53564 phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli gb AAA60534.1 (U00007) fructose-specific IIA/FPR component [Escherichia coli] gb AAB31084.1 (S72443) DTP, FruB-phosphoenolpyruvate: sugar phosphotransferase system
6880	PL-2161.1	1148802 to 1149422	66%	sp S53063 Fimb protein - Escherichia coli emb CAA85725.1 (Z37500) Fimb protein [Escherichia coli]	diphosphoryl transfer protein [Escherichia coli, Peptide, 376 aa] gb AAC75230.1 (AE000306) PTS system, fructose-specific IIA/fpr component [Escherichia coli K12] prf 2014253BV phosphotransferase FPR protein [Escherichia coli]
6881	PL-4191.1	1149422 to 1149616	56%	sp P45545 YHFS_ECOLI HYPOTHETICAL 38.6 KD PROTEIN IN CYSG-TRPS INTERGENIC REGION (F361) pir C65132 hypothetical 38.6 kD protein in cysg-trps intergenic region - Escherichia coli (strain K-12) gb AA58173.1 (U18997) ORF_f361 [Escherichia coli] gb AAC76401.1 (AE000413) orf, hypothetical protein [Escherichia coli K12]	

TABLEAU II

SEQ ID n° 6882	PL-2162.1	Contig9 from 1150399 to 1151940	p	56%	pir D70180 phosphotransferase system enzyme II (EC 2.7.1.69) glucose-specific factor II - Lyme disease spirochete gb AAC6998.1 (AE001166) PTS system, glucose- specific IIBC component (ptsG) [Borrelia burgdorferi] sp D06901 MAEF_FUSMF MALTOSF-6'-PHOSPHATE GLUCOSIDASE (6-PHOSPHO-ALPHA-D-GLUCOSIDASE) gb AAB63015.1 (U81185) MalH [Fusobacterium mortiferum] gb AAD11507.1 -(U60828) unknown [Lactococcus lactis] gb AAK06083.1 AE006429_1 (AE006429) transcription regulator [Lactococcus lactis subsp. lactis] SEQ ID n-3315
SEQ ID n° 6883	PL-2163.1	Contig9 from 1151954 to 1153312	p	65%	gb AAD11507.1 -(U60828) unknown [Lactococcus lactis] gb AAK06083.1 AE006429_1 (AE006429) transcription regulator [Lactococcus lactis subsp. lactis] SEQ ID n-3316
SEQ ID n° 6884	PL-2164.1	Contig9 from 1153569 to 1154348	p	42%	transcription regulator [Lactococcus lactis subsp. lactis] SEQ ID n-3317
SEQ ID n° 6885	PL-4188.1	Contig9 from 1155267 to 1155404	p	No Hits found	#N/A
SEQ ID n° 6886	PL-3980.1	Contig9 from 1155444 to 1155893	p	44%	pir B82381 transcription regulator LuxR family VCA1078 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96971.1 (AB004433) transcriptional regulator, luxR family [Vibrio cholerae] pir CB3477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AB004564_5 (AB004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-3139
SEQ ID n° 6887	PL-2165.1	Contig9 from 1156074 to 1156769	p	43%	pir T37066 probable integral membrane protein - Streptomyces coelicolor emb CAB52363.1 (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)] SEQ ID n-3318
SEQ ID n° 6888	PL-2166.1	Contig9 from 1157089 to 1158345	m	68%	dbj BAB03941.1 (AP001507) BH0222-unknown conserved protein [Bacillus halodurans] #N/A
SEQ ID n° 6889	PL-4187.1	Contig9 from 1158359 to 1158664	m	50%	

TABLEAU II

SEQ ID n° 6890	PL-3979.1	Contig9 from 1158676 to 1159119	m	59%	dbj BAB03939.1 (AP001507) BH0220-unknown conserved protein [Bacillus halodurans]	SEQ ID n-9137
SEQ ID n° 6891	PL-2167.1	Contig9 from 1159358 to 1160401	p	48%	gb AAK02875.1 (AE006117) unknown [Pasteurella multocida]	SEQ ID n-2320
SEQ ID n° 6892	PL-3978.1	Contig9 from 1160460 to 1160924	m	46%	emb CAB71827.1 (AL138662) hypothetical protein SC8E4A.22 [Streptomyces coelicolor A3(2)]	SEQ ID n-9136
SEQ ID n° 6893	PL-4186.1	Contig9 from 1161131 to 1161532	m	37%	pir C83418 hypothetical protein PA1817 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05206.1 AE004608_5 (AE004608) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 6894	PL-2168.1	Contig9 from 1161714 to 1162769	m	76%	pir D83102 xenobiotic reductase PA4356 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07744.1 AE004851_12 (AE004851) xenobiotic reductase [Pseudomonas aeruginosa]	SEQ ID n-2321
SEQ ID n° 6895	PL-3977.1	Contig9 from 1163153 to 1163482	m	No Hits found		SEQ ID n-9135
SEQ ID n° 6896	PL-4185.1	Contig9 from 1163451 to 1163687	m	No Hits found		#N/A
SEQ ID n° 6897	PL-2169.1	Contig9 from 1164203 to 1165924	p	72%	ref NP_047871.1 murine toxin [Yersinia pestis] pir T14986 toxin protein - Yersinia pestis plasmid pMT1 gb AAC82729.1 (AF074611) murine toxin [Yersinia pestis]	SEQ ID n-2322

TABLEAU II

SEQ ID n° 6898	PL-2170.1	Contig9 from 1166142 to 1167473	m	76%	sp P00926 SDHD_ECOLI D-SERINE DEHYDRATASE (D-SERINE DEAMINASE) pir [DWECS D-serine dehydratase (EC 4.2.1.14) - Escherichia coli gb AAC75425.1 (AE000324) D-serine dehydratase (deaminase) [Escherichia coli K12] dbj BAAL6229.1 (D90866) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] dbj BAAL6237.1 (D90867) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] sp P08555 DSDX_ECOLI DSDX PERMEASE pir [S54140 D-serine permease - Escherichia coli] emb CAA60138.1 (X86379) D-serine permease [Escherichia coli] emb CAA62932.1 (X91821) dsdx [Escherichia coli] gb AAC75424.1 (AE000324) transport system permease (serine?) [Escherichia coli K12] dbj BAAL6225.1 (D90866) DSDX PERMEASE. [Escherichia coli] dbj BAAL6233.1 (D90867) DSDX PERMEASE. [Escherichia coli] sp P46068 DSDC_ECOLI D-SERINE DEAMINASE ACTIVATOR pir [A65010 D-serine deaminase activator - Escherichia coli (strain K-12) gb AAC75423.1 (AE000324) D-serine dehydratase (deaminase) transcriptional activator [Escherichia coli K12] dbj BAAL6224.1 (D90866) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] dbj BAAL6232.1 (D90867) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] gb AAG58105.1 AE005527_8 (AE005527) putative PagC-like membrane protein [Escherichia coli O157:H7] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-1324
SEQ ID n° 6899	PL-2171.1	Contig9 from 1168158 to 1169495	m	89%	sp P00926 SDHD_ECOLI D-SERINE DEHYDRATASE (D-SERINE DEAMINASE) pir [DWECS D-serine dehydratase (EC 4.2.1.14) - Escherichia coli gb AAC75425.1 (AE000324) D-serine dehydratase (deaminase) [Escherichia coli K12] dbj BAAL6229.1 (D90866) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] dbj BAAL6237.1 (D90867) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] sp P08555 DSDX_ECOLI DSDX PERMEASE pir [S54140 D-serine permease - Escherichia coli] emb CAA60138.1 (X86379) D-serine permease [Escherichia coli] emb CAA62932.1 (X91821) dsdx [Escherichia coli] gb AAC75424.1 (AE000324) transport system permease (serine?) [Escherichia coli K12] dbj BAAL6225.1 (D90866) DSDX PERMEASE. [Escherichia coli] dbj BAAL6233.1 (D90867) DSDX PERMEASE. [Escherichia coli] sp P46068 DSDC_ECOLI D-SERINE DEAMINASE ACTIVATOR pir [A65010 D-serine deaminase activator - Escherichia coli (strain K-12) gb AAC75423.1 (AE000324) D-serine dehydratase (deaminase) transcriptional activator [Escherichia coli K12] dbj BAAL6224.1 (D90866) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] dbj BAAL6232.1 (D90867) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] gb AAG58105.1 AE005527_8 (AE005527) putative PagC-like membrane protein [Escherichia coli O157:H7] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-1325
SEQ ID n° 6900	PL-2172.1	Contig9 from 1169737 to 1170675	p	73%	sp P00926 SDHD_ECOLI D-SERINE DEHYDRATASE (D-SERINE DEAMINASE) pir [DWECS D-serine dehydratase (EC 4.2.1.14) - Escherichia coli gb AAC75425.1 (AE000324) D-serine dehydratase (deaminase) [Escherichia coli K12] dbj BAAL6229.1 (D90866) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] dbj BAAL6237.1 (D90867) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] sp P08555 DSDX_ECOLI DSDX PERMEASE pir [S54140 D-serine permease - Escherichia coli] emb CAA60138.1 (X86379) D-serine permease [Escherichia coli] emb CAA62932.1 (X91821) dsdx [Escherichia coli] gb AAC75424.1 (AE000324) transport system permease (serine?) [Escherichia coli K12] dbj BAAL6225.1 (D90866) DSDX PERMEASE. [Escherichia coli] dbj BAAL6233.1 (D90867) DSDX PERMEASE. [Escherichia coli] sp P46068 DSDC_ECOLI D-SERINE DEAMINASE ACTIVATOR pir [A65010 D-serine deaminase activator - Escherichia coli (strain K-12) gb AAC75423.1 (AE000324) D-serine dehydratase (deaminase) transcriptional activator [Escherichia coli K12] dbj BAAL6224.1 (D90866) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] dbj BAAL6232.1 (D90867) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] gb AAG58105.1 AE005527_8 (AE005527) putative PagC-like membrane protein [Escherichia coli O157:H7] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-1326
SEQ ID n° 6901	PL-3975.1	Contig9 from 1170985 to 1171533	p	48%	sp P00926 SDHD_ECOLI D-SERINE DEHYDRATASE (D-SERINE DEAMINASE) pir [DWECS D-serine dehydratase (EC 4.2.1.14) - Escherichia coli gb AAC75425.1 (AE000324) D-serine dehydratase (deaminase) [Escherichia coli K12] dbj BAAL6229.1 (D90866) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] dbj BAAL6237.1 (D90867) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] sp P08555 DSDX_ECOLI DSDX PERMEASE pir [S54140 D-serine permease - Escherichia coli] emb CAA60138.1 (X86379) D-serine permease [Escherichia coli] emb CAA62932.1 (X91821) dsdx [Escherichia coli] gb AAC75424.1 (AE000324) transport system permease (serine?) [Escherichia coli K12] dbj BAAL6225.1 (D90866) DSDX PERMEASE. [Escherichia coli] dbj BAAL6233.1 (D90867) DSDX PERMEASE. [Escherichia coli] sp P46068 DSDC_ECOLI D-SERINE DEAMINASE ACTIVATOR pir [A65010 D-serine deaminase activator - Escherichia coli (strain K-12) gb AAC75423.1 (AE000324) D-serine dehydratase (deaminase) transcriptional activator [Escherichia coli K12] dbj BAAL6224.1 (D90866) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] dbj BAAL6232.1 (D90867) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] gb AAG58105.1 AE005527_8 (AE005527) putative PagC-like membrane protein [Escherichia coli O157:H7] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-1327
SEQ ID n° 6902	PL-2173.1	Contig9 from 1172158 to 1173003	p	17%	sp P00926 SDHD_ECOLI D-SERINE DEHYDRATASE (D-SERINE DEAMINASE) pir [DWECS D-serine dehydratase (EC 4.2.1.14) - Escherichia coli gb AAC75425.1 (AE000324) D-serine dehydratase (deaminase) [Escherichia coli K12] dbj BAAL6229.1 (D90866) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] dbj BAAL6237.1 (D90867) D-serine dehydratase (EC 4.2.1.14) [Escherichia coli] sp P08555 DSDX_ECOLI DSDX PERMEASE pir [S54140 D-serine permease - Escherichia coli] emb CAA60138.1 (X86379) D-serine permease [Escherichia coli] emb CAA62932.1 (X91821) dsdx [Escherichia coli] gb AAC75424.1 (AE000324) transport system permease (serine?) [Escherichia coli K12] dbj BAAL6225.1 (D90866) DSDX PERMEASE. [Escherichia coli] dbj BAAL6233.1 (D90867) DSDX PERMEASE. [Escherichia coli] sp P46068 DSDC_ECOLI D-SERINE DEAMINASE ACTIVATOR pir [A65010 D-serine deaminase activator - Escherichia coli (strain K-12) gb AAC75423.1 (AE000324) D-serine dehydratase (deaminase) transcriptional activator [Escherichia coli K12] dbj BAAL6224.1 (D90866) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] dbj BAAL6232.1 (D90867) D-SERINE DEAMINASE ACTIVATOR. [Escherichia coli] gb AAG58105.1 AE005527_8 (AE005527) putative PagC-like membrane protein [Escherichia coli O157:H7] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-1328

THIS PAGE BLANK (USPTO)

TABLEAU II

SEQ ID n° 6903	PL-2174.1	1173716 to 1175122	p	81%	sp P39312 CYCA_ECOLI D-SERINE/D-ALANINE/GLYCINE TRANSPORTER. pir [S56433 D-serine/D-alanine/glycine transporter - Escherichia coli gb AAA97104.1 (U14003) ORF_0470 [Escherichia coli] gb AAC77165.1 (AE000492) transport of D-alanine, D-serine, and glycine [Escherichia coli K12] gb ARG59406.1 AE005653_7 (AE005653) transport of D-alanine, D-serine, and glycine sp P30849 WRBA_ECOLI TRP REPRESSOR BINDING PROTEIN. pir [B84842 trp repressor-binding protein - Escherichia coli gb AAC74089.1 (AE000202) trp repressor binding protein; affects association of trp repressor and operator [Escherichia coli K12] dbj BAA35771.1 (D90737) Trp repressor binding protein [Escherichia coli] dbj BAA35781.1 (D90738) Trp repressor binding protein [Escherichia coli] SEQ ID n-1328
SEQ ID n° 6904	PL-2175.1	1175502 to 1176101	p	77%	ref NP_052901.1 transposase for Tn21 [Plasmid R100] dbj BAA78805.1 (AP000342) transposase for Tn21 [Plasmid R100] gb AAG14402.1 AF188331.1 (AF188331) putative transposase [Shigella flexneri] sp O42184 REST_CHICK RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170) gb AAC60344.1 (AF014012) restin [Gallus gallus] pir [T29999 hypothetical protein ZC8.4 - Caenorhabditis elegans gb AAB52624.1 (U64862) strong similarity to Onchocerca volvulus major antigen (SP:P212249) [Caenorhabditis elegans] SEQ ID n-1329
SEQ ID n° 6905	PL-4180.2	1176159 to 1176440	m	30%	gb AAA25324.1 (L34345) xylytol dehydrogenase [Morganella morganii] SEQ ID n-1332
SEQ ID n° 6906	PL-2176.3	1176730 to 1177968	p	40%	
SEQ ID n° 6907	PL-4179.2	1178011 to 1179039	p	40%	
SEQ ID n° 6908	PL-2178.1	1179680 to 1180708	p	82%	

TABLEAU II

SEQ ID n°	Contig9 from	P	SEQ ID n°	SEQ ID n°
6909	1180712 to 1182223	56%	6911	1182223
PL-2179.1			PL-2180.1	
6910	1182302 to 1183786	80%	6912	1183786
PL-2180.1			PL-2181.1	
6911	1184273 to 1188253	86%	6913	1188253
PL-2181.1			PL-2182.1	
6912	1188330 to 1188842	89%	6914	1188842
PL-2182.1			PL-2183.1	
6913	1188895 to 1189617	88%	6915	1189617
PL-2183.1			PL-2184.1	
6914	1189864 to 1190931	74%	6916	1190931
PL-2184.1			PL-2185.1	
6915	1191206 to 1192627	83%	6917	1192627
PL-2185.1			PL-2186.1	
6916	1192640 to 1193050	70%	6918	1193050
PL-2186.1			PL-2187.1	

gb|AAK03455.1| (AE006175) unknown [Pasteurella multocida]

SEQ ID n-1333

sp|P07117|PUTP_ECOLI_SODIUM/PROLINE SYMPORTER (PROLINE PERMEASE) pir||JGBCPP sodium/proline symporter - Escherichia coli emb|CAA29143.1| (X05653) putp proline carrier (AA 1-502)

[Escherichia coli] dbj|BAA35793.1| (D90738)

Proline carrier protein [Escherichia coli]

gb|AAC74100.1| (AE000203) major sodium/proline

symporter [Escherichia coli K12] yff||1404369A

Pro carrier protein [Escherichia coli]

gb|AAG55630.1|AE005301_2 (AE005301) proline

dehydrogenase, P5C dehydrogenase [Escherichia

coli O157:H7]

emb|CAF46361.1| (AJ131736) Fliz protein

[Xenorhabdus nematophilus]

emb|CAB46360.1| (AJ131736) Flia, sigma 28

[Xenorhabdus nematophilus]

sp|P13713|PLIC_SERMA_FLAGELLIN pir||JU0056

flagellin - Serratia marcescens gb|AAA26556.1|

(M27219) flagellin [Serratia marcescens]

pir||JCS755 hook-associated protein 2 -

Xenorhabdus nematophilus emb|CAA62510.1|

(X91047) hook-associated protein 2 [Xenorhabdus

nematophilus]

sp|P26609|FLIS_SALTY_FLAGELLAR PROTEIN FLIS

gb|AAA27077.1| (M85241) flagellar protein

[Salmonella typhimurium]

SEQ ID n-1339

#N/A

TABLEAU II

SEQ ID n° 6917	PL-3973.1	Contig9 from 1193050 to 1193427	p	50%	sp P26610 FLIT_ECOLI FLAGELLAR PROTEIN FLIT pir C64956 flagellar protein flit - Escherichia coli gb AA23792.1 (M85240) flagellar protein [Escherichia coli] dbj BAAL5754.1 (D90833) Flagellar protein FLIT. [Escherichia coli] gb AAC74993.1 (AE000285) flagellar biosynthesis; repressor of class 3a and 3b operons (RFLA activity) [Escherichia coli K12] gb AAG56941.1 AE005415_6 (AE005415) flagellar biosynthesis; repressor of class 3a and 3b Operons (RFLA activity) [Escherichia coli O157:H7]	SEQ ID n-3132
SEQ ID n° 6918	PL-2185.1	Contig9 from 1193829 to 1194641	m	No Hits found	sp P25797 FLIE_ECOLI FLAGELLAR HOOK-BASAL BODY COMPLEX PROTEIN FLIE pir A42376 flagellar hook- basal body complex protein flie - Escherichia coli gb AA23800.1 (M84992) flagellar protein [Escherichia coli] dbj BAAL5760.1 (D90833) Flagellar hook-basal body 11K protein Flie [Escherichia coli] dbj BAAL5762.1 (D90834) Flagellar hook-basal body 11K protein Flie [Escherichia coli] gb AAC75004.1 (AE000286) flagellar biosynthesis; basal-body component, possibly at (MS-ring)-rod junction [Escherichia coli K12] gb AAG56952.1 AE005416_6 (AE005416) flagellar biosynthesis; basal-body component, possibly at (MS-ring)-rod junction [Escherichia coli O157:H7]	SEQ ID n-3340
SEQ ID n° 6919	PL-4174.1	Contig9 from 1195239 to 1195550	m	69%		#N/A

TABLEAU II

SEQ ID n° 6927 PL-2191.1	Contig9 from 1203059 to 1204063	p 85%	sp P06974 FLIM_ECOLI FLAGELLAR MOTOR SWITCH	SEQ ID n° 1347
			PROTEIN FLIM pir XMECF2 flagellar motor switch	
SEQ ID n° 6928 PL-4171.1	Contig9 from 1204056 to 1204475	p 77%	protein flim - Escherichia coli gb AA23786.1 (M12784) FlaAII protein [Escherichia coli]	#N/A
			dbj BAAL5770.1 (D90834) Flagellar motor switch	
SEQ ID n° 6929 PL-3970.1	Contig9 from 1204582 to 1204929	p 53%	protein flim. [Escherichia coli] gb AAC75012.1 --(AE000286) flagellar biosynthesis, component of motor switch and energizing, enabling rotation and determining its direction [Escherichia coli K12]	
			sp P26419 FLIN_SALTY FLAGELLAR MOTOR SWITCH	
SEQ ID n° 6930 PL-2192.1	Contig9 from 1204961 to 1205695	p 80%	PROTEIN FLIN pir D30929 flagellar motor switch	
			protein flin - Salmonella typhimurium	
SEQ ID n° 6931 PL-2193.1	Contig9 from 1205700 to 1206400	p 77%	gb AA27105.1 (M24463) flin flagellar switch	#N/A
			protein [Salmonella typhimurium]	
SEQ ID n° 6932 PL-2194.1	Contig9 from 1206401 to 1207100	p 53%	sp P34199 MOPB_ERWCA MOPB PROTEIN pir S35275	
			probable flagellar biosynthesis protein mopB - Erwinia carotovora subsp. atroseptica	
SEQ ID n° 6933 PL-2195.1	Contig9 from 1207101 to 1207800	p 53%	emb CAA51475.1 (X72969) mopB [Erwinia carotovora]	SEQ ID n° 9129
			sp P33133 FLIP_ECOLI FLAGELLAR BIOSYNTHETIC	
SEQ ID n° 6934 PL-2196.1	Contig9 from 1207801 to 1208500	p 80%	PROTEIN FLIP pir B36869 probable export	
			protein flip precursor - Escherichia coli	
SEQ ID n° 6935 PL-2197.1	Contig9 from 1208501 to 1209200	p 80%	gb AAC36859.1 (L22182) flagellar protein	
			[Escherichia coli] dbj BAAL5773.1 (D90834)	
SEQ ID n° 6936 PL-2198.1	Contig9 from 1209201 to 1209900	p 80%	Flagellar biosynthetic protein FlpP.	
			[Escherichia coli] dbj BAAL5779.1 (D90835)	
SEQ ID n° 6937 PL-2199.1	Contig9 from 1209901 to 1210600	p 80%	Flagellar biosynthetic protein FlpP.	
			[Escherichia coli] gb AAC75015.1 (AE000287)	
SEQ ID n° 6938 PL-2200.1	Contig9 from 1210601 to 1211300	p 80%	flagellar biosynthesis [Escherichia coli K12]	
			gb AAG56963.1 AE005417_5 (AE005417) flagellar biosynthesis [Escherichia coli O157:H7]	

TABLEAU II

SEQ ID n° 6931	PL-4170.1	Contig9 from 1205716 to 1205985	p	85%	sp P54701 FLIQ_SALTY FLAGELLAR BIOSYNTHETIC PROTEIN FLIQ pir S78699 probable export protein fliQ - Salmonella typhimurium gb AAB81320.1 (L49021) fliQ [Salmonella typhimurium]	#N/A
SEQ ID n° 6932	PL-2193.1	Contig9 from 1205988 to 1206770	p	76%	sp P34202 FLIR_ERWCA FLAGELLAR BIOSYNTHETIC PROTEIN FLIR (FLAGELLAR BIOSYNTHETIC PROTEIN MOPE) pir S42698 probable export protein mope Erwinia carotovora subsp. atroseptica emb CAA51478.1 (X72969) mope [Erwinia carotovora]	SEQ ID n° 1349
SEQ ID n° 6933	PL-2194.1	Contig9 from 1207194 to 1209281	m	40%	ref NP_071283.1 Predicted DNA methylase containing a Zn-ribbon module [Archaeoglobus fulgidus]	SEQ ID n° 1350
SEQ ID n° 6934	PL-2195.1	Contig9 from 1209382 to 1210125	m	No Hits found		SEQ ID n° 1351
SEQ ID n° 6935	PL-4168.1	Contig9 from 1210587 to 1210871	p	53%	ref NP_052450.1 yaca [Plasmid Colib-P9] dbj BAA75089.1 (AB021078) yaca [Plasmid Colib- P9]	#N/A
SEQ ID n° 6936	PL-4167.1	Contig9 from 1211353 to 1211613	p	38%	sp Q58503 YB03_METJA HYPOTHETICAL PROTEIN MJ1103 pir P64437 hypothetical protein MJ1103 - Methanococcus jannaschii gb AAB99106.1 (U67553) conserved hypothetical protein [Methanococcus jannaschii] pir G82793 hypothetical protein XF0534 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF83344.1 AE003901.7 (AE003901) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 6937	PL-4166.1	Contig9 from 1211690 to 1212054	p	44%	pir D82498 conserved hypothetical protein VCA0105 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96019.1 (AE004353) conserved hypothetical protein [Vibrio cholerae]	#N/A
SEQ ID n° 6938	PL-4165.1	Contig9 from 1212311 to 1212580	m	48%		#N/A

TABLEAU II

SEQ ID n° 6939	PL-2196.1	Contig9 from 1212707 to 1213726	m	No Hits found	SEQ ID n-3352
SEQ ID n° 6940	PL-2197.1	Contig9 from 1213734 to 1215335	m	No Hits found	SEQ ID n-3353
SEQ ID n° 6941	PL-2198.1	Contig9 from 1215356 to 1216285	m	No Hits found	SEQ ID n-3354
SEQ ID n° 6942	PL-2199.1	Contig9 from 1216282 to 1218249	m	50%	SEQ ID n-3355
SEQ ID n° 6943	PL-2200.1	Contig9 from 1218862 to 1219827	m	72%	SEQ ID n-3358
SEQ ID n° 6944	PL-2201.1	Contig9 from 1219902 to 1221551	m	63%	
SEQ ID n° 6945	PL-2202.1	Contig9 from 1221678 to 1222622	m	69%	SEQ ID n-3359

gb|AAC62387.1| (AF044506) VgrG protein
[Escherichia coli]

sp|P16326|FLGL_SALTY_FLAGELLAR_HOOK-ASSOCIATED
PROTEIN 3 (HAP3) (HOOK-FILAMENT JUNCTION
PROTEIN) pir||S10362 hook-associated protein 3
Salmonella typhimurium emb|CAA36028.1| (X51739)
HAP3 [Salmonella typhimurium]

sp|P33235|FLGK_ECOLI_FLAGELLAR_HOOK-ASSOCIATED
PROTEIN 1 (HAP1) pir||G64851 flagellar hook-
associated protein 1 - Escherichia coli
dbj|BAA35891.1| (D90744) Flagellar hook-
associated protein 1 (hap1) . [Escherichia
coli] gb|AAC74166.1| (AE000209) flagellar
biosynthesis, hook-filament junction protein 1
[Escherichia coli K12]

sp|P15931|FLGJ_SALTY_FLAGELLAR_PROTEIN_FLGJ
pir||C30930 flagellar protein flgJ - Salmonella
typhimurium gb|AA27070.1| (M24466) flgJ
flagellar protein [Salmonella typhimurium]

TABLEAU II

SEQ ID n° 6946	PL-2203.1	Contig9 from 1222619 to 1223728	m	83%	sp P75941 FLGI_ECOLI_FLAGELLAR_P-RING_PROTEIN PRECURSOR...pir E64851 flagellar basal body P- ring protein precursor - Escherichia coli gb AAC7A164.1 (AE000208) homolog of Salmonella P-ring of flagella basal body [Escherichia coli K12] dbj BAA35889.1 (D90744) ---Flagellar basal body P-ring protein precursor--- [Escherichia coli] SEQ ID n-2361
SEQ ID n° 6947	PL-2204.1	Contig9 from 1223741 to 1224493	m	70%	dbj BAA35888.1 (D90744) Flagellar basal body L- ring protein precursor [Escherichia coli] SEQ ID n-2362
SEQ ID n° 6948	PL-2205.1	Contig9 from 1224568 to 1225350	m	86%	sp P16439 FLGG_SALTY_FLAGELLAR_BASAL-BODY_ROD PROTEIN FLGG (DISTAL ROD PROTEIN) pir XMEBFG flagellar basal body rod protein flgg - Salmonella typhimurium emb CAA36314.1 (X52094) flgg protein product (AA 1-260) [Salmonella typhimurium] SEQ ID n-2363
SEQ ID n° 6949	PL-2206.1	Contig9 from 1225374 to 1226129	m	76%	sp P16323 FLGG_SALTY_FLAGELLAR_BASAL-BODY_ROD PROTEIN FLGF (PUTATIVE PROXIMAL ROD PROTEIN) pir XMEBFF flagellar basal body rod protein flgf - Salmonella typhimurium emb CAA36313.1 (X52094) flgf protein product (AA 1-251) [Salmonella typhimurium] SEQ ID n-2364
SEQ ID n° 6950	PL-2208.1	Contig9 from 1226148 to 1227362	m	72%	sp P16322 FLGG_SALTY_FLAGELLAR_HOOK_PROTEIN_FLGE pir S10365 flagellar hook protein flge - Salmonella typhimurium emb CAA36022.1 (X51737) flge protein (AA 1-403) [Salmonella typhimurium] SEQ ID n-2365
SEQ ID n° 6951	PL-2209.2	Contig9 from 1227390 to 1228085	m	74%	sp P16321 FLGD_SALTY_BASAL-BODY_ROD_MODIFICATION PROTEIN FLGD pir S47641 flagellar hook formation protein flgd - Salmonella typhimurium dbj BAA04982.1 (D25293) flagella [Salmonella typhimurium] #N/A

TABLEAU II

SEQ ID n° 6952	PL-4162.2	Contig9 from 1228098 to 1228502	m	85%	sp Q56894 FLGC_YEREN FLAGELLAR BASAL-BODY ROD PROTEIN FLGC pir S54220 flagellar basal body rod protein flgc - Yersinia enterocolitica emb CAA88193.1 (Z48169) flgc (Yersinia enterocolitica)	#N/A
SEQ ID n° 6953	PL-3969.2	Contig9 from 1228508 to 1228921	m	62%	gb AAC45657.1 (U82214) FlgB [Proteus mirabilis]	#N/A
SEQ ID n° 6954	PL-2210.1	Contig9 from 1229170 to 1229829	p	62%	gb AAC45658.1 (U82214) FlgA [Proteus mirabilis]	SEQ ID n-2368
SEQ ID n° 6955	PL-4161.1	Contig9 from 1229954 to 1230256	p	67%	sp P96974 FLGM_PROMI NEGATIVE REGULATOR OF FLAGELLIN SYNTHESIS (ANTI-SIGMA-28 FACTOR)	#N/A
SEQ ID n° 6956	PL-3968.1	Contig9 from 1230268 to 1230708	p	66%	gb AAC45659.1 (U82214) FlgM [Proteus mirabilis] sp P96975 FLGM_PROMI FLAGELLA SYNTHESIS PROTEIN FLGN gb AAC45660.1 (U82214) FlgN [Proteus mirabilis]	SEQ ID n-3126
SEQ ID n° 6957	PL-2211.1	Contig9 from 1231156 to 1232184	p	28%	pir A45592 liver stage antigen LSA-1 - malaria parasite (Plasmodium falciparum) emb CAA39663.1 (X56203) liver stage antigen [Plasmodium falciparum]	SEQ ID n-2369
SEQ ID n° 6958	PL-2212.1	Contig9 from 1232321 to 1233796	m	No Hits found		SEQ ID n-2370
SEQ ID n° 6959	PL-4159.1	Contig9 from 1233842 to 1234006	m	No Hits found		#N/A
SEQ ID n° 6960	PL-2213.1	Contig9 from 1234876 to 1236348	m	No Hits found		SEQ ID n-2371
SEQ ID n° 6961	PL-2214.1	Contig9 from 1236407 to 1237870	m	No Hits found		SEQ ID n-2372
SEQ ID n° 6962	PL-3941.2	Contig9 from 1237919 to 1239421	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 6963	PL-2216.2	Contig9 from 1239484 to 1240947	m	No Hits found	SEQ ID n~2374
SEQ ID n° 6964	PL-2215.2	Contig9 from 1240996 to 1242498	m	No Hits found	SEQ ID n~2373
SEQ ID n° 6965	PL-3150.1	Contig9 from 1242561 to 1244075	m	14%	sp P26007 ITA6_CHICK INTEGRIN ALPHA-6-PRECURSOR (VLA-6) pir A38457 integrin alpha-6 chain precursor - chicken emb CAA39909.1 (X56559) integrin alpha 6 subunit [Gallus gallus]
SEQ ID n° 6966	PL-3151.1	Contig9 from 1244134 to 1245627	m	No Hits found	SEQ ID n~2396
SEQ ID n° 6967	PL-4155.1	Contig9 from 1245677 to 1246078	m	No Hits found	SEQ ID n~2397
SEQ ID n° 6968	PL-3152.1	Contig9 from 1246097 to 1247668	m	No Hits found	#N/A
SEQ ID n° 6969	PL-4154.1	Contig9 from 1247850 to 1248293	m	No Hits found	SEQ ID n~2398
SEQ ID n° 6970	PL-3153.1	Contig9 from 1249069 to 1250082	m	72%	ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]
SEQ ID n° 6971	PL-4152.1	Contig9 from 1250314 to 1250733	m	No Hits found	SEQ ID n~2399
SEQ ID n° 6972	PL-3154.1	Contig9 from 1251255 to 1253336	m	88%	#N/A sp Q56887 FLHA_YEREN FLAGELLAR BIOSYNTHESIS PROTEIN FLHA pir S54214 flagellar biosynthesis protein flha - Yersinia enterocolitica emb CAA88186.1 (Z48169) flha [Yersinia enterocolitica]
					SEQ ID n~2400

TABLEAU II

SEQ ID n° 6973	PL-3156.1	Contig9 from 1253329 to 1254480	m	81%	sp Q56886 FLHB_YEREN_FLAGELLAR_BIOSYNTHETIC PROTEIN FLHB pir S54213 flagellar biosynthetic protein flhb - Yersinia enterocolitica emb CAA88185.1 (Z48169) flhb [Yersinia enterocolitica]	SEQ ID n-2402
SEQ ID n° 6974	PL-3157.2	Contig9 from 1254786 to 1256474	p	31%	sp Q06584 PYS2_PSEAE_PYOCIN_S2 (KILLER PROTEIN) pir D83501 pyocin S2 PA1150 [imported] - Pseudomonas aeruginosa (strain PA01) gb AA04539.1 AE004545_2 (AE004545) pyocin S2 [Pseudomonas aeruginosa]	SEQ ID n-2403
SEQ ID n° 6975	PL-4149.1	Contig9 from 1256471 to 1256728	p	65%	sp P04482 IMM2_ECOLI_COLICIN_E2_IMMUNITY_PROTEIN (IMME2) (MICROCIN E2 IMMUNITY PROTEIN) pir IMECE2 colicin E2 immunity protein - Escherichia coli plasmids emb CAA26146.1 (X02227) immE2 polypeptide [Escherichia coli] gb AAA23069.1 (M29885) colicin immunity protein (ceiB) [Plasmid ColE2] emb CAA25610.1 (X01163) E2 immunity protein (aa 1-86) [Escherichia coli]	#N/A
SEQ ID n° 6976	PL-3943.1	Contig9 from 1256825 to 1257313	p	54%	pir A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa]	SEQ ID n-3102
SEQ ID n° 6977	PL-3944.1	Contig9 from 1257310 to 1257780	p	37%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa]	SEQ ID n-3103
SEQ ID n° 6978	PL-3945.1	Contig9 from 1257884 to 1258351	p	35%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa]	SEQ ID n-3104
SEQ ID n° 6979	PL-4147.1	Contig9 from 1258449 to 1258634	p	44%	pir D82027 hypothetical protein NMA0318 [imported] - Neisseria meningitidis (group A strain Z2491) emb CA883623.1 (AL162752) hypothetical protein NMA0318 [Neisseria meningitidis Z2491]	#N/A

TABLEAU II

SEQ ID n° 6980	PL-4145.1	Contig9 from 1259259 to 1259510	m	51%	pir T44274 hypothetical protein [imported] - Synecococcus sp. (strain PCC7942) dbj BAA37108.1 (AB010691) putative ORF-3 [Synecococcus sp.]	#N/A
SEQ ID n° 6981	PL-4143.1	Contig9 from 1260345 to 1260767	m	NO Hits found		#N/A
SEQ ID n° 6982	PL-2029.1	Contig9 from 1261416 to 1263266	m	54%	sp P40803 PKSK_BACSU PUTATIVE POLYKETIDE SYNTHASE PKSK (PKS) pir A69679 polyketide synthase pksK - Bacillus subtilis gb AAA85144.1 (U11039) polyketide synthase [Bacillus subtilis] emb CAB13590.1 (Z99112) polyketide synthase of type I [Bacillus subtilis] emb CAB13601.1 (Z99113) polyketide synthase of type I [Bacillus subtilis] dbj BAB06372.1 (AP001516) pyruvate dehydrogenase E2 (dihydrolipoamide acetyltransferase) [Bacillus halodurans] pir H72128 3-methyl-2-oxobutanate dehydrogenase (lipoamide) (EC 1.2.4.4) alpha/beta E1 chain CP0743 [similarity] - Chlamydomophila pneumoniae (strains CWL029 and AR39) gb AAD18186.1 (AE001583) (pyruvate) Oxoisovalerate Dehydrogenase Alpha & Beta Fusion [Chlamydomophila pneumoniae CWL029] gb AAF38548.1 (AE002233) 2- oxoisovalerate dehydrogenase, E1 component, alpha and beta subunit [Chlamydomophila pneumoniae AR39] dbj BAA98245.1 (AP002545) (pyruvate) oxoisovalerate dehydrogenase alpha and beta fusion [Chlamydomophila pneumoniae J138]	SEQ ID n-1168
SEQ ID n° 6983	PL-2030.2	Contig9 from 1263259 to 1264824	m	32%		#N/A
SEQ ID n° 6984	PL-2031.2	Contig9 from 1264834 to 1266831	m	53%		#N/A
SEQ ID n° 6985	PL-2032.1	Contig9 from 1268501 to 1269907	p	68%	gb AAC59094.1 AE005621_6 (AE005621) putative glycoporin [Escherichia coli O157:H7]	SEQ ID n-1172

TABLEAU II

SEQ ID n° 6986	PL-2033.1	Contig9 from 1270940 to 1271758	p	No Hits found			SEQ ID n-1173
SEQ ID n° 6987	PL-2034.1	Contig9 from 1271894 to 1284376	p	26%	gb AAF17281.1 (AF204805) NosD [Nostoc sp. GSV224]		
SEQ ID n° 6988	PL-2035.1	Contig9 from 1284373 to 1285638	p	45%	pir H75515 tetracycline-efflux transporter - Deinococcus radiodurans (strain R1) gb AAF10051.1 AE001906_7 (AE001906) tetracycline efflux transporter [Deinococcus radiodurans]	SEQ ID n-1174	
SEQ ID n° 6989	PL-2036.1	Contig9 from 1285667 to 1288864	p	60%	pir T14591 actinomycin synthetase II acmB [imported] - Streptomyces chrysomallus gb AAC38442.1 (AF047717) actinomycin synthetase II [Streptomyces chrysomallus]	SEQ ID n-1175	
SEQ ID n° 6990	PL-4135.1	Contig9 from 1288916 to 1289275	p	No Hits found		#N/A	
SEQ ID n° 6991	PL-2037.1	Contig9 from 1289663 to 1290526	m	No Hits found			SEQ ID n-1176
SEQ ID n° 6992	PL-2038.1	Contig9 from 1290648 to 1291886	m	29%	pir D82481 multidrug resistance protein D VCA0267 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96178.1 (AE004366) multidrug resistance protein D [Vibrio cholerae]	SEQ ID n-1177	
SEQ ID n° 6993	PL-2039.1	Contig9 from 1291883 to 1293022	m	No Hits found			SEQ ID n-1178
SEQ ID n° 6994	PL-2040.1	Contig9 from 1293019 to 1294182	m	28%	emb CAC11114.1 (AJ250581) Niks protein [Streptomyces tendae]	SEQ ID n-1179	
SEQ ID n° 6995	PL-3947.1	Contig9 from 1294179 to 1294583	m	31%	dbj BAB05302.1 (AF001512) BH1583-unknown conserved protein in others [Bacillus halodurans]	SEQ ID n-1181	SEQ ID n-3105

TABLEAU II

SEQ ID n° 6996	PL-2041.2	Contig9 from 1294640 to 1295425	m	29%	emb CAC12469.1 (AL445067) conserved hypothetical protein [Thermoplasma acidophilum]	#N/A
SEQ ID n° 6997	PL-3948.2	Contig9 from 1295422 to 1295979	m	42%	ref NP_070589.1 3-isopropylmalate dehydratase, small subunit (leuD-2) [Archaeoglobus fulgidus] sp O28513 LE24_ARCFU PUTATIVE 3- ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI) pir H69469 3-isopropylmalate dehydratase, small subunit (leuD-2) homolog - Archaeoglobus fulgidus gb AAB89489.1 (AE000981) 3-isopropylmalate dehydratase, small subunit (leuD-2) [Archaeoglobus fulgidus]	#N/A
SEQ ID n° 6998	PL-2042.2	Contig9 from 1295972 to 1297213	m	53%	pir C72394 hypothetical protein TM0291 - Thermotoga maritima (strain MSB8) gb AAD35379.1 AE001711_2 (AB001711) 3- isopropylmalate dehydratase, large subunit, putative [Thermotoga maritima]	#N/A
SEQ ID n° 6999	PL-4132.1	Contig9 from 1297210 to 1297653	m	63%	emb CAB91069.1 (AJ239033) homocitrate synthase 1 [Anabaena variabilis]	#N/A
SEQ ID n° 7000	PL-2043.1	Contig9 from 1297660 to 1298346	m	54%	emb CAB91068.1 (AJ239032) homocitrate synthase 2 [Anabaena variabilis]	SEQ ID n° 1184
SEQ ID n° 7001	PL-2044.1	Contig9 from 1298383 to 1299714	m	66%	sp P54950 YXK_BACSU HYPOTHETICAL 49.3 XD PROTEIN IN IDH-DEOR INTERGENIC REGION pir E70075 nitrilotriacetate monooxygenase (EC 1.14.13.-) component A homolog yxk - Bacillus subtilis dbj BAA08327.1 (D45912) homologous to dazA gene product of Rhodococcus sp. [Bacillus subtilis] emb CAB15988.1 (Z99124) similar to monooxygenase [Bacillus subtilis]	SEQ ID n° 1185

TABLEAU II

SEQ ID n° 7002 PL-2045.1	Contig9 from 1299896 to 1300636	m	65%	gb AAG26465.1 AF285774.5 (AF285774) putative phosphoenolpyruvate phosphomutase [Bacteroides fragilis]	SEQ ID n-2185
SEQ ID n° 7003 PL-4130.1	Contig9 from 1301662 to 1301877	p	No Hits found		#N/A
SEQ ID n° 7004 PL-2046.1	Contig9 from 1301867 to 1302406	p	50%	prf 1919464A rmpB gene [Klebsiella pneumoniae] pir B83589 probable transposase PA0445 [imported] - Pseudomonas aeruginosa (strain PA01) pir B83355 probable transposase PA2319 [imported] - Pseudomonas aeruginosa (strain PA01) pir B83309 probable transposase PA2690 [imported] - Pseudomonas aeruginosa (strain PA01) pir H83216 probable transposase PA3434 [imported] - Pseudomonas aeruginosa (strain PA01) pir B83145 probable transposase PA3993 [imported] - Pseudomonas aeruginosa (strain PA01) pir B83045 probable transposase PA4797 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03834.1 AE004482_1 (AE004482) probable transposase [Pseudomonas aeruginosa] gb AAG05707.1 AE004658_1 (AE004658) probable transposase [Pseudomonas aeruginosa] gb AAG06078.1 AE004697_3 (AE004697) probable transposase [Pseudomonas aeruginosa] gb AAG06822.1 AE004764_8 (AE004764) probable transposase [Pseudomonas aeruginosa] gb AAG07380.1 AE004817_4 (AE004817) probable transposase [Pseudomonas aeruginosa] pir F75337 transposase - Deinococcus radiodurans (strain R1) gb AAF11477.1 AE002031_6 (AE002031) transposase [Deinococcus radiodurans]	SEQ ID n-2187
SEQ ID n° 7005 PL-4129.1	Contig9 from 1302461 to 1302589	p	63%		#N/A
SEQ ID n° 7006 PL-3950.1	Contig9 from 1302635 to 1303063	p	62%		SEQ ID n-3108

TABLEAU II

SEQ ID n° 7007	PL-2047.1	Contig9 from 1303143 to 1303793	m	81%	sp P07800 CHEZ_SALTY CHEMOTAXIS PROTEIN CHEZ pir A27088_chemotaxis protein chez - Salmonella typhimurium gb AAD15120.1 (M16691) chez gene product [Salmonella typhimurium] SEQ ID n°1188
SEQ ID n° 7008	PL-4127.1	Contig9 from 1303803 to 1304192	m	88%	sp P06657 CHEY_SALTY CHEMOTAXIS PROTEIN CHEY pir QREBCY chemotaxis protein chey [validated] salmonella typhimurium gb AA27037.1 (M12131) #N/A Chey protein [Salmonella typhimurium] sp P07330 CHEB_ECOLI PROTEIN-GLUTAMATE METHYLESTERASE pir XYECEB protein-glutamate methylesterase (EC 3.1.1.61) - Escherichia coli dbj BAA15699.1 (D90830) Protein-glutamate methylesterase (EC 3.1.1.61).
SEQ ID n° 7009	PL-2048.1	Contig9 from 1304512 to 1305564	m	89%	[Escherichia coli] gb AAC74953.1 (AE000282) response regulator for chemotaxis (cheA sensor); protein methylesterase [Escherichia coli K12] SEQ ID n°1189
SEQ ID n° 7010	PL-2049.1	Contig9 from 1305557 to 1306444	m	73%	sp P07801 CHER_SALTY CHEMOTAXIS PROTEIN METHYLTRANSFERASE pir XYEGBM protein-glutamate O-methyltransferase (EC 2.1.1.80) - Salmonella typhimurium gb AAA27035.1 (J02757) methyltransferase (cheR; EC 2.1.1.24) [Salmonella typhimurium] SEQ ID n°1190
SEQ ID n° 7011	PL-2050.2	Contig9 from 1306451 to 1308085	m	64%	dbj BAB38738.1 (AP002569) methyl-accepting chemotaxis protein I [Escherichia coli O157:H7] #N/A
SEQ ID n° 7012	PL-2051.2	Contig9 from 1308139 to 1309833	m	75%	sp P21822 MCPS_ENTAE METHYL-ACCEPTING CHEMOTAXIS SERINE TRANSDUCER pir C32302 serine transducer tse - Enterobacter aerogenes gb AAA24797.1 (M26411) tse [Enterobacter aerogenes] #N/A

TABLEAU II

SEQ ID n° 7013	PL-3951.2	Contig9 from 1310010 to 1310507	m 78%	sp P07365 CHEW_ECOLI CHEMOTAXIS PROTEIN CHEW pir QRECCW purine binding chemotaxis protein chew - Escherichia coli gb AA23565.1 (M13463) chew peptide [Escherichia coli] dbj BAA15703.1 (D90830) Chemotaxis protein CHEW [Escherichia coli] dbj BAA15708.1 (D90831) Chemotaxis protein CHEW [Escherichia coli] gb AAC74957.1 (AE000282) positive regulator of CheA protein activity [Escherichia coli K12] dbj BAB36020.1 (AF002559) positive regulator of CheA protein activity [Escherichia coli O157:H7] #N/A	SEQ ID n-1194
SEQ ID n° 7014	PL-2052.1	Contig9 from 1310561 to 1312612	m 77%	sp P09384 CHEA_SALTY CHEMOTAXIS PROTEIN CHEA pir A28959 chemotaxis protein cheA - Salmonella typhimurium gb AA27034.1 (J03611) sensory protein (cheA, gta start codon) [Salmonella typhimurium] sp P09349 MOTB_ECOLI CHEMOTAXIS MOTB PROTEIN (MOTILITY PROTEIN B) pir QRECCW chemotaxis protein motB - Escherichia coli gb AA24178.1 (J01652) motB protein for chemotaxis [Escherichia coli] dbj BAA15710.1 (D90831) Chemotaxis MotB protein (Motility protein B). [Escherichia coli] gb AAC74959.1 (AE000282) enables flagellar motor rotation, linking torque machinery to cell wall [Escherichia coli K12] gb AAG56879.1 AE005411_3 (AE005411) enables flagellar motor rotation, linking torque machinery to cell wall [Escherichia coli O157:H7] SEQ ID n-1195	
SEQ ID n° 7015	PL-2053.1	Contig9 from 1312615 to 1313616	m 69%	sp P55891 MOTA_SALTY CHEMOTAXIS MOTA PROTEIN (MOTILITY PROTEIN A) gb AAC45265.1 (U81861) Mota [Salmonella typhimurium] dbj BAA85316.1 (D43640) Mota protein [Salmonella typhimurium] SEQ ID n-1196	

TABLEAU II

SEQ ID n° 7017	PL-3952.1	Contig9 from 1314637 to 1315218	m	94%	sp Q9X9F3 FLHC_XENNE FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHC emb CAB41408.1 (AJ012828) FLHC protein [Xenorhabdus nematophilus]	SEQ ID n-9110
SEQ ID n° 7018	PL-4123.1	Contig9 from 1315222 to 1315575	m	89%	sp Q9X9F2 FLHD_XENNE FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHD emb CAB41407.1 (AJ012828) FLHD protein [Xenorhabdus nematophilus]	#N/A
SEQ ID n° 7019	PL-4121.1	Contig9 from 1317840 to 1317998	m	41%	pir C83044 Mg(2+) transport ATPase, P-type 2 PA4825 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08210.1 AE004895_10 (AE004895) Mg(2+) transport ATPase, P-type 2 [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 7020	PL-4120.1	Contig9 from 1318135 to 1318317	m	50%	pir C83044 Mg(2+) transport ATPase, P-type 2 PA4825 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08210.1 AE004895_10 (AE004895) Mg(2+) transport ATPase, P-type 2 [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 7021	PL-4119.1	Contig9 from 1318611 to 1318781	p	No Hits found	sp P22037 ATMC_SALTY MG(2+) TRANSPORT ATPASE PROTEIN C pir A39083 Mg2+-transporting ATPase (EC 3.6.1.-) mgTC - Salmonella typhimurium gb AAA72083.1 (M57715) Mg2+ transport ATPase [Salmonella typhimurium] gb AAD16960.1 (AF106566) MgTC [Salmonella typhimurium]	#N/A
SEQ ID n° 7022	PL-2055.3	Contig9 from 1319372 to 1320082	m	69%		
SEQ ID n° 7023	PL-7224.1	Contig9 from 1320612 to 1320845	p	No Hits found		

TABLEAU II

sp P77523 YLAC_ECOLI HYPOTHETICAL 19.8 KDA PROTEIN IN TFSB_HHA INTERGENIC REGION pir A64776 probable membrane protein ylaC - Escherichia coli gb AAB40213.1 (U82664) hypothetical [Escherichia coli] gb AAC73560.1 (AE000152) orf, hypothetical protein [Escherichia coli K12] gb AAG54807.1 AE005225_1 (AE005225) orf, hypothetical protein [Escherichia coli O157:H7 BDL933] dbj BAB33934.1 (AP002551) hypothetical protein [Escherichia coli O157:H7]	Contig9 from 1321242 to 1321748	p	54%	SEQ ID n° 7024 PL-3953.3	1321242 to 1321748	m	No Hits found	SEQ ID n-2198 #N/A
	Contig9 from 1322114 to 1323190	m	No Hits found	SEQ ID n° 7025 PL-2056.1	1322114 to 1323190	m	No Hits found	SEQ ID n-2199 #N/A
	Contig9 from 1324941 to 1325198	p	47%	SEQ ID n° 7026 PL-4115.1	1324941 to 1325198	p	47%	SEQ ID n-2200 #N/A
	Contig9 from 1325101 to 1326204	p	66%	SEQ ID n° 7027 PL-2057.1	1325101 to 1326204	p	66%	SEQ ID n-2201 #N/A
	Contig9 from 1326288 to 1328021	m	20%	SEQ ID n° 7028 PL-2058.1	1326288 to 1328021	m	20%	SEQ ID n-2202 #N/A
	Contig9 from 1328081 to 1329166	m	No Hits found	SEQ ID n° 7029 PL-2059.1	1328081 to 1329166	m	No Hits found	SEQ ID n-2203 #N/A
	Contig9 from 1329583 to 1329696	m	No Hits found	SEQ ID n° 7030 PL-4114.1	1329583 to 1329696	m	No Hits found	SEQ ID n-2204 #N/A
	Contig9 from 1329883 to 1331478	p	5%	SEQ ID n° 7031 PL-2060.2	1329883 to 1331478	p	5%	SEQ ID n-2205 #N/A

TABLEAU II

SEQ ID n° 7032	PL-2061.1	Contig9 from 1331534 to 1332514	p	No Hits found	SEQ ID n-1204
SEQ ID n° 7033	PL-4113.1	Contig9 from 1332511 to 1332648	m	No Hits found	#N/A
SEQ ID n° 7034	PL-4112.1	Contig9 from 1332849 to 1333169	m	No Hits found	#N/A
SEQ ID n° 7035	PL-4111.1	Contig9 from 1333159 to 1333548	m	No Hits found	#N/A
SEQ ID n° 7036	PL-4110.1	Contig9 from 1333991 to 1334191	p	No Hits found	#N/A
SEQ ID n° 7037	PL-2062.1	Contig9 from 1334349 to 1335863	p	25%	ref NP_047290.1 nicking enzyme (traA) [Lactococcus lactis] pir [T43077 probable relaxase - Lactococcus lactis plasmid pMRC01 gb AAC55993.1 (AE001272) nicking enzyme (traA) [Lactococcus lactis] SEQ ID n-1205
SEQ ID n° 7038	PL-2063.1	Contig9 from 1335924 to 1337798	p	47%	pir [S77439 hypothetical protein slr1135 - Synechocystis sp. (strain PCC 6803) dbj BAA17286.1 (D90905) hypothetical protein [Synechocystis sp.] SEQ ID n-1206
SEQ ID n° 7039	PL-4108.1	Contig9 from 1338055 to 1338228	p	No Hits found	#N/A
SEQ ID n° 7040	PL-4106.1	Contig9 from 1338456 to 1338803	m	62%	gb AAC58108.1 AE005527_11 (AE005527) putative transposase [Escherichia coli O157:H7] #N/A

TABLEAU II

SEQ ID n° 7041	PL-2064.1	Contig9 from 1339178 to 1340146	p	60%	pir C81839 probable transposase for IS1655 NMA1481 [imported] - Neisseria meningitidis (group B strain MD58, group A strain Z2491) emb CAB84714.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] emb CAB84719.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] SEQ ID n-2207	#N/A
SEQ ID n° 7042	PL-4104.1	Contig9 from 1340221 to 1340532	m	No Hits found		#N/A
SEQ ID n° 7043	PL-4103.1	Contig9 from 1340620 to 1340949	m	No Hits found		#N/A
SEQ ID n° 7044	PL-2065.1	Contig9 from 1341477 to 1342325	m	43%	gb AAG57759.1 AE005493_12 (AE005493) Z3947 gene product [Escherichia coli O157:H7]	SEQ ID n-2208
SEQ ID n° 7045	PL-2066.1	Contig9 from 1342672 to 1343556	p	59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]	SEQ ID n-2209
SEQ ID n° 7046	PL-2067.1	Contig9 from 1343947 to 1344999	p	78%	sp P05020 PYRC_ECOLI DIHYDROOROTASE (DHQASE) pir DEECOO dihydroorotase (EC 3.5.2.3) - Escherichia coli emb CAA28157.1 (X04469) dihydroorotase [Escherichia coli] gb AAA24482.1 (M16752) dihydroorotase (EC 3.5.2.3) [Escherichia coli] dbj EAA35870.1 (D90743) Dihydroorotase (EC 3.5.2.3). [Escherichia coli] gb AAC74146.1 (AE000207) dihydro-orotase [Escherichia coli K12] dbj BAA35857.1 (D90742) ORF_ID:o233#8 [Escherichia coli] dbj BAA35868.1 (D90743) ORF_ID:o233#8 [Escherichia coli] pir A45828 colanic acid capsular biosynthesis activation protein A - Erwinia amylovora	SEQ ID n-2210
SEQ ID n° 7047	PL-4101.1	Contig9 from 1345192 to 1345446	p	68%		#N/A
SEQ ID n° 7048	PL-2068.1	Contig9 from 1345650 to 1346252	p	40%		SEQ ID n-2211

TABLEAU II

SEQ ID n° 7049	PL-2069.1	Contig9 from 1346298 to 1347356	m 83%	pir S16889 hypothetical protein 39.9 - Escherichia coli emb CAA43318.1 (X61000) Orf39.9 [Escherichia coli] SEQ ID n-2212
SEQ ID n° 7050	PL-4100.1	Contig9 from 1347600 to 1347860	m 58%	sp Q9S3S0 DINI_SERMA DNA-DAMAGE-INDUCIBLE PROTEIN I gb AAD50308.1 AF175466.2 (AF175466) DNA damage-inducible protein Dini [Serratia marcescens] #N/A
SEQ ID n° 7051	PL-2070.1	Contig9 from 1348123 to 1349064	p 77%	sp P24187 HTRB_ECOLI LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (HEAT SHOCK PROTEIN B) pir S16888 lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-) - Escherichia coli emb CAA43317.1 (X61000) HtrB protein [Escherichia coli] dbj BAA35863.1 (D90743) HtrB protein. [Escherichia coli] gb AAC74138.1 (AE000206) heat shock protein [Escherichia coli KL2] dbj BAA35852.1 (D90742) HtrB protein. [Escherichia coli] gb AAG55800.1 AE005316_5 (AE005316) Z1690 gene product [Escherichia coli O157:H7] sp P94408 YCLF_BACSU HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION SEQ ID n-2214
SEQ ID n° 7052	PL-2071.1	Contig9 from 1349788 to 1351326	p 56%	pir C69762 di-tripeptide ABC transporter (membrane pr) homolog yclF - Bacillus subtilis dbj BAA09000.1 (D50453) homologue of Di-tripeptide transporter Dtp of L. lactis [Bacillus subtilis] emb CAB12175.1 (Z99106) similar to di-tripeptide ABC transporter (membrane protein) [Bacillus subtilis] SEQ ID n-2215
SEQ ID n° 7053	PL-4099.1	Contig9 from 1351534 to 1351860	m 67%	pir E82467 probable antidote protein VCA0392 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF6298.1 (AE004374) antidote protein, putative [Vibrio cholerae] #N/A

TABLEAU II

SEQ ID n° 7054-PL-2072.1	Contig9 from 1352230 to 1352937	m	47%	pir H83242 probable transcription regulator PA3220 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06608.1 AE004745_5 (AE004745) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-1216
SEQ ID n° 7055 PL-4097.2	Contig9 from 1352994 to 1353329	m	73%	pir A83243 CsaA protéin PA3221 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06609.1 AE004745_6 (AE004745) CsaA protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 7056 PL-4095.2	Contig9 from 1353599 to 1353958	m	No Hits found		#N/A
SEQ ID n° 7057 PL-2073.1	Contig9 from 1354167 to 1355000	m	38%	dbj BAB06659.1 (AP001517) BH2940-unknown conserved protein [Bacillus halodurans]	SEQ ID n-1217
SEQ ID n° 7058 PL-2074.1	Contig9 from 1355304 to 1356815	p	67%	pir D83628 probable aldehyde dehydrogenase PA0130 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG03520.1 AE004451_1 (AE004451) probable aldehyde dehydrogenase [Pseudomonas aeruginosa]	SEQ ID n-1218
SEQ ID n° 7059 PL-2075.1	Contig9 from 1356832 to 1358766	p	70%	dbj BAB06037.1 (AP001515) malonic semialdehyde oxidative decarboxylase [Bacillus halodurans]	SEQ ID n-1219
SEQ ID n° 7060 PL-2076.1	Contig9 from 1359132 to 1360118	p	57%	sp O68965 MI2D RHIME MYO-INOSITOL 2- DEHYDROGENASE gb AAC70005.1 (AF059313) myo- inositol dehydrogenase [Sinorhizobium meliloti]	SEQ ID n-1220
SEQ ID n° 7061 PL-2077.1	Contig9 from 1360222 to 1361937	p	60%	gb AAG58882.1 AE005599_14 (AE005599) putative cotransporter [Escherichia coli O157:H7]	SEQ ID n-1221
SEQ ID n° 7062 PL-2078.1	Contig9 from 1362472 to 1363605	p	56%	dbj BAB04429.1 (AP001509) BH0710-unknown conserved protein [Bacillus halodurans]	SEQ ID n-1222
SEQ ID n° 7063 PL-2079.1	Contig9 from 1363681 to 1365585	p	27%	dbj BAB06038.1 (AP001515) myo-inositol catabolism [Bacillus halodurans]	SEQ ID n-1223

TABLEAU II

SEQ ID n° 7064	PL-2080.1	Contig9 from 1365615 to 1366505	p	64%	gb AAC31180.1 (AF076240) Mocc [Rhizobium leguminosarum bv. viciae]	SEQ ID n° 1225
SEQ ID n° 7065	PL-2081.1	Contig9 from 1366553 to 1367380	p	57%	sp P42413 IOLB_EACSU IOLB PROTEIN pir B69645 myo-inositol catabolism iolB - Bacillus subtilis dbj BAA03291.1 (D14399) hypothetical protein [Bacillus subtilis] emb CAB16011.1 (Z99124) alternate gene name: yxdB-myo-inositol catabolism [Bacillus subtilis] pir T33922 hypothetical protein Y8A9A.2 - Caenorhabditis elegans gb AAD12852.1 (AF125461) contains similarity to thrombospondin type 1 domains (Pfam:PF00090, Score=1.1 E= 0.49, N=8) [Caenorhabditis elegans]	SEQ ID n° 1226
SEQ ID n° 7066	PL-3955.1	Contig9 from 1367343 to 1367786	m	35%	pir T33922 hypothetical protein Y8A9A.2 - Caenorhabditis elegans gb AAD12852.1 (AF125461) contains similarity to thrombospondin type 1 domains (Pfam:PF00090, Score=1.1 E= 0.49, N=8) [Caenorhabditis elegans]	SEQ ID n° 9113
SEQ ID n° 7067	PL-3956.1	Contig9 from 1367832 to 1368311	m	44%	pir T33922 hypothetical protein Y8A9A.2 - Caenorhabditis elegans gb AAD12852.1 (AF125461) contains similarity to thrombospondin type 1 domains (Pfam:PF00090, Score=1.1 E= 0.49, N=8) [Caenorhabditis elegans]	SEQ ID n° 9114
SEQ ID n° 7068	PL-3957.1	Contig9 from 1368965 to 1369519	m	50%	gb AAK02392.1 (AE006066) unknown [Pasteurella multocida]	SEQ ID n° 9115
SEQ ID n° 7069	PL-2082.1	Contig9 from 1369529 to 1370542	m	67%	gb AAK02391.1 (AE006066) unknown [Pasteurella multocida]	SEQ ID n° 1227
SEQ ID n° 7070	PL-2083.1	Contig9 from 1370566 to 1371534	m	50%	gb AAK02390.1 (AE006066) unknown [Pasteurella multocida]	SEQ ID n° 1228
SEQ ID n° 7071	PL-2084.1	Contig9 from 1371531 to 1372889	m	45%	gb AAK02389.1 (AE006066) unknown [Pasteurella multocida]	SEQ ID n° 1229

TABLEAU II

SEQ ID n° 7072	PL-4090.1	Contig9 from 1373569 to 1373829	m	50%	pir B82474 hypothetical protein VCA0312 VCA0386 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAC38426.1 (AF055586) unknown [Vibrio cholerae] gb AAF96220.1 (AE004370) hypothetical protein [Vibrio cholerae] gb AAF96292.1 (AE004374) hypothetical protein [Vibrio cholerae]	#N/A
SEQ ID n° 7073	PL-2085.1	Contig9 from 1373923 to 1377204	m	58%	gb AAK02396.1 (AE006067) unknown [Pasteurella multocida]	SEQ ID n° 2230
SEQ ID n° 7074	PL-4088.1	Contig9 from 1377201 to 1377329	m	No Hits found		#N/A
SEQ ID n° 7075	PL-4087.1	Contig9 from 1377380 to 1377520	p	No Hits found		#N/A
SEQ ID n° 7076	PL-3958.1	Contig9 from 1378106 to 1378645	m	No Hits found		SEQ ID n° 9116
SEQ ID n° 7077	PL-2086.1	Contig9 from 1378849 to 1379874	m	21%	dbj BAB06239.1 (AF001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n° 2231
SEQ ID n° 7078	PL-4085.1	Contig9 from 1380672 to 1380956	m	No Hits found		#N/A
SEQ ID n° 7079	PL-7014.1	Contig9 from 1380961 to 1381053	m	59%	dbj BAA35736.1 (D90734) ORF_ID:0224#4 [Escherichia coli]	#N/A
SEQ ID n° 7080	PL-4084.1	Contig9 from 1381238 to 1381573	p	88%	gb AA055455.1 AE005287_2 (AE005287) yccK gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7081	PL-4083.1	Contig9 from 1381587 to 1381865	m	58%	dbj BAA35733.1 (D90734) Acylphosphatase (EC 3.6.1.7) Ch2, skeletal muscle [Escherichia coli]	#N/A

TABLEAU II

SEQ ID n° 7082	PL-4082.1	Contig9 from 1382089 to 1382409	P	80%	sp P75875 YCCV_ECOLI_HYPOTHETICAL_13.8_KDA PROTEIN IN MGS-A-HYAA INTERGENIC REGION pir E64837 yccv protein - Escherichia coli gb AAC74052.1 (AE000198) orf, hypothetical protein [Escherichia coli K12] dbj BAA35731.1 (D90734) ORF_ID:0223#11 [Escherichia coli] ---gb AAG55452.1 AE005286_11 (AE005286) yccv gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7083	PL-4079.1	Contig9 from 1382882 to 1383109	P	No Hits found		#N/A
SEQ ID n° 7084	PL-3959.1	Contig9 from 1383163 to 1383528	M	27%	gb AAK03925.1 (AE006222) unknown [Pasteurella multocida]	SEQ ID n-9117
SEQ ID n° 7085	PL-3960.1	Contig9 from 1384340 to 1384753	M	70%	dbj BAA35730.1 (D90734) ORF_ID:0223#10 [Escherichia coli] pir B64837 methylglyoxal synthase (EC 4.2.99.11) - Escherichia coli gb AAC74049.1 (AE000198) methylglyoxal synthase [Escherichia coli K12] dbj BAA35728.1 (D90734) Hypothetical protein in held 3'region . [Escherichia coli] gb AAG55449.1 AE005286_8 (AE005286) methylglyoxal synthase [Escherichia coli O157:H7]	SEQ ID n-9119
SEQ ID n° 7086	PL-3961.1	Contig9 from 1384876 to 1385334	P	77%	sp P15038 HELD_ECOLI_HELICASE_IV (75 KD HELICASE) pir HJEC4 helicase (EC 3.6.1.-) IV Escherichia coli dbj BAA35727.1 (D90734) Helicase (EC 3.6.1.-) IV. [Escherichia coli] gb AAC74048.1 (AE000198) DNA helicase IV [Escherichia coli K12]	SEQ ID n-9120
SEQ ID n° 7087	PL-2087.1	Contig9 from 1385457 to 1387511	M	76%		SEQ ID n-9132

TABLEAU II

SEQ ID n° 7088	PL-2088.1	Contig9 from 1387722 to 1389863	p	76%	sp P75870 YCCS_ECOLI HYPOTHETICAL 82.0 KDA PROTEIN IN SULA-HELD INTERGENIC REGION pir G64836 probable membrane protein yccs - Escherichia coli gb AAC74046.1 (AE000198) orf, hypothetical protein [Escherichia coli K12] dbj BAA35718.1 (D90733) Hypothetical protein HI1680 [Escherichia coli] dbj BAA35725.1 (D90734) Hypothetical protein HI1680 [Escherichia coli] SEQ ID n-1233
SEQ ID n° 7089	PL-2089.2	Contig9 from 1389923 to 1390525	m	47%	sp P75869 YCCR_ECOLI HYPOTHETICAL 24.1 KDA PROTEIN IN SULA-HELD INTERGENIC REGION pir F64836 probable membrane protein b0959 - Escherichia coli gb AAC74045.1 (AE000198) orf, hypothetical protein [Escherichia coli K12] dbj BAA35717.1 (D90733) ORF ID:0223#4 [Escherichia coli] dbj BAA35724.1 (D90734) ORF ID:0223#4 [Escherichia coli] sp P08845 SULA_SERMA CELL DIVISION INHIBITOR pir D29016 cell division inhibitor sula - Serratia marcescens gb AAA26582.1 (M16468) sula protein [Serratia marcescens] SEQ ID n-1234
SEQ ID n° 7090	PL-3962.2	Contig9 from 1390774 to 1391307	p	60%	sp P04845 OMPA_SERMA OUTER MEMBRANE PROTEIN A PRECURSOR pir S07298 outer membrane protein ompA precursor - Serratia marcescens emb CAA25254.1 (X00618) ompA protein [Serratia marcescens] SEQ ID n-2375
SEQ ID n° 7091	PL-3131.2	Contig9 from 1391992 to 1393098	p	81%	

TABLEAU II

Contig9 from 1393248 to 1393703	m	85%	sp P45569 YCBG_ECOLI HYPOTHETICAL 17.7 KDA PROTEIN IN FABG-OMPA INTERGENIC REGION pir [C64836 ycbg protein - Escherichia coli gb AAC74042.1 (AE000198) putative dehydrogenase [Escherichia coli K12] dbj BAA35714.1 (D90733) Hypothetical protein in ompA 3'region . [Escherichia coli] dbj BAA35721.1 (D90734) Hypothetical protein in ompA 3'region . [Escherichia coli] gb AAG55442.1 AE005286_1 (AE005286) putative dehydrogenase [Escherichia coli O157:H7]	SEQ ID n-9122
Contig9 from 1393910 to 1395640	p	63%	gb AAG55441.1 AE005285_8 (AE005285) putative ATP- dependent protease [Escherichia coli O157:H7] sp P18391 FABA_ECOLI 3-HYDROXYDECANOYL-[ACYL- CARRIER-PROTEIN] DEHYDRATASE (BETA- HYDROXYDECANOYL THIOESTER DEHYDRASE) pir [DWECHD 3-hydroxydecanoyl-(acyl-carrier- protein] dehydratase (EC 4.2.1.60) Escherichia coli gb AAG96496.1 (J03186) D-3- hydroxydecanoyl-(acyl carrier-protein) dehydratase [Escherichia coli] dbj BAA35712.1 (D90733) 3-hydroxydecanoyl-[acyl- carrier-protein] dehydratase (EC 4.2.1.60) (beta-hydroxydecanoyl thioester dehydratase). [Escherichia coli] gb AAC74040.1 (AE000197) beta-hydroxydecanoyl thioester dehydratase, trans-2-decenoyl- ACP isomerase [Escherichia coli K12] gb AAG55440.1 AE005285_7 (AE005285) beta- hydroxydecanoyl thioester dehydratase, trans-2-decenoyl-ACP isomerase [Escherichia coli O157:H7]	SEQ ID n-9123
Contig9 from 1395724 to 1396242	p	81%		
Contig9 from 1396367 to 1396555	m	No Hits found		#N/A

TABLEAU II

SEQ ID n°	Contig9 from	p	No Hits found		#N/A
1396668 to 1397006	Contig9 from				
1397588 to 1397755	Contig9 from	m	48%	pir S36191 ribosome modulation factor - Escherichia coli emb CAA49706.1 (X70111) ribosome modulation factor [Escherichia coli]	#N/A
1398002 to 1398565	Contig9 from	m	69%	dbj BAA35710.1 (D90733) ORF_ID:0222#5 [Escherichia coli]	#N/A
1398562 to 1400211	Contig9 from	m	79%	gb AAG55437.1 AE005285_4 (AE005285) paraquat- inducible protein B [Escherichia coli O157:H7 EDL933] dbj BAB34458.1 (AP002554) paraquat- inducible protein B [Escherichia coli O157:H7] sp P43670 PQIA_ECOLI PARAQUAT-INDUCIBLE PROTEIN A pir B64835 paraquat-inducible protein pqia - Escherichia coli dbj BAA35708.1 (D90733) Paraquat-inducible protein A. [Escherichia coli] gb AAC74036.1 (AE000197) paraquat-inducible protein A [Escherichia coli K12]	#N/A
1400232 to 1401479	Contig9 from	m	74%	sp P43672 UUP_ECOLI ABC TRANSPORTER ATP-BINDING PROTEIN UUP pir D64835 ABC-type transport protein uup - Escherichia coli gb AAC74035.1 (AE000197) putative ATP-binding component of a transport system [Escherichia coli K12] dbj BAA35707.1 (D90733) Hypothetical protein H11300 [Escherichia coli]	SEQ ID n-2378
1401569 to 1403479	Contig9 from	m	86%	sp P75864 YCBY_ECOLI HYPOTHETICAL 78.9 KDA PROTEIN IN PYRD-PQIA INTERGENIC REGION pir C64835 hypothetical protein b0948 - Escherichia coli gb AAC74034.1 (AE000197) putative oxidoreductase [Escherichia coli K12] dbj BAA35703.1 (D90732) Hypothetical protein HI0115 [Escherichia coli] dbj BAA35706.1 (D90733) Hypothetical protein HI0115 [Escherichia coli]	SEQ ID n-2379
1403485 to 1405617	Contig9 from	m	84%		SEQ ID n-2380

TABLEAU II

SEQ ID n° 7103	PL-3137.1	Contig9 from 1405705 to 1406820	p 76%	gb AAG55433.1 AE005284_11 (AE005284) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2381
SEQ ID n° 7104	PL-3138.2	Contig9 from 1407098 to 1408396	p 48%	dbj BAA83130.1 (AB023953) N-glycosylation [Saccharothrix aerocolonigenes]	#N/A
SEQ ID n° 7105	PL-3139.2	Contig9 from 1408614 to 1409498	p 59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]	#N/A
SEQ ID n° 7106	PL-3140.1	Contig9 from 1409620 to 1410915	p 50%	dbj BAA83130.1 (AB023953) N-glycosylation [Saccharothrix aerocolonigenes]	SEQ ID n-2385
SEQ ID n° 7107	PL-3966.1	Contig9 from 1411301 to 1411846	m 63%	gb AAG55432.1 AE005284_10 (AE005284) orf, hypothetical protein [Escherichia coli O157:H7] sp P05021 PYRD_ECOLI DIHYDROOROTATE DEHYDROGENASE (DIHYDROOROTATE OXIDASE) (DHODHASE) (DHOD) (DHOD) pir DEFCO dihydroorotate oxidase (EC 1.3.3.1) Escherichia coli emb CAA26594.1 (X02826) dihydroorotate dehydrogenase (aa 1-336) [Escherichia coli] dbj BAA35700.1 (D90732) Dihydroorotate oxidase (EC 1.3.3.1) [Escherichia coli] gb AAC74031.1 (AE000196) dihydro-orotate dehydrogenase [Escherichia coli K12] gb AAG55431.1 AE005284_9 (AE005284) dihydro-orotate dehydrogenase [Escherichia coli O157:H7]	SEQ ID n-9125
SEQ ID n° 7108	PL-3141.1	Contig9 from 1412163 to 1413173	m 85%		
SEQ ID n° 7109	PL-4072.1	Contig9 from 1413239 to 1413397	m No Hits found		#N/A
SEQ ID n° 7110	PL-4071.1	Contig9 from 1413517 to 1413684	m No Hits found		#N/A

TABLEAU II

Contig9 from 1413860 to 1416472	m	85%	gb AG55417.1 AE005283_4 (AE005283) aminopeptidase N [Escherichia coli O157:H7] sp P18133 PNCB_ECOLI NICOTINATE PHOSPHORIBOSYLTRANSFERASE (NAPRTASE) pir JQ0756 nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Escherichia coli gb AAA24400.1 (J05568) nicotinic acid phosphoribosyl transferase (pncB) (EC 2.4.2.11) [Escherichia coli] dbj BAA35683.1 (D90731) Nicotinate phosphoribosyltransferase (EC 2.4.2.11) [Escherichia coli] gb AAC74017.1 (AE000195) nicotinate phosphoribosyltransferase [Escherichia coli K12] sp P17242 SYN_ECOLI ASPARAGINYL-TRNA SYNTHETASE (ASPARAGINE--TRNA LIGASE) (ASNRS) pir SYECNT asparagine--trna ligase (EC 6.1.1.22) - Escherichia coli emb CAA48274.1 (X68192) Asparaginyl-trna synthetase [Escherichia coli] gb AA24666.1 (M33145) asparaginyl-trna synthetase (asns) [Escherichia coli] dbj BAA35682.1 (D90731) Asparaginyl-trna synthetase (EC 6.1.1.22) (asparagine- trna ligase) (asnrs) . [Escherichia coli] gb AAC74016.1 (AE000195) asparagine trna synthetase [Escherichia coli K12] sp Q56828 OMPX_XENNE OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF) (OUTER MEMBRANE PROTEIN OMP) pir S70847 outer membrane porin ompF precursor - Xenorhabdus nematophilus gb AAB41114.1 (L40919) OmpF-like protein precursor [Xenorhabdus nematophila] prf 2204378A OmpF-like porin [Xenorhabdus nematophilus]	SEQ ID n-2387
Contig9 from 1416818 to 1418032	p	78%		SEQ ID n-2388
Contig9 from 1418237 to 1419637	p	93%		SEQ ID n-2389
Contig9 from 1419974 to 1421119	p	72%		#N/A

TABLEAU II

SEQ ID n° 7115	PL-6661.2	Contig9 from 1421625 to 1422791	p	75%	sp Q56828 OMP_F_XENNE OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF) (OUTER MEMBRANE PROTEIN OMPF) pir S70847 outer membrane porin ompF precursor - Xenorhabdus nematophilus gb AAB41114.1 (L40919) OmpF-like protein precursor [Xenorhabdus nematophila] prf 2204378A OmpF-like porin [Xenorhabdus nematophilus] #N/A
SEQ ID n° 7116	PL-3035.2	Contig9 from 1423013 to 1424203	p	84%	pdb 1ART Aspartate Aminotransferase (E.C.2.6.1.1) Complexed With Pyridoxal-5'-Phosphate And 2-Methylaspartate #N/A
SEQ ID n° 7117	PL-3034.1	Contig9 from 1424620 to 1425267	m	77%	gb AAG55412.1 AE005282_7 (AE005282) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2267
SEQ ID n° 7118	PL-3033.1	Contig9 from 1425313 to 1425861	m	73%	sp P75848 YCBK_ECOLI HYPOTHETICAL 20.4 KDA PROTEIN IN MUKB-ASPC INTERGENIC REGION pir E64832-ycbK protein precursor - Escherichia coli gb AAC74012.1 (AE000195) orf, hypothetical protein [Escherichia coli K12] dbj BAA35672.1 (D90730) Hypothetical protein H11666 [Escherichia coli] dbj BAA35678.1 (D90731) Hypothetical protein H11666 [Escherichia coli] SEQ ID n-2266
SEQ ID n° 7119	PL-3032.1	Contig9 from 1425954 to 1427309	m	74%	gb AAG55410.1 AE005282_5 (AE005282) putative amidase [Escherichia coli O157:H7] SEQ ID n-2265
SEQ ID n° 7120	PL-3031.1	Contig9 from 1427356 to 1428972	m	29%	gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae] sp P22525 YCBK_ECOLI HYPOTHETICAL 67.8 KDA PROTEIN IN MUKB-ASPC INTERGENIC REGION pir D64832 ycbB protein precursor - Escherichia coli gb AAC74011.1 (AE000194) putative amidase [Escherichia coli K12] dbj BAA35671.1 (D90730) Hypothetical protein 63 (MukB 3' region) [Escherichia coli] #N/A
SEQ ID n° 7121	PL-6658.1	Contig9 from 1429075 to 1429440	m	32%	

TABLEAU II

Contig9 from 1429776 to 1430450	SEQ ID n° 7122 PL-3030.1	m 38%	pir C83186 probable transcription regulator PA3678 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07066.1 AE004787_6 (AE004787) probable transcriptional regulator [Pseudomonas aeruginosa] sp Q01911 TETX_BACFR TETRACYCLINE RESISTANCE PROTEIN (TRANSPONON TN4351/TN4400) pir A39191 probable oxidoreductase (EC 1.-.-.-) - Bacteroides fragilis gb AA27471.1 (M37699) tetracycline resistance protein [Transposon Tn4351] ref NP_053071.1 BfpE [Escherichia coli] pir S70972 bfpE protein - Escherichia coli emb CAA92332.1 (Z68186) BfpE [Escherichia coli] gb AAC44044.1 (U27184) BfpE [Escherichia coli] dbj BAA84844.1 (AB024946) BfpE [Escherichia coli] ref NP_052543.1 ATP-binding protein [Plasmid Colib-P9] dbj BAA75182.1 (AB021078) ATP- binding protein [Plasmid Colib-P9] dbj BAA77977.1 (AB027308) nucleotide-binding protein [Plasmid R64] SEQ ID n-2261	SEQ ID n-2263
Contig9 from 1430613 to 1431926	SEQ ID n° 7123 PL-3029.1	p 38%	gb AAF14815.2 (AF000001) Pilo [Salmonella typhi] gb AAF81211.1 AF247502_6 (AF247502) Pilo [Salmonella dublin] ref NP_052546.1 lipoprotein [Plasmid Colib-P9] dbj BAA75185.1 (AB021078) lipoprotein [Plasmid Colib-P9] dbj BAA77974.1 (AB027308) lipoprotein [Plasmid R64] gb AAF14812.2 (AF000001) PILL [Salmonella typhi] gb AAF81207.1 AF247502_2 (AF247502) PILL [Salmonella dublin] #N/A	SEQ ID n-2258
Contig9 from 1432599 to 1433696	SEQ ID n° 7124 PL-3028.1	m 51%	Contig9 from 1433703 to 1435265	SEQ ID n-2259
Contig9 from 1435287 to 1435829	SEQ ID n° 7125 PL-3027.1	m 45%	Contig9 from 1435816 to 1437108	SEQ ID n-2260
Contig9 from 1437112 to 1438716	SEQ ID n° 7126 PL-3913.1	m No Hits found	Contig9 from 1438721 to 1439062	SEQ ID n-2257
Contig9 from 1439062 to 1439062	SEQ ID n° 7127 PL-3026.1	m 40%		
Contig9 from 1439062 to 1439062	SEQ ID n° 7128 PL-3025.1	m 54%		
Contig9 from 1439062 to 1439062	SEQ ID n° 7129 PL-6656.1	m 47%		

SEQ ID n°	7130 PL-6655.1	1439059 to 1439151	Contig9 from	m	No Hits found	#N/A	SEQ ID n-3077
SEQ ID n°	7131 PL-3912.1	1439166 to 1439690	Contig9 from	m	No Hits found		
SEQ ID n°	7132 PL-3024.1	1439807 to 1440982	Contig9 from	m	35%		SEQ ID n-2255
SEQ ID n°	7133 PL-3023.1	1441022 to 1441816	Contig9 from	m	59%		SEQ ID n-2255
SEQ ID n°	7134 PL-3022.1	1441974 to 1442546	Contig9 from	m	41%		SEQ ID n-2254
SEQ ID n°	7135 PL-3021.1	1443224 to 1445011	Contig9 from	m	10%		SEQ ID n-2253
SEQ ID n°	7136 PL-6651.1	1445697 to 1446146	Contig9 from	p	34%		SEQ ID n-2252
SEQ ID n°	7137 PL-3020.1	1446161 to 1447225	Contig9 from	p	31%		SEQ ID n-2252

TABLEAU II

SEQ ID n° 7138	PL-3019.1	Contig9 from 1447237 to 1448628	p	22%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-2250
SEQ ID n° 7139	PL-3018.1	Contig9 from 1448677 to 1449861	p	35%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-2249
SEQ ID n° 7140	PL-3910.1	Contig9 from 1449875 to 1450333	p	No Hits found		SEQ ID n-9076
SEQ ID n° 7141	PL-3017.1	Contig9 from 1450496 to 1451179	p	No Hits found		#N/A
SEQ ID n° 7142	PL-3016.1	Contig9 from 1451176 to 1452777	p	31%	emb CAB77340.1 (AL160331) hypothetical protein SCD8A.19c [Streptomyces coelicolor A3(2)]	SEQ ID n-2248
SEQ ID n° 7143	PL-3015.1	Contig9 from 1452790 to 1453509	p	24%	emb CAB77339.1 (AL160331) hypothetical protein SCD8A.18c [Streptomyces coelicolor A3(2)]	SEQ ID n-2247
SEQ ID n° 7144	PL-6648.1	Contig9 from 1453506 to 1453922	p	No Hits found		#N/A
SEQ ID n° 7145	PL-3014.1	Contig9 from 1453966 to 1456683	p	No Hits found		SEQ ID n-2246
SEQ ID n° 7146	PL-3013.2	Contig9 from 1456676 to 1459582	p	No Hits found		#N/A
SEQ ID n° 7147	PL-3012.1	Contig9 from 1459770 to 1461074	p	21%	ref NP_050293.1 fiber protein [fowl adenovirus 8] gb AAC71676.1 (AF021254) fibre homolog [fowl adenovirus 8] gb AAD50350.1 AF083975_17 (AF083975) fiber protein [fowl adenovirus 8]	SEQ ID n-2244
SEQ ID n° 7148	PL-3011.1	Contig9 from 1461138 to 1462793	p	No Hits found		SEQ ID n-2243

TABLEAU II

SEQ ID n° 7149	PL-3010.2	Contig9 from 1462803 to 1464887	p	42%	emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)]	SEQ ID n-2242
SEQ ID n° 7150	PL-2586.2	Contig9 from 1464912 to 1465814	p	23%	emb CAB77354.1 (AL160331) hypothetical protein SCD8A.33c (fragment) [Streptomyces coelicolor A3(2)]	SEQ ID n-2778
SEQ ID n° 7151	PL-3908.2	Contig9 from 1465916 to 1466398	p	No Hits found		#N/A
SEQ ID n° 7152	PL-2585.2	Contig9 from 1466737 to 1467579	p	No Hits found		#N/A
SEQ ID n° 7153	PL-2584.1	Contig9 from 1467699 to 1468721	p	41%	ref NP_065279.1 SepC [Serratia entomophila] gb AAG09644.1 (AF135182) SepC [Serratia entomophila]	SEQ ID n-2776
SEQ ID n° 7154	PL-2583.1	Contig9 from 1469215 to 1470237	p	66%	gb AAF81206.1 AF247502_1 (AF247502) Ytl2 [Salmonella dublin]	SEQ ID n-2775
SEQ ID n° 7155	PL-6647.1	Contig9 from 1470230 to 1470631	p	44%	ref NP_047874.1 putative transposase [Yersinia pestis] pir T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CAB55253.1 (AL117211) hypothetical protein YPMT1.71 [Yersinia pestis]	#N/A
SEQ ID n° 7156	PL-6646.1	Contig9 from 1470688 to 1470858	m	No Hits found		#N/A
SEQ ID n° 7157	PL-6645.1	Contig9 from 1471265 to 1471714	p	No Hits found		#N/A
SEQ ID n° 7158	PL-2582.1	Contig9 from 1471768 to 1472844	p	29%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-2774
SEQ ID n° 7159	PL-2581.1	Contig9 from 1472856 to 1474340	p	20%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-2773

TABLEAU II

SEQ ID n° 7160	PL-2580.1	Contig9 from 1474389 to 1475594	p	33%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-1772
SEQ ID n° 7161	PL-3906.1	Contig9 from 1475608 to 1476066	p	No Hits found		SEQ ID n-3073
SEQ ID n° 7162	PL-6642.1	Contig9 from 1476063 to 1476242	p	No Hits found		#N/A
SEQ ID n° 7163	PL-2579.1	Contig9 from 1476229 to 1476912	p	No Hits found		#N/A
SEQ ID n° 7164	PL-2578.1	Contig9 from 1476909 to 1478510	p	13%	pir D82202 vgrG protein VC1416 [imported] - Vibrio cholerae (group O1 strain N16951) gb AAF94573.1 (AE004220) vgrG protein [Vibrio cholerae]	SEQ ID n-1770
SEQ ID n° 7165	PL-3905.1	Contig9 from 1478523 to 1479014	p	38%	emb CAB77339.1 (AL160331) hypothetical protein SCD8A.18c [Streptomyces coelicolor A3(2)]	SEQ ID n-3072
SEQ ID n° 7166	PL-6639.1	Contig9 from 1479011 to 1479427	p	No Hits found		#N/A
SEQ ID n° 7167	PL-2577.1	Contig9 from 1479524 to 1482226	p	No Hits found		SEQ ID n-1769
SEQ ID n° 7168	PL-2576.1	Contig9 from 1482223 to 1485129	p	No Hits found		SEQ ID n-1768
SEQ ID n° 7169	PL-2575.2	Contig9 from 1485331 to 1486281	p	27%	pir JQ1866 hypothetical 87.1K protein - bovine adenovirus 3	#N/A
SEQ ID n° 7170	PL-2574.1	Contig9 from 1486331 to 1487356	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-1766

TABLEAU II

SEQ ID n° 7171	PL-2573.1	Contig9 from 1487535 to 1489097	p	12%	ref NP_065040.1 AMV258 [Amsacta moorei entomopoxvirus] gb AA02964.1 AF250284_258 (AF250284) AMV258 [Amsacta moorei entomopoxvirus]	SEQ ID n-1765
SEQ ID n° 7172	PL-2572.1	Contig9 from 1489107 to 1491173	p	22%	emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)]	SEQ ID n-1764
SEQ ID n° 7173	PL-2571.1	Contig9 from 1491198 to 1492100	p	No Hits found		SEQ ID n-1763
SEQ ID n° 7174	PL-2570.1	Contig9 from 1492181 to 1493110	p	No Hits found		SEQ ID n-1762
SEQ ID n° 7175	PL-2569.1	Contig9 from 1493302 to 1494249	p	No Hits found		SEQ ID n-1760
SEQ ID n° 7176	PL-6634.1	Contig9 from 1495180 to 1495629	p	35%	emb CAB77342.1 (AL160331) hypothetical protein SCD8A.21c [Streptomyces coelicolor A3(2)]	#N/A
SEQ ID n° 7177	PL-2568.1	Contig9 from 1495682 to 1496887	p	28%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-1759
SEQ ID n° 7178	PL-2567.1	Contig9 from 1496899 to 1498284	p	22%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-1758
SEQ ID n° 7179	PL-2566.1	Contig9 from 1498340 to 1499515	p	33%	emb CAB77347.1 (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]	SEQ ID n-1757
SEQ ID n° 7180	PL-3903.1	Contig9 from 1499551 to 1500009	p	No Hits found		SEQ ID n-3071
SEQ ID n° 7181	PL-6631.1	Contig9 from 1500006 to 1500185	p	No Hits found		#N/A

TABLEAU II

SEQ ID n° 7182	PL-2565.1	Contig9 from 1500172 to 1500855	p	No Hits found	emb CAB77340.1 (AL160331) hypothetical protein SCD8A.19c [Streptomyces coelicolor A3(2)]	#N/A
SEQ ID n° 7183	PL-2564.1	Contig9 from 1500852 to 1502453	p	38%		SEQ ID n-2756
SEQ ID n° 7184	PL-3902.1	Contig9 from 1502466 to 1502912	p	42%	emb CAB77339.1 (AL160331) hypothetical protein SCD8A.18c [Streptomyces coelicolor A3(2)]	SEQ ID n-3070
SEQ ID n° 7185	PL-6630.1	Contig9 from 1502909 to 1503325	p	No Hits found		#N/A
SEQ ID n° 7186	PL-2563.1	Contig9 from 1503402 to 1506104	p	No Hits found		SEQ ID n-2755
SEQ ID n° 7187	PL-2562.1	Contig9 from 1506097 to 1508976	p	No Hits found		SEQ ID n-2754
SEQ ID n° 7188	PL-2561.1	Contig9 from 1509119 to 1510150	p	38%	sp P33666 YDBA_ECOLI HYPOTHETICAL 205.9 KDA PROTEIN IN PAAY-ACPD INTERGENIC REGION	SEQ ID n-2753
SEQ ID n° 7189	PL-2560.1	Contig9 from 1510207 to 1511886	p	No Hits found		SEQ ID n-2752
SEQ ID n° 7190	PL-2559.1	Contig9 from 1511896 to 1513980	p	23%	emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)]	SEQ ID n-2750
SEQ ID n° 7191	PL-2558.1	Contig9 from 1514005 to 1514697	p	No Hits found		SEQ ID n-2749
SEQ ID n° 7192	PL-6628.1	Contig9 from 1514796 to 1515032	p	No Hits found		#N/A
SEQ ID n° 7193	PL-2557.1	Contig9 from 1515235 to 1516245	p	No Hits found		SEQ ID n-2748

TABLEAU II

SEQ ID n°	7194 PL-2556.1	Contig9 from 1517293	p	No Hits found	SEQ ID n-2747
SEQ ID n°	7195 PL-6627.1	Contig9 from 1517483 to 1517620	p	42%	#N/A
SEQ ID n°	7196 PL-2555.1	Contig9 from 1517721 to 1518647	p	77%	SEQ ID n-2746
SEQ ID n°	7197 PL-6626.1	Contig9 from 1518730 to 1518831	p	No Hits found	#N/A
SEQ ID n°	7198 PL-6625.1	Contig9 from 1519396 to 1519845	p	No Hits found	#N/A
SEQ ID n°	7199 PL-2554.1	Contig9 from 1520981	p	28%	SEQ ID n-2745
SEQ ID n°	7200 PL-2553.1	Contig9 from 1522426	p	21%	SEQ ID n-2744
SEQ ID n°	7201 PL-2552.1	Contig9 from 1522474 to 1523709	p	31%	SEQ ID n-2743
SEQ ID n°	7202 PL-3900.1	Contig9 from 1524181	p	No Hits found	SEQ ID n-3069
SEQ ID n°	7203 PL-6624.1	Contig9 from 1524160 to 1524357	p	No Hits found	#N/A
SEQ ID n°	7204 PL-2551.1	Contig9 from 1524344 to 1525027	p	No Hits found	SEQ ID n-2742

ref|NP_052862.1| hypothetical protein [Coxiella burnetii] gb|AAD33494.1|AF131076_20 (AF131076) hypothetical protein [Coxiella burnetii]

ref|NP_073263.1|orf39 [Salmonella enterica serovar Choleraesuis] dbj|BAB20546.1| (AB040415) orf39 [Salmonella enterica serovar Choleraesuis]

emb|CAB77347.1| (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]

emb|CAB77347.1| (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]

emb|CAB77347.1| (AL160331) hypothetical protein SCD8A.26c [Streptomyces coelicolor A3(2)]

TABLEAU II

SEQ ID n° 7205	PL-2550.1	Contigs from 1525090 to 1526625	p	12%	pir D82202 vgrg protein VC1416 [imported] - vibrio cholerae (group O1 strain N16961) gb AAF94573.1 (AE004220) vgrg protein [Vibrio cholerae]	SEQ ID n-2741
SEQ ID n° 7206	PL-3899.1	Contigs from 1526638 to 1527129	p	38%	emb CAB77339.1 (AL160331) hypothetical protein SCD8A.18c [Streptomyces coelicolor A3(2)]	SEQ ID n-3066
SEQ ID n° 7207	PL-6622.1	Contigs from 1527126 to 1527542	p	No Hits found		#N/A
SEQ ID n° 7208	PL-2549.1	Contigs from 1527585 to 1530293	p	No Hits found		SEQ ID n-2739
SEQ ID n° 7209	PL-2548.1	Contigs from 1530290 to 1533643	p	No Hits found		SEQ ID n-2738
SEQ ID n° 7210	PL-2547.1	Contigs from 1533753 to 1534970	p	23%	pir JQ1866 hypothetical 87.1K protein - bovine adenovirus 3	SEQ ID n-2737
SEQ ID n° 7211	PL-2545.2	Contigs from 1535034 to 1536998	p	No Hits found		SEQ ID n-2735
SEQ ID n° 7212	PL-2851.1	Contigs from 1537008 to 1539107	p	24%	emb CAB77353.1 (AL160331) putative AAA family ATPase [Streptomyces coelicolor A3(2)]	SEQ ID n-2066
SEQ ID n° 7213	PL-2850.1	Contigs from 1539131 to 1540033	p	No Hits found		SEQ ID n-2065
SEQ ID n° 7214	PL-2849.1	Contigs from 1540138 to 1541124	p	17%	sp Q47279 HRPN_ERWCA HARPIN (HARPIN-ECC) gb AAB49733.1 (L78834) putative [Pectobacterium carotovorum]	SEQ ID n-2063
SEQ ID n° 7215	PL-2848.1	Contigs from 1541592 to 1542269	m	55%	gb AAA96022.1 (U38815) halovibrin [Vibrio fischeri] gb AAG42286.1 AF206719_1 (AF206719) Hvna [Vibrio fischeri]	SEQ ID n-2062

TABLEAU II

SEQ ID n° 7216	PL-2847.1	Contig9 from 1542148 to 1543035	p	47%	pir G83406 conserved hypothetical protein PA1914 [imported] - Pseudomonas aeruginosa (strain PA01)	SEQ ID n-2061
SEQ ID n° 7217	PL-2846.1	Contig9 from 1543554 to 1544351	p	No Hits found		SEQ ID n-2060
SEQ ID n° 7218	PL-6620.1	Contig9 from 1544413 to 1544673	p	35%	gb AAF97407.1 (AY004319) photopexin A [Photorhabdus luminescens]	#N/A
SEQ ID n° 7219	PL-2845.1	Contig9 from 1544661 to 1545545	p	59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]	SEQ ID n-2059
SEQ ID n° 7220	PL-2844.1	Contig9 from 1545596 to 1546453	p	68%	gb AAF97407.1 (AY004319) photopexin A [Photorhabdus luminescens]	SEQ ID n-2058
SEQ ID n° 7221	PL-6619.1	Contig9 from 1546575 to 1546784	m	48%	ref NP_073263.1 orf39 [Salmonella enterica serovar Choleraesuis] dbj BAE20546.1 (AB040415) orf39 [Salmonella enterica serovar Choleraesuis]	#N/A
SEQ ID n° 7222	PL-2843.1	Contig9 from 1546847 to 1547809	m	76%	ref NP_073263.1 orf39 [Salmonella enterica serovar Choleraesuis] dbj BAE20546.1 (AB040415) orf39 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-2057
SEQ ID n° 7223	PL-6618.1	Contig9 from 1547956 to 1548195	m	56%	sp P46147 YEFM_ECOLI HYPOTHETICAL 9.3 KD PROTEIN IN SBCB-HISL INTERGENIC REGION	#N/A
SEQ ID n° 7224	PL-2842.1	Contig9 from 1548439 to 1549059	p	No Hits found		SEQ ID n-2056
SEQ ID n° 7225	PL-2841.1	Contig9 from 1549098 to 1549781	m	No Hits found		SEQ ID n-2055

TABLEAU II

SEQ ID n° 7226 PL-2840.1	Contig9 from 1550089 to 1554537	m 88%	sp P22523 MUKB_ECOLI CELL DIVISION PROTEIN MUKB pir C64832 cell division protein mukB - Escherichia coli (strain K-12, substrain MG1655) dbj BAA35670.1 (D90730) MukB protein [Escherichia coli] gb AAC74010.1 (AE000194) kinesin-like cell division protein involved in chromosome partitioning [Escherichia coli K12] SEQ ID n-2054
SEQ ID n° 7227 PL-2839.1	Contig9 from 1554534 to 1555229	m 88%	pir S43912 kicA protein - Escherichia coli dbj BAA35669.1 (D90730) MukE protein [Escherichia coli] SEQ ID n-2052
SEQ ID n° 7228 PL-2838.1	Contig9 from 1555237 to 1556559	m 88%	sp P36567 MUKF_ECOLI MUKF PROTEIN (KILLING FACTOR KICB) pir S43911 mukF protein - Escherichia coli dbj BAA05457.1 (D26440) MukF [Escherichia coli] dbj BAA35668.1 (D90730) MukF protein (killing factor KicB). [Escherichia coli] gb AAC74008.1 (AE000194) mukF protein (killing factor KICB) [Escherichia coli K12] SEQ ID n-2051
SEQ ID n° 7229 PL-2837.1	Contig9 from 1556570 to 1557349	m 73%	gb AAG55406.1 AE005282_1 (AE005282) S- adenosylmethionine-dependent methyltransferase [Escherichia coli O157:H7] sp P36565 YCBC_ECOLI HYPOTHETICAL 28.7 KDA PROTEIN IN KDSB-MUKF INTERGENIC REGION pir G64831 probable membrane protein ycbC - Escherichia coli gb AAC74006.1 (AE000194) orf, hypothetical protein [Escherichia coli K12] dbj BAA35666.1 (D90730) Hypothetical protein in kdsB-mukF intergenic region [Escherichia coli] gb AAG55405.1 AE005281_8 (AE005281) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2050
SEQ ID n° 7230 PL-2836.1	Contig9 from 1557628 to 1558467	p 70%	sp P36565 YCBC_ECOLI HYPOTHETICAL 28.7 KDA PROTEIN IN KDSB-MUKF INTERGENIC REGION pir G64831 probable membrane protein ycbC - Escherichia coli gb AAC74006.1 (AE000194) orf, hypothetical protein [Escherichia coli K12] dbj BAA35666.1 (D90730) Hypothetical protein in kdsB-mukF intergenic region [Escherichia coli] gb AAG55405.1 AE005281_8 (AE005281) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2049

TABLEAU II

SEQ ID n° 7231-PL-2835.1	Contig9 from 1558696 to 1559445	m 81%	sp P04951 KDSB_ECOLI_3-DEOXY-MANNO-OCTULOSONATE CYTIDYLYLTRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS) pir A26322 3-deoxy-manno- octulosonate cytidylyltransferase (EC 2.7.7.38) Escherichia coli gb AA83877.1 (J02614) CMP- KDO synthetase [Escherichia coli] dbj BAA35664.1 (D90730) 3-deoxy-manno- octulosonate cytidylyltransferase (EC 2.7.7.38) [Escherichia coli] gb AAC74004.1 (AE000193) CTP: CMP-3-deoxy-D-manno-octulosonate transferase [Escherichia coli K12] sp P75844 YCAR_ECOLI_PROTEIN_YCAR_pir D64831 ycar protein - Escherichia coli gb AAC74003.1 (AE000193) orf, hypothetical protein [Escherichia coli K12] dbj BAA35663.1 (D90730) ORF_ID: o218#3 [Escherichia coli] gb AGS5402.1 AE005281_5 (AE005281) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 7232 PL-6612.1	Contig9 from 1559449 to 1559628	m 74%	gb AAB40823.1 (U82598) cold shock-like protein [Escherichia coli] #N/A
SEQ ID n° 7233 PL-6611.1	Contig9 from 1560007 to 1560249	m 59%	gb AGS5400.1 AE005281_3 (AE005281) putative EC 1.2 enzyme [Escherichia coli O157:H7] SEQ ID n-2047
SEQ ID n° 7234 PL-2834.1	Contig9 from 1560804 to 1561799	m 69%	

TABLEAU II

SEQ ID n° 7235	PL-2832.2	Contig9 from 1561796 to 1563541	m	89%	sp P27299 MSBA_ECOLI PROBABLE TRANSPORT ATP-BINDING PROTEIN MSBA pir S27998 probable ABC-type transport protein msba - Escherichia coli emb CAA77839.1 (Z11796) member of ATP-dependent transport family, very similar to mdr proteins and hemolysin B, export protein [Escherichia coli] dbj BAA35658.1 (D90729) Msba protein. [Escherichia coli] gb AAC74000.1 (AE000193) ATP-binding transport protein; multicopy suppressor of htrB [Escherichia coli K12] gb AAG55399.1 AE005281_2 (AE005281) ATP-binding transport protein; multicopy suppressor of htrB [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7236	PL-2831.1	Contig9 from 1563580 to 1565907	m	56%	gb AAG55398.1 AE005281_1 (AE005281) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2044
SEQ ID n° 7237	PL-2830.1	Contig9 from 1566816 to 1567628	p	39%	dbj BAB06652.1 (AP001517) BH2933-unknown [Bacillus halodurans]	SEQ ID n-2043
SEQ ID n° 7238	PL-2829.1	Contig9 from 1567633 to 1568268	p	46%	dbj BAB05889.1 (AP001514) BH2170-unknown conserved protein [Bacillus halodurans]	SEQ ID n-2041
SEQ ID n° 7239	PL-6606.1	Contig9 from 1568779 to 1568937	p	No Hits found		#N/A
SEQ ID n° 7240	PL-2828.1	Contig9 from 1569001 to 1569900	p	No Hits found		#N/A
SEQ ID n° 7241	PL-6605.1	Contig9 from 1570170 to 1570409	m	No Hits found		SEQ ID n-2040

TABLEAU II

SEQ ID n° 7242 PL-6603.1	Contig9 from 1570864 to 1571148	m 89%	sp P23303 IHFB_SERMA INTEGRATION HOST FACTOR BETA-SUBUNIT (IHFB-BETA) pir B38173 integration host factor beta chain - Serratia marcescens gb AA26557.1 (M62643) integration host factor beta-subunit [Serratia marcescens] sp P02349 RS1_ECOLI 30S RIBOSOMAL PROTEIN S1 pir R3EC1 ribosomal protein S1 [validated] - Escherichia coli dbj BAA35655.1 (D90729) 30S ribosomal protein S1. [Escherichia coli] gb AAC73997.1 (AE000193) 30S ribosomal subunit protein S1 [Escherichia coli K12] gb AAG55396.1 AE005280_7 (AE005280) 30S ribosomal subunit protein S1 [Escherichia coli O157:H7]	#N/A	SEQ ID n-2039
SEQ ID n° 7243 PL-2827.1	Contig9 from 1571214 to 1572887	m 96%	sp P23863 KCY_ECOLI CYTIDYLATE KINASE (CK) (CYTIDINE MONOPHOSPHATE KINASE) (CMP KINASE) (MSSA PROTEIN) (P25) pir B64830 cytidylate kinase (EC 2.7.4.14) [validated] - Escherichia coli pdb 2CMK A Chain A, Cytidine Monophosphate Kinase In Complex With Cytidine-Di- Phosphate dbj BAA35645.1 (D90728) Cytidylate kinase (EC 2.7.4.14) (ck) (cytidine monophosphate kinase) (CMP kinase) (Mssa protein) (p25). dbj BAA35654.1 (D90729) Cytidylate kinase (EC 2.7.4.14) (ck) (cytidine monophosphate kinase) (CMP kinase) (Mssa protein) (p25). gb AAC73996.1 (AE000193) cytidylate kinase [Escherichia coli K12] gb AAG55395.1 AE005280_6 (AE005280) cytidylate kinase [Escherichia coli O157:H7]		SEQ ID n-2038
SEQ ID n° 7244 PL-2825.1	Contig9 from 1573069 to 1573752	m 86%			

TABLEAU II

SEQ ID n° 7245	PL-2824.1	Contig9 from 1574057 to 1575343	m	84%	sp P19688 AROA_YEREN 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS) pir XUEBY 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) [validated] - Versinia enterocolitica gb AA27666.1 (M32213) 5-enolpyruvylshikimate 3-phosphate synthase (aroA) [Versinia enterocolitica] SEQ ID n-2037
SEQ ID n° 7246	PL-2823.1	Contig9 from 1575593 to 1576681	m	88%	sp P19689 SERC_YEREN PHOSPHOSERINE AMINOTRANSFERASE (PSAT) pir XNEBPY phosphoserine transaminase (EC 2.6.1.52) - Versinia enterocolitica gb AA27665.1 (M32213) 3-phosphoserine aminotransferase (serC) [Versinia enterocolitica] SEQ ID n-2036
SEQ ID n° 7247	PL-3897.1	Contig9 from 1576853 to 1577356	m	41%	pir G70582 hypothetical protein Rv0919 - Mycobacterium tuberculosis (strain H37RV) emb CAB08501.1 (Z95210) hypothetical protein Rv0919 [Mycobacterium tuberculosis] sp P43995 Y420_HAEN HYPOTHETICAL PROTEIN HI0420 pir D64007 hypothetical protein HI0420 - Haemophilus influenzae (strain Rd KW20) gb AAC22082.1 (U32725) H. influenzae predicted coding region HI0420 [Haemophilus influenzae Rd] #N/A
SEQ ID n° 7248	PL-6600.1	Contig9 from 1577353 to 1577628	m	58%	
SEQ ID n° 7249	PL-2822.1	Contig9 from 1577798 to 1578841	m	82%	gb AAG58088.1 AE005526_1 (AE005526) periplasmic L-asparaginase II [Escherichia coli O157:H7] SEQ ID n-2035
SEQ ID n° 7250	PL-2821.1	Contig9 from 1578971 to 1580743	p	86%	sp P75838 YCAO_ECOLI HYPOTHETICAL 65.7 KD PROTEIN IN FOCA-SERC INTERGENIC REGION SEQ ID n-2034

TABLEAU II

SEQ ID n° 7251 PL-2820.1	Contig9 from 1581063 to 1581920	p 81%	sp P21501 FOCA_ECOLI PROBABLE FORMATE TRANSPORTER 1 (FORMATE CHANNEL 1) pir A32305 probable formate transport protein - Escherichia coli dbj BAA35639.1 (D90728) Probable formate transporter [Escherichia coli] dbj BAA35648.1 (D90729) Probable formate transporter [Escherichia coli] gb AAC73990.1 (AE000192) probable formate transporter (formate channel 1) [Escherichia coli K12] gb AGS5389.1 AE005279_9 (AE005279) probable formate transporter (formate channel 1) [Escherichia coli O157:H7] SEQ ID n-2033
			sp P09373 PFLB_ECOLI FORMATE ACETYLTRANSFERASE 1 (PYRUVATE FORMATE-LYASE 1) pir S01788 formate C-acetyltransferase (EC 2.3.1.54) 1 - Escherichia coli emb CAA30828.1 (X08035) pyruvate formate-lyase (AA 1-760) [Escherichia coli] dbj BAJ35638.1 (D90728) Formate c- acetyltransferase (EC 2.3.1.54). [Escherichia coli] gb AAC73989.1 (AE000192) formate acetyltransferase 1 [Escherichia coli K12] sp P09374 PFLA_ECOLI PYRUVATE FORMATE-LYASE 1 ACTIVATING ENZYME (PFL-ACTIVATING ENZYME) pir S01789 pyruvate formate-lyase activating enzyme (EC 1.97.1.4), lyase 1- specific - Escherichia coli (strain K-12) emb CAA30829.1 (X08035) pyruvate formate-lyase activating enzyme (AA 1-246) [Escherichia coli] gb AAC73988.1 (AE000192) pyruvate formate lyase activating enzyme 1 [Escherichia coli K12] dbj BAA35637.1 (D90728) Pyruvate formate-lyase 1 activating enzyme (EC 1.97.1.4). [Escherichia coli] gb AGS5387.1 AE005279_7 (AE005279) pyruvate formate lyase activating enzyme 1 [Escherichia coli O157:H7] SEQ ID n-2030
SEQ ID n° 7252 PL-2819.1	Contig9 from 1581976 to 1584358	p 94%	
SEQ ID n° 7253 PL-2818.1	Contig9 from 1584332 to 1585072	p 80%	

TABLEAU II

SEQ ID n° 7254	PL-2817.1	Contig9 from 1585489 to 1586427	m	71%	gb AAF81206.1 AF247502_1 (AF247502) Yt12 [Salmonella dublin]	SEQ ID n-2029
SEQ ID n° 7255	PL-6598.1	Contig9 from 1586905 to 1587174	m	53%	gb AAG54517.1 AE005197_6 (AE005197) 20248 gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7256	PL-2816.2	Contig9 from 1587691 to 1588659	p	60%	pir c81839 probable transposase for IS1655 NMAL481 [imported] - Neisseria meningitidis (group B strain MD58, group A strain Z2491) emb CAB84714.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] emb CAB84719.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491]	#N/A
SEQ ID n° 7257	PL-6597.1	Contig9 from 1588842 to 1589165	p	No Hits found		#N/A
SEQ ID n° 7258	PL-2600.2	Contig9 from 1589204 to 1589776	p	No Hits found		
SEQ ID n° 7259	PL-2601.1	Contig9 from 1591689 to 1593305	m	29%	gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae]	SEQ ID n-2793
SEQ ID n° 7260	PL-2602.1	Contig9 from 1593424 to 1594182	p	39%	pir F83105 hypothetical protein PA4317 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07705.1 AE004848_4 (AE004848) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2794
						SEQ ID n-2795

TABLEAU II

SEQ ID n° 7261	PL-2603.1	Contig9 from 1594278 to 1595567	m	90%	sp P09156 SYS_ECOLI_SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE)..(SERRS) pir YSEC serine-- trna ligase [EC 6.1.1.11] - Escherichia coli emb CAA28673.1 (X05017) seryl-trna synthetase [Escherichia coli] dbj BAA35625.1 (D90727) Serine-TRNA ligase [EC 6.1.1.11] [Escherichia coli] gb AAC73979.1 (AE000191) serine trna synthetase; also charges selenocystein trna with serine [Escherichia coli K12] gb AAG55379.1 AE005278_5 (AE005278) putative polynucleotide enzyme [Escherichia coli O157:H7] SEQ ID n-2796 SEQ ID n-2797
SEQ ID n° 7262	PL-2604.1	Contig9 from 1595799 to 1597142	m	92%	sp P39178 LOLA_ECOLI_OUTER-MEMBRANE LIPOPROTEINS CARRIER PROTEIN PRECURSOR (P20) SEQ ID n-2798
SEQ ID n° 7263	PL-2605.1	Contig9 from 1597150 to 1597761	m	74%	sp P46889 FTSK_ECOLI_CELL DIVISION PROTEIN FTSK pir A64828 cell division protein ftsk - Escherichia coli dbj BAA35615.1 (D90726) Cell division protein ftsk. [Escherichia coli] dbj BAA35622.1 (D90727) cell division protein Ftsk. [Escherichia coli] gb AAC73976.1 (AE000191) cell division protein [Escherichia coli K12] SEQ ID n-2799
SEQ ID n° 7265	PL-6593.1	Contig9 from 1601389 to 1601523	m	No Hits found	#N/A
SEQ ID n° 7266	PL-3895.1	Contig9 from 1601545 to 1602039	m	95%	emb CAA71443.1 (Y10417) lrp [Proteus mirabilis] SEQ ID n-9063
SEQ ID n° 7267	PL-7215.1	Contig9 from 1602172 to 1602330	p	No Hits found	#N/A

TABLEAU II

SEQ ID n° 7268 PL-2607.1	Contig9 from 1602538 to 1603497	p 88%	sp P09625 TRXB_ECOLI THIOREDOKIN REDUCTASE (TRXR) pir RDECT thioredoxin reductase (NADPH) (EC 1.6.4.5) [validated]	SEQ ID n-1800
			Escherichia coli gb AA24697.1 (J03762) thioredoxin reductase [Escherichia coli]	
			dbj BAA35613.1 (D90726) Thioredoxin reductase (NADPH) (EC 1.6.4.5) [Escherichia coli] dbj BAA35620.1 (D90727) Thioredoxin reductase (NADPH) (EC 1.6.4.5) [Escherichia coli] gb AAC73974.1 (AE000190) thioredoxin reductase [Escherichia coli K12]	
SEQ ID n° 7269 PL-2608.1	Contig9 from 1603632 to 1605401	p 82%	gb AAG55375.1 AE005278_1 (AE005278) thioredoxin reductase [Escherichia coli O157:H7] sp Q52402 AARD_PROST TRANSPORT ATP-BINDING PROTEIN AARD pir S70900 ABC-type transport protein aard - Providencia stuartii gb AAB18930.1 (U30383) Aard [Providencia stuartii]	SEQ ID n-1801
			sp P23886 CYDC_ECOLI TRANSPORT ATP-BINDING PROTEIN CYDC pir B36888 ABC-type transport protein cydc - Escherichia coli gb AAA03230.1 (L10383) putative [Escherichia coli]	
			dbj BAA35611.1 (D90726) Probable transport protein mdrH [Escherichia coli] gb AAC73972.1 (AE000190) ATP-binding component of cytochrome- related transport [Escherichia coli K12]	
SEQ ID n° 7270 PL-2609.1	Contig9 from 1605404 to 1607152	p 77%		SEQ ID n-1802

TABLEAU II

WO 02/094867

641

PCT/IB02/03040

SEQ ID n° 7271 PL-2610.1	Contig9 from 1607156 to 1607851	p	71%	sp P23885 LPTP_ECOLI_LEUCYL-PHENYLALANYL-TRNA-- PROTEIN TRANSFERASE pir [A36888 leucyl, phenylalanyl]-trna--protein transferase (EC 2.3.2.-) - Escherichia coli gb AAA03231.1 (L10383) Leu/Phe-trna-protein transferase [Escherichia coli] gb AAC36910.1 (M63145) orf 2 [Escherichia coli] dbj BAA35610.1 (D90726) Leucyltransferase (EC 2.3.2.6). [Escherichia coli] gb AAC73971.1 (AE000190) leucyl, phenylalanyl-trna-protein transferase [Escherichia coli K12] SEQ ID n°1804
SEQ ID n° 7272 PL-6591.1	Contig9 from 1608008 to 1608226	p	98%	sp P02998 IF1_ECOLI_TRANSLATION_INITIATION FACTOR IF-1 pir [FIEC1 translation initiation factor IF-1 - Escherichia coli emb CAA68446.1 (Y00373) initiation factor IF1 (AA 1 -72) [Escherichia coli] gb AAA03232.1 (L10383) putative [Escherichia coli] dbj BAA35602.1 (D90725) Translation initiation factor IF-1 [Escherichia coli] dbj BAA35607.1 (D90726) Translation initiation factor IF-1 [Escherichia coli] gb AAC73970.1 (AE000190) protein chain initiation factor IF-1 [Escherichia coli K12] gb AAG55371.1 AE005277_12 (AE005277) protein chain initiation factor IF-1 [Escherichia coli] O157:H7 sp P15716 CLPA_ECOLI_ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA pir [SUECCA endopeptidase Clp ATP-binding chain A - Escherichia coli dbj BAA35601.1 (D90725) ATP- dependent Clp protease ATP-binding subunit ClpA. [Escherichia coli] gb AAC73969.1 (AE000190) ATP-binding component of serine protease [Escherichia coli K12] gb AAG55264.1 AE005269_8 (AE005269) ATP-binding component of serine protease [Escherichia coli O157:H7] SEQ ID n°1805
SEQ ID n° 7273 PL-2611.1	Contig9 from 1608326 to 1610602	m	89%	

TABLEAU II

SEQ ID n° 7274	PL-6589.1	Contig9 from 1610635 to 1610955	m	77%	sp P75832 YLJA_ECOLI PROTEIN YLJA pir A64827 ylja protein - Escherichia coli gb AAC73968.1 (AE000190) orf, hypothetical protein [Escherichia coli K12] dbj BAA35600.1 (D90725) ORF_ID:0213#6 [Escherichia coli] gb AAG55263.1 AE005269_7 (AE005269) orf, hypothetical protein [Escherichia coli O157:H7] sp P24245 CSPD_ECOLI COLD SHOCK-LIKE PROTEIN CSPD (CSP-D) pir H64826 cold shock protein homolog cspD - Escherichia coli dbj BAA35599.1 (D90725) Cold shock-like protein CspD. [Escherichia coli] gb AAC73967.1 (AE000190) cold shock protein [Escherichia coli K12] gb AAG55262.1 AE005269_6 (AE005269) cold shock protein [Escherichia coli O157:H7] sp P75831 YBJZ_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBJZ pir G64826 probable ABC transporter ybjZ - Escherichia coli gb AAC73966.1 (AE000189) putative ATP-binding component of a transport system [Escherichia coli K12] dbj BAA35598.1 (D90725) ABC transporter probable ATP-binding subunit homolog [Escherichia coli]	#N/A
SEQ ID n° 7275	PL-6588.1	Contig9 from 1611298 to 1611519	p	60%	gb AAG55260.1 AE005269_4 (AE005269) putative membrane protein [Escherichia coli O157:H7] sp P75826 YBJE_ECOLI HYPOTHETICAL 34.4 KD PROTEIN IN POXB-AQEZ INTERGENIC REGION pir B64826 probable membrane protein ybjE - Escherichia coli gb AAC73961.1 (AE000189) putative surface protein [Escherichia coli K12]	SEQ ID n-2806 SEQ ID n-2807 SEQ ID n-2808
SEQ ID n° 7276	PL-2612.2	Contig9 from 1611600 to 1613543	m	80%		
SEQ ID n° 7277	PL-2613.1	Contig9 from 1613543 to 1614655	m	73%		
SEQ ID n° 7278	PL-2614.1	Contig9 from 1614976 to 1615875	p	76%		

TABLEAU II

SEQ ID n° 7279	PL-2615.1	Contig9 from 1616179 to 1616907	p	86%	sp P30858 ARTP_ECOLI ARGININE TRANSPORT ATP-BINDING PROTEIN ARTP pir H64824 arginine transport protein artp - Escherichia coli dbj BAA35578.1 (D90724) Periplasmic transport system protein artp. [Escherichia coli] gb AAC73951.1 (AE000188) ATP-binding component of 3rd arginine transport system [Escherichia coli K12] gb AGS5243.1 AE005267_8 (AE005267) ATP-binding component of 3rd arginine transport system [Escherichia coli K12] gb H7	SEQ ID n° 1809
SEQ ID n° 7280	PL-2616.1	Contig9 from 1616927 to 1617661	p	82%	sp P30859 ARTI_ECOLI ARGININE-BINDING PERIPLASMIC PROTEIN 1 PRECURSOR pir G64824 arginine-binding periplasmic protein 1 precursor - Escherichia coli dbj BAA35577.1 (D90724) Arginine binding protein artI [Escherichia coli] gb AAC73950.1 (AE000188) arginine 3rd transport system periplasmic binding protein [Escherichia coli K12]	SEQ ID n° 1810
SEQ ID n° 7281	PL-2617.1	Contig9 from 1617676 to 1618392	p	84%	sp P30861 ARTQ_ECOLI ARGININE TRANSPORT SYSTEM PERMEASE PROTEIN ARTQ pir F64824 arginine transport system permease protein artQ - Escherichia coli dbj BAA35576.1 (D90724) Arginine transport system protein ArtQ. [Escherichia coli] gb AAC73949.1 (AE000188) arginine 3rd transport system permease protein [Escherichia coli K12]	SEQ ID n° 1811

TABLEAU II

SEQ ID n° 7282 PL-2618.1	Contig9 from 1618392 to 1619060	p 84%	sp P30862 ARTM_ECOLI ARGININE TRANSPORT SYSTEM PERMEASE PROTEIN ARTM pir [E64824 arginine transport system permease protein artm - Escherichia coli dbj BAA35575.1 (D90724) Arginine transport system protein ArtM. [Escherichia coli] gb AAC73948.1 (AE000188) arginine 3rd transport system permease protein [Escherichia coli K12] gb AAG55240.1 AE005267_5 (AE005267) arginine 3rd transport system permease protein [Escherichia coli O157:H7]	SEQ ID n°1812
SEQ ID n° 7283 PL-2619.3	Contig9 from 1619114 to 1620247	m 77%	sp P75817 YBJF_ECOLI HYPOTHETICAL RNA METHYLTRANSFERASE IN POTI-ARTJ INTERGENIC REGION pir [C64824 probable RNA methyltransferase ybjf Escherichia coli gb AAC73946.1 (AE000187) putative enzyme [Escherichia coli K12] dbj BAA35573.1 (D90724) Hypothetical RNA methyltransferase HI0958 (BC 2.1.1.-). [Escherichia coli]	#N/A
SEQ ID n° 7284 PL-3894.2	Contig9 from 1620272 to 1620784	m 74%	sp P75815 YBJN_ECOLI HYPOTHETICAL 17.7 KDA PROTEIN IN RIMK-POTF INTERGENIC REGION pir [E64823 hypothetical protein ybjn - Escherichia coli gb AAC73940.1 (AE000187) putative sensory transduction regulator [Escherichia coli K12] dbj BAA35564.1 (D90723) ORF_ID:c210#11 [Escherichia coli]	#N/A
SEQ ID n° 7285 PL-6585.1	Contig9 from 1620876 to 1621178	m 39%	gb AAG55226.1 AE005266_5 (AE005266) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7286 PL-6583.1	Contig9 from 1621369 to 1621629	p 83%	pir [G82236 glutaredoxin 1 VC1146 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94305.1 (AE004194) glutaredoxin 1 [Vibrio cholerae]	#N/A

TABLEAU II

SEQ ID n° 7287	PL-7214.1	Contig9 from 1621862 to 1622047	p	No Hits found	#N/A
SEQ ID n° 7288	PL-2620.1	Contig9 from 1622178 to 1622786	p	65%	gb AAG55217.1 AE005265_7 (AE005265) orf, hypothetical protein [Escherichia coli O157:H7] sp P36559 SDAC_ECOLI_SERINE_TRANSPORTER pir S45633 serine transport protein sdac - Escherichia coli gb AAA50169.1 (U01233) putative serine transporter [Escherichia coli] gb AAB40446.1 (U29581) putative serine transporter [Escherichia coli] gb AAC75838.1 (AE000363) probable serine transporter [Escherichia coli K12] gb AAG57910.1 AE005508_1 (AE005508) probable serine transporter [Escherichia coli O157:H7] SEQ ID n-3815
SEQ ID n° 7289	PL-2621.1	Contig9 from 1623693 to 1624991	p	87%	sp P36559 SDAC_ECOLI_SERINE_TRANSPORTER pir S45633 serine transport protein sdac - Escherichia coli gb AAA50169.1 (U01233) putative serine transporter [Escherichia coli] gb AAB40446.1 (U29581) putative serine transporter [Escherichia coli] gb AAC75838.1 (AE000363) probable serine transporter [Escherichia coli K12] gb AAG57910.1 AE005508_1 (AE005508) probable serine transporter [Escherichia coli O157:H7] SEQ ID n-3816
SEQ ID n° 7290	PL-2622.2	Contig9 from 1625069 to 1625890	m	No Hits found	#N/A
SEQ ID n° 7291	PL-6581.1	Contig9 from 1626604 to 1626918	p	81%	gb AAA27616.1 (M97630) crystalline inclusion protein type II [Xenorhabdus luminescens] #N/A
SEQ ID n° 7292	PL-6580.1	Contig9 from 1628069 to 1628407	p	No Hits found	#N/A
SEQ ID n° 7293	PL-2623.1	Contig9 from 1628995 to 1629849	p	No Hits found	SEQ ID n-3818

TABLEAU II

SEQ ID n° 7294 PL-2624.2	Contig9 from 1630066 to 1631268	m	77%	sp P08506 DACC_ECOLI_PENICILLIN-BINDING PROTEIN 6 PRECURSOR (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE FRACTION C) (DD-PEPTIDASE) (DD-CARBOXYPEPTIDASE) (PBP-6) pir G64821 serine-type D-Ala-D-Ala carboxypeptidase (EC 3.4.16.4) dacC precursor - Escherichia coli dbj BAA35542.1 (D90722) Penicillin-binding protein 6 precursor. [Escherichia coli] gb AAC73926.1 (AE000186) D- alanyl-D-alanine carboxypeptidase; penicillin- binding protein 6 [Escherichia coli K12]	#N/A
SEQ ID n° 7295 PL-2625.1	Contig9 from 1631702 to 1632322	p	64%	pir C83294 probable glutathione S-transferase PA2813 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06201.1 AE004708_7 (AE004708) probable glutathione S-transferase [Pseudomonas aeruginosa] sp P76370 YEEZ_ECOLI_PROTEIN YEEZ PRECURSOR pir G64966 hypothetical protein b2016 - Escherichia coli gb AAC75077.1 (AE000293) putative enzyme of sugar metabolism [Escherichia coli K12]	SEQ ID n-1820
SEQ ID n° 7296 PL-2626.1	Contig9 from 1632329 to 1633156	m	66%	sp P10366 HIS1_ECOLI_ATP PHOSPHORIBOSYLTRANSFERASE pir I56436 ATP phosphoribosyltransferase - Escherichia coli pir XREC ATP phosphoribosyltransferase (EC 2.4.2.17) - Escherichia coli emb CAA45224.1 (X63697) ATP-phosphoribosyl transferase [Escherichia coli] gb AA19742.1 (U02070) ATP phosphoribosyltransferase [Escherichia coli] dbj BAA15850.1 (D90840) ATP phosphoribosyltransferase (EC 2.4.2.17) . [Escherichia coli] gb AAC75080.1 (AE000293) ATP phosphoribosyltransferase [Escherichia coli K12]	SEQ ID n-1821
SEQ ID n° 7297 PL-2627.1	Contig9 from 1633585 to 1634496	p	90%		SEQ ID n-1822

TABLEAU II

SEQ ID n° 7298	PL-2628.1	Contig9 from 1634503 to 1636926	p 43%	sp P10370 HISX_SALTY HISTIDINOL DEHYDROGENASE (HDH) pir DEEBHT histidinol dehydrogenase (EC 1.1.1.23) - Salmonella typhimurium emb CAA31823.1 (X13464) hisD ORF (AA 1-434) [Salmonella typhimurium] gb AA88615.1 (J01804) histidinol dehydrogenase [Salmonella typhimurium] gb AAA73023.1 (M64753) histidinol dehydrogenase [unidentified cloning vector] gb AAA73024.1 (M64754) histidinol dehydrogenase [unidentified cloning vector] gb AAG57081.1 AE005427_9 (AE005427) imidazoleglycerolphosphate dehydratase and histidinol-phosphate phosphatase [Escherichia coli O157:H7] SEQ ID n° 1823
SEQ ID n° 7299	PL-2629.1	Contig9 from 1636926 to 1637993	p 84%	sp P10375 HIS5_ECOLI AMIDOTRANSFERASE HIS5 pir XQECHH imidazole glycerol phosphate synthase (EC 2.4.2.-) chain hisH - Escherichia coli emb CAA31815.1 (X13462) hisH ORF (AA 1-196) [Escherichia coli] dbj BAAL5854.1 (D90840) Amidotransferase HisH (EC 2.4.2.-) [Escherichia coli] dbj BAA15862.1 (D90841) Amidotransferase HisH (EC 2.4.2.-) [Escherichia coli] gb AAC75084.1 (AE000293) glutamine amidotransferase subunit of heterodimer with HisF = imidazole glycerol phosphate synthase holoenzyme [Escherichia coli K12] dbj BAA77742.1 (AB008676) aminotransferase [Escherichia coli] gb AAG57083.1 AE005427_11 (AE005427) N-(5'- phospho-L-ribosyl-formimino)-5-amino-1-(5'- phosphoribosyl)-4-imidazolecarboxamide isomerase [Escherichia coli O157:H7] sp P10374 HIS6_SALTY HISF PROTEIN (CYCLASE) pir OYEBHF cyclase hisF - Salmonella typhimurium emb CAA31828.1 (X13464) hisF ORF (AA 1-258) [Salmonella typhimurium] SEQ ID n° 1828
SEQ ID n° 7300	PL-2630.1	Contig9 from 1637993 to 1638598	p 69%	
SEQ ID n° 7301	PL-2631.1	Contig9 from 1638604 to 1639341	p 77%	
SEQ ID n° 7302	PL-2632.1	Contig9 from 1639323 to 1640099	p 89%	

TABLEAU II

SEQ ID n° 7303	PL-2633.1	Contig9 from 1640093 to 1640698	p 81%	dbj BAA77739.1 (AB008676) phosphoribosyl-AMP cyclohydrolase [Escherichia coli] gb AAG57085.1 AE005427_13 (AE005427) phosphoribosyl-amp cyclohydrolase; phosphoribosyl-ATP [Escherichia coli O157:H7] pyrophosphatase [Escherichia coli O157:H7]	SEQ ID n-1829
SEQ ID n° 7304	PL-2634.1	Contig9 from 1640980 to 1642131	m 79%	gb AAG58733.1 AE005585_7 (AE005585) putative oxidoreductase [Escherichia coli O157:H7] sp P76238 YEAK_ECOLI HYPOTHETICAL 17.9 KD PROTEIN IN GAP-RND INTERGENIC REGION pir [C64939 hypothetical protein b1787 - Escherichia coli (strain K-12) gb AAC74857.1 (AE000273) orf, hypothetical protein [Escherichia coli K12] gb AAG56776.1 AE005402_2 (AE005402) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-1830
SEQ ID n° 7305	PL-3893.1	Contig9 from 1642553 to 1643044	p 71%	sp P54657 CAD1_DICDI CALCIUM-DEPENDENT CELL ADHESION MOLECULE-1 (DDCAD-1) (GP24) gb AAC47135.1 (U49650) dictyostelium discoideum calcium-dependent cell adhesion molecule-1 DDCAD-1 [Dictyostelium discoideum] sp P14062 6PGD_SALTY 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING pir [S04397 phosphoglucuronate dehydrogenase (decarboxylating) (EC 1.1.1.44) - Salmonella typhimurium emb CAA33677.1 (X15651) 6- phosphoglucuronate dehydrogenase (AA 1-468) [Salmonella enterica] gb AAA27137.1 (M64332) 6-phosphoglucuronate dehydrogenase [Salmonella typhimurium]	SEQ ID n-1831
SEQ ID n° 7307	PL-2636.1	Contig9 from 1644930 to 1646336	m 89%	sp P76389 YEGH_ECOLI HYPOTHETICAL 59.5 KDA PROTEIN IN WZA-ASMA INTERGENIC REGION	SEQ ID n-1832
SEQ ID n° 7308	PL-2637.1	Contig9 from 1646582 to 1648153	p 83%		SEQ ID n-1833

TABLEAU II

SEQ ID n° 7309	PL-2638.1	Contig9 from 1648644 to 1650476	m	61%	gb AAG57126.1 AE005432_7 (AE005432) suppressor of ompF assembly mutants [Escherichia coli O157:H7]	SEQ ID n° 1834
SEQ ID n° 7310	PL-2639.1	Contig9 from 1650535 to 1651116	m	79%	gb AAG57127.1 AE005432_8 (AE005432) 2'- deoxycytidine 5'-triphosphate deaminase [Escherichia coli O157:H7]	SEQ ID n° 1835
SEQ ID n° 7311	PL-2640.1	Contig9 from 1651170 to 1651811	m	78%	pir [A64973 uridine kinase (EC 2.7.1.48) - Escherichia coli gb AAC75127.1 (AE000296) uridine/cytidine kinase [Escherichia coli K12] gb AAG57128.1 AE005432_9 (AE005432) uridine/cytidine kinase [Escherichia coli O157:H7]	SEQ ID n° 1837
SEQ ID n° 7312	PL-2641.1	Contig9 from 1652069 to 1653181	m	85%	pir [H64978 probable ATPase mrp - Escherichia coli gb AAA60527.1 (U000007) mrp [Escherichia coli] gb AAC75174.1 (AE000300) putative ATPase [Escherichia coli K12] prf [2014253F ATPase [Escherichia coli]	SEQ ID n° 1838
SEQ ID n° 7313	PL-2643.1	Contig9 from 1653443 to 1655470	p	89%	gb AAG57175.1 AE005437_10 (AE005437) methionine tRNA synthetase [Escherichia coli O157:H7] pir [B83613 secreted protein Hcp PA0263 [imported] - Pseudomonas aeruginosa (strain PA01) pir [C83455 secreted protein Hcp PAJ512 [imported] - Pseudomonas aeruginosa (strain PA01) pir [G82987 secreted protein Hcp PAS267 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03652.1 AE004464_5 (AE004464) secreted protein Hcp [Pseudomonas aeruginosa] gb AAG04901.1 AE004580_1 (AE004580) secreted protein Hcp [Pseudomonas aeruginosa] gb AAG08652.1 AE004939_4 (AE004939) secreted protein Hcp [Pseudomonas aeruginosa]	SEQ ID n° 1839
SEQ ID n° 7314	PL-3892.1	Contig9 from 1656211 to 1656519	p	48%		SEQ ID n° 3060
SEQ ID n° 7315	PL-6574.1	Contig9 from 1656546 to 1656701	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 7316	PL-2644.1	Contig9 from 1656793 to 1657329	m	No Hits found	SEQ ID n-1840
SEQ ID n° 7317	PL-3891.1	Contig9 from 1657613 to 1658050	p	52%	SEQ ID n-3059
SEQ ID n° 7318	PL-2645.1	Contig9 from 1658053 to 1658748	p	84%	SEQ ID n-1841
SEQ ID n° 7319	PL-2646.1	Contig9 from 1658890 to 1659774	p	62%	SEQ ID n-1842

gb|AA057279.1|AE005446_7 (AE005446)orf,
 hypothetical protein [Escherichia coli O157:H7]
 sp|P33373|YOHK_ECOLI-HYPOTHETICAL 24.5 KD
 PROTEIN IN PBPG-CDD INTERGENIC REGION
 pir||E64982 yohk protein - Escherichia coli
 (strain K-12) gb|AAC75203.1| (AE000303)
 putative serotonin transporter [Escherichia coli
 K12]
 sp|F13652|CDD_ECOLI CYTIDINE DEAMINASE (CYTIDINE
 AMINOHYDROLASE) (Cda) pir||F64982 cytidine
 deaminase (EC 3.5.4.5) - Escherichia coli
 pdb|1C7T| Cytidine Deaminase (Cda)
 (E.C.3.5.4.5) Complexed With 3,4-
 Dihydrozebularine (Dhz) pdb|1AF2|A Chain A,
 Crystal Structure Of Cytidine Deaminase
 Complexed With Uridine pdb|1ALN|
 Crystal Structure Of Cytidine Deaminase
 Complexed With 3-Deazacytidine
 pdb|1CTU| Cytidine Deaminase (Cda)
 (E.C.3.5.4.5) Complexed With 3,4 Hydrated
 Pyrimidine-2-One Riboside (Zeb) gb|AA23542.1|
 (M60916) cytidine deaminase [Escherichia coli]
 gb|AAA60533.1| (U00007) cytidine deaminase
 [Escherichia coli] gb|AAC75204.1| (AE000303)
 cytidine/deoxycytidine deaminase [Escherichia
 coli K12] prf||2014253BU cytidine deaminase
 [Escherichia coli]

TABLEAU II

SEQ ID n° 7320 PL-2647.1	Contig9 from 1660025 to 1661722	p	77%	sp P26616 NAO1_ECOLI_NAD-DEPENDENT MALIC ENZYME (NAD-ME) pir B64901 malate dehydrogenase (oxaloacetate-decarboxylating) (EC 1.1.1.38), NAD-linked - Escherichia coli dbj BAA15127.1 (D90788) SfcA protein (fragment). [Escherichia coli] dbj BAA15136.1 (D90789) SfcA protein (fragment). [Escherichia coli] dbj BAA15145.1 (D90790) SfcA protein (fragment). [Escherichia coli] gb AAC74552.1 (AE000245) NAD-linked malate dehydrogenase (malic enzyme) [Escherichia coli K12]	SEQ ID n-1843
SEQ ID n° 7321 PL-2648.1	Contig9 from 1661989 to 1662729	p	80%	sp P33017 SANA_ECOLI_SANA PROTEIN pir G64982 sana protein - Escherichia coli (strain K-12) gb AAC75205.1 (AE000303) vancomycin sensitivity [Escherichia coli K12] gb AAG57282.1 AE005446_10 (AE005446) vancomycin sensitivity [Escherichia coli O157:H7]	SEQ ID n-1844
SEQ ID n° 7322 PL-2649.1	Contig9 from 1662701 to 1663825	m	62%	gb AAG57290.1 AE005447_5 (AE005447) 23408 gene product [Escherichia coli O157:H7] sp P27511 GCH1_ECOLI_GTP CYCLOHYDROLASE I (GTP- CH-I) pir H64983 GTP cyclohydrolase I (EC 3.5.4.16) [validated] - Escherichia coli emb CAA45365.1 (X63910) GTP cyclohydrolase I [Escherichia coli] gb AAA60535.1 (U00007) GTP cyclohydrolase I [Escherichia coli] gb AAC75214.1 (AE000304) GTP cyclohydrolase I [Escherichia coli K12] gb AAG57291.1 AE005447_6 (AE005447) GTP cyclohydrolase I [Escherichia coli O157:H7] prf 2014253AX GTP cyclohydrolase I [Escherichia coli] pir C83470 hypothetical protein PA1412 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04801.1 AE004570_9 (AE004570) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-1845
SEQ ID n° 7323 PL-2650.1	Contig9 from 1663871 to 1664530	m	85%		
SEQ ID n° 7324 PL-2651.1	Contig9 from 1664724 to 1665896	m	55%		

TABLEAU II

SEQ ID n° 7325	PL-2652.1	Contig9 from 1666396 to 1667142	p	53%	dbj BAB06210.1 (AF001515) 3-oxoacyl-(acyl- carrier protein) reductase [Bacillus halodurans]	SEQ ID n° 1849
SEQ ID n° 7326	PL-2653.1	Contig9 from 1667364 to 1668605	p	77%	gb AAG55200.1 AE005263_9 (AE005263) molybdopterin biosynthesis [Escherichia coli O157:H7]	SEQ ID n° 1850
SEQ ID n° 7327	PL-2654.1	Contig9 from 1668605 to 1669357	p	78%	sp P12282 MOEB_ECOLI MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN pir B32352 molybdopterin biosynthesis protein moeb - Escherichia coli gb AAA23580.1 (M21151) chlN protein [Escherichia coli] dbj BAA35514.1 (D90720) Molybdopterin biosynthesis Moeb protein. [Escherichia coli] dbj BAA35521.1 (D90721) Molybdopterin biosynthesis Moeb protein. [Escherichia coli] gb AAC73913.1 (AE000185) molybdopterin biosynthesis [Escherichia coli K12] sp P75790 YBIT_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBIT	SEQ ID n° 1851
SEQ ID n° 7328	PL-2655.3	Contig9 from 1669456 to 1671051	m	85%	pir D64819 probable ABC-type transport protein ybit - Escherichia coli gb AAC73907.1 (AE000184) putative ATP-binding component of a transport system [Escherichia coli K12] dbj BAA35501.1 (D90719) Hypothetical protein HI0658 [Escherichia coli] dbj BAA35508.1 (D90720) Hypothetical protein HI0658 [Escherichia coli] gb AAG55192.1 AE005263_1 (AE005263) putative ATP- binding component of a transport system [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7329	PL-3940.2	Contig9 from 1672156 to 1672566	p	No Hits found		#N/A
SEQ ID n° 7330	PL-3183.2	Contig9 from 1672885 to 1673448	m	74%	dbj BAB06803.1 (AF001517) BH3084-unknown conserved protein [Bacillus halodurans]	#N/A

SEQ ID n°	Contig9 from	m	No Hits found	#N/A
SEQ ID n° 7331 PL-6571.1	1674055 to 1674141			
				pir E64818 probable membrane protein ybif - Escherichia coli gb AAC73900.1 (AE000183) putative transmembrane subunit [Escherichia coli X12] dbj BAA35485.1 (D90718) Hypothetical protein 1 [Escherichia coli] dbj BAA35495.1 (D90719) Hypothetical protein 1 [Escherichia coli] gb AAG55185.1 AE005262_5 (AE005262) putative transmembrane subunit [Escherichia coli O157:H7]
SEQ ID n° 7332 PL-3182.1	1674128 to 1675021	p	77%	SEQ ID n-2431
SEQ ID n° 7333 PL-6570.1	1675316 to 1675663	p	84%	
				pir I69619 pexB protein - Escherichia coli gb AAA21955.1 (U04242) PexB [Escherichia coli] pir H81436 phnA-like protein Cj0185c [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB72668.1 (AL139074) phnA-like protein [Campylobacter jejuni]
SEQ ID n° 7334 PL-6569.1	1675955 to 1676176	p	65%	#N/A
SEQ ID n° 7335 PL-3181.1	1676581 to 1677276	p	37%	SEQ ID n-2430
				pir D70329 hypothetical protein aq_327 - Aquifex aeolicus gb AAC06629.1 (AE000684) putative protein [Aquifex aeolicus] pir D69790 probable halide peroxidase (EC 1.11.1.-) ydJP - Bacillus subtilis dbj BAA22772.1 (AB007638) peroxidase [Bacillus subtilis] emb CAB12447.1 (Z99107) similar to arylesterase [Bacillus subtilis]
SEQ ID n° 7336 PL-3180.1	1677341 to 1678279	p	38%	SEQ ID n-2429
				gb AAF13753.1 AF117351_10 (AF117351) dihydroadipicolinate synthetase [Zymomonas mobilis]
SEQ ID n° 7337 PL-3179.1	1678296 to 1679189	p	55%	SEQ ID n-2427
				ref NP_061701.1 hypothetical protein [Xylella fastidiosa] pir E82866 hypothetical protein Xfa0046 [imported] - Xylella fastidiosa (strain 9a5c) gb AAP85614.1 AE003851_45 (AE003851) hypothetical protein [Xylella fastidiosa]
SEQ ID n° 7338 PL-6567.1	1679261 to 1679560	p	41%	#N/A

TABLEAU II

SEQ ID n° 7339	PL-6566.1	Contig9 from 1679668 to 1680000	m	31%	ref NP_058361.1 putative transposase [Salmonella typhi] gb AAF69986.1 AF250878_147 (AF250878) putative transposase [Salmonella typhi]	#N/A
SEQ ID n° 7340	PL-3178.1	Contig9 from 1680307 to 1681113	p	85%	gb AAG54503.1 AE005196_1 (AE005196) putative aldose reductase (EC 1.1.1.21) [Escherichia coli O157:H7]	SEQ ID n-2426
SEQ ID n° 7341	PL-3177.1	Contig9 from 1681376 to 1682488	p	81%	pir B83480 probable oxidoreductase PA1334 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04723.1 AE004562_10 (AE004562) probable oxidoreductase [Pseudomonas aeruginosa]	SEQ ID n-2425
SEQ ID n° 7342	PL-3176.1	Contig9 from 1682622 to 1683530	m	82%	gb AAG54504.1 AE005196_2 (AE005196) putative transcriptional regulator LYSR-type [Escherichia coli O157:H7]	SEQ ID n-2424
SEQ ID n° 7343	PL-3175.1	Contig9 from 1683530 to 1685677	m	76%	gb AAG55171.1 AE005261_1 (AE005261) putative ATP- dependent helicase [Escherichia coli O157:H7]	SEQ ID n-2423
SEQ ID n° 7344	PL-3174.1	Contig9 from 1686073 to 1686909	p	58%	gb AAG57635.1 AE005482_2 (AE005482) putative thiosulfate sulfurtransferase [Escherichia coli O157:H7]	SEQ ID n-2422
SEQ ID n° 7345	PL-3939.1	Contig9 from 1687019 to 1687591	p	59%	ref NP_052816.1 pXO1-120 [Bacillus anthracis] pir H59105 hypothetical protein pXO1-120 - Bacillus anthracis virulence plasmid pXO1 gb AAD32424.1 AAD32424 (AF065404) pXO1-120 [Bacillus anthracis]	SEQ ID n-3099
SEQ ID n° 7346	PL-3938.1	Contig9 from 1687708 to 1688412	p	42%	dbj BAB16031.1 (AB030747) transposase [Streptococcus pyogenes]	SEQ ID n-3098
SEQ ID n° 7347	PL-1787.1	Contig9 from 1689123 to 1690247	p	20%	emb CAA70510.1 (Y09330) ferulic acid esterase A [Aspergillus niger]	SEQ ID n-906
SEQ ID n° 7348	PL-1788.1	Contig9 from 1690842 to 1691960	p	15%	emb CAC15040.1 (AJ012575) triacylglycerol lipase [Candida ernobii]	SEQ ID n-907

TABLEAU II

SEQ ID n° 7349	PL-1789.1	Contig9 from 1692331 to 1693461	P. 18%	gb AAB07724.1 (U55867) Ipomoea nil Pn47p	SEQ ID n-908
SEQ ID n° 7350	PL-1790.1	Contig9 from 1693870 to 1694988	P. No Hits found		SEQ ID n-910
SEQ ID n° 7351	PL-1791.1	Contig9 from 1695297 to 1696355	P. 64%	emb CAA40809.1 (X57583) mccb [Escherichia coli]	SEQ ID n-911
SEQ ID n° 7352	PL-1792.1	Contig9 from 1696382 to 1697527	P. 43%	pir E64665 tetracycline resistance protein tetA(P) homolog Helicobacter pylori (strain 26695) gb AAD08210.1 (AE000622) tetracycline resistance protein tetA(P), putative [Helicobacter pylori 26695] SEQ ID n-912 pir D69887 conserved hypothetical protein ynaD Bacillus subtilis gb AAB41084.1 (U66480) ynaD [Bacillus subtilis] emb CAB13636.1 (Z99113) similar to hypothetical proteins [Bacillus subtilis] sp P33371 YOHI_ECOLI HYPOTHETICAL 35.2 KD PROTEIN IN PBP-CDD INTERGENIC REGION pir C64982 hypothetical 35.2 kD protein in pbpg- cdd intergenic region - Escherichia coli (strain K-12) gb AA60503.1 (U00007) yohi [Escherichia coli] gb AAC75201.1 (AE000303) putative regulator protein [Escherichia coli K12] prf 2014253AN yohi gene [Escherichia coli]	SEQ ID n-913
SEQ ID n° 7353	PL-3937.1	Contig9 from 1697509 to 1698051	P. 41%		
SEQ ID n° 7354	PL-1793.1	Contig9 from 1698285 to 1699217	M. 91%		

TABLEAU II

SEQ ID n° 7355	PL-1794.1	Contig9 from 1699221 to 1700525	m	84%	sp P25888 RHLE_ECOLI PUTATIVE ATP-DEPENDENT RNA HELICASE RHLE pir B64816 probable ATP- dependent RNA helicase rhle - Escherichia coli gb AA53653.1 (I02123) ATP-dependent RNA helicase [Escherichia coli] dbj BAA35463.1 (D90717) Putative ATP-dependent RNA helicase RHLE. [Escherichia coli] SEQ ID n-914
SEQ ID n° 7356	PL-1795.1	Contig9 from 1700803 to 1701495	p	63%	gb AAC73884.1 (AE000182) putative ATP-dependent RNA helicase [Escherichia coli K12] dbj BAA35457.1 (D90716) Putative ATP-dependent RNA helicase RHLE. [Escherichia coli] SEQ ID n-914 pir D64816 probable transcription regulator ybiH - Escherichia coli gb AAC73883.1 (AE000181) putative transcriptional regulator [Escherichia coli K12] gb AAG55167.1 AE005260_6 (AE005260) putative transcriptional regulator [Escherichia coli O157:H7] SEQ ID n-915
SEQ ID n° 7357	PL-1796.1	Contig9 from 1701512 to 1702504	p	75%	pir C64816 hypothetical protein b0795 precursor - Escherichia coli gb AAC73882.1 (AE000181) putative membrane protein [Escherichia coli K12] dbj BAA35455.1 (D90716) Hypothetical protein f355 [Escherichia coli] dbj BAA35461.1 (D90717) Hypothetical protein f355 [Escherichia coli] SEQ ID n-916
SEQ ID n° 7358	PL-1797.1	Contig9 from 1702514 to 1704253	p	82%	sp P75776 YBHF_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBHF gb AAG50553.1 AF250767_1 (AF250767) Elad [uncultured bacterium pCosFS1] SEQ ID n-917
SEQ ID n° 7359	PL-1798.1	Contig9 from 1704250 to 1705410	p	84%	sp P75774 YBHR_ECOLI HYPOTHETICAL 41.6 KDA PROTEIN IN MOAE-RHLE INTERGENIC REGION pir H64815 ybhr protein - Escherichia coli gb AAC73879.1 (AE000181) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-918
SEQ ID n° 7360	PL-1799.1	Contig9 from 1705423 to 1706529	p	86%	protein [Escherichia coli K12] SEQ ID n-919

TABLEAU II

SEQ ID n° 7361	PL-1800.1	Contig9 from 1706816 to 1707970	m	40%	pir S44207 hypothetical protein 337 - Coxiella burnetii	SEQ ID n-922
SEQ ID n° 7362	PL-1801.3	Contig9 from 1708078 to 1709424	m	34%	emb CAB71247.1 (A1138598) 2-amino-3- ketobutyrate coenzyme A ligase. [Streptomyces coelicolor A3(2)]	#N/A
SEQ ID n° 7363	PL-1802.1	Contig9 from 1710137 to 1710847	m	80%	sp P75768 YBHL_ECOLI HYPOTHETICAL 25.9 KDA PROTEIN IN MOAE-RHLE INTERGENIC REGION pir [B64815 ybhl protein - Escherichia coli gb AAC73873.1 (AE000181) orf, hypothetical protein-[Escherichia coli K12] dbj BAA35444.1 (D90716) Hypothetical protein, 23.5K	SEQ ID n-924
SEQ ID n° 7364	PL-3936.1	Contig9 from 1711030 to 1711482	m	84%	sp P30749 MOAE_ECOLI MOLYBDOPTERIN [MPT] CONVERTING FACTOR, SUBUNIT 2 (MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN E) (MOLYBDOPTERIN CONVERTING FACTOR LARGE SUBUNIT) pir [S31883 molybdopterin biosynthesis protein E chain [validated] - Escherichia coli emb CAA49865.1 (X70420) moae [Escherichia coli] gb AAC73872.1 (AE000181) molybdopterin converting factor, subunit 2 [Escherichia coli K12] dbj BAA35443.1 (D90716) Molybdopterin-converting factor 16k chain [Escherichia coli]	SEQ ID n-3096
SEQ ID n° 7365	PL-6556.1	Contig9 from 1711486 to 1711731	m	78%	gb AGS5155.1 AE005259_6 (AE005259) molybdopterin biosynthesis [Escherichia coli O157:H7]	#N/A

TABLEAU II

SEQ ID n° 7366	PL-3935.1	1711728 to 1712207	m	84%	Contig9 from	sp P30747 MOAC_ECOLI MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN C pir [G64814 molybdenum cofactor biosynthesis.protein_C-[validated] - Escherichia coli dbj BAA35441.1 (D90716) Moac protein. [Escherichia coli] gb AAC73870.1 (AE000181) molybdopterin biosynthesis, protein C [Escherichia coli K12] gb AAG55154.1 AE005259_5 (AE005259) molybdopterin biosynthesis, protein C [Escherichia coli O157:H7] gb AAG55152.1 AE005259_3 (AE005259) molybdopterin biosynthesis, protein A [Escherichia coli O157:H7]	SEQ ID n-9095
SEQ ID n° 7367	PL-1803.1	1712247 to 1713230	m	79%	Contig9 from	sp P75767 YBHK_ECOLI HYPOTHETICAL 32.8 KDA PROTEIN IN UVRB-MOAA INTERGENIC REGION pir [D64814 ybhk protein - Escherichia coli gb AAC73867.1 (AE000180) putative structural protein [Escherichia coli K12] dbj BAA35438.1 (D90716) Hypothetical protein 1 [Escherichia coli]	SEQ ID n-926
SEQ ID n° 7368	PL-6554.1	1713246 to 1713353	p	No Hits found	Contig9 from	ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAE20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-927
SEQ ID n° 7369	PL-1804.1	1713639 to 1714547	p	83%	Contig9 from	pir [H83457 hypothetical protein PA1508 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04897.1 AE004579_9 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 7370	PL-1805.1	1715372 to 1716385	m	72%	Contig9 from		
SEQ ID n° 7371	PL-6552.1	1716806 to 1717078	m	44%	Contig9 from		

TABLEAU II

SEQ ID n° 7372	PL-1806.1	Contig9 from 1717082 to 1718227	m	30%	pir E83542 hypothetical protein PA0821 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04210.1 AE004517.5 (AE004517) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-928
SEQ ID n° 7373	PL-1807.1	Contig9 from 1718265 to 1719410	m	27%	pir E83542 hypothetical protein PA0821 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04210.1 AE004517.5 (AE004517) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-929
SEQ ID n° 7374	PL-1808.1	Contig9 from 1719425 to 1720630	m	No Hits found	SEQ ID n-930
SEQ ID n° 7375	PL-1809.1	Contig9 from 1720786 to 1722900	m	41%	gb AAG54536.1 AE005199_6 (AE005199) Z0267 gene product [Escherichia coli O157:H7] SEQ ID n-931 sp P07025 UVRB_ECOLI EXCINUCLEASE ABC SUBUNIT B pir BVECB excinuclease ABC chain B - Escherichia coli emb CAA27357.1 (X03722) uvrB gene product (AA 1 - 673) [Escherichia coli] gb AAC73866.1 (AE000180) DNA repair; excision nuclease subunit B [Escherichia coli K12] gb AAG55150.1 AE005259_1 (AE005259) DNA repair; excision nuclease subunit B [Escherichia coli O157:H7] SEQ ID n-933
SEQ ID n° 7376	PL-1811.1	Contig9 from 1723550 to 1725559	m	90%	SEQ ID n-934
SEQ ID n° 7377	PL-1812.1	Contig9 from 1727233 to 1727847	p	No Hits found	SEQ ID n-935
SEQ ID n° 7378	PL-1813.1	Contig9 from 1727848 to 1728741	p	39%	pir A72517 hypothetical protein APE2110 - Aeropyrum pernix (strain K1) dbj BA08111.1 (AP000063) 247aa long hypothetical protein [Aeropyrum pernix]

TABLEAU II

SEQ ID n° 7379	PL-1814.1	Contig9 from 1729058 to 1729738	m	76%	sp P13000 BIOD_ECOLI DETHIOBIOTIN SYNTHETASE (DETHIOBIOTIN SYNTHASE) (DTB SYNTHETASE) (DTBS) pir SYECDB dethiobiotin synthase (EC 6.3.3.3) - Escherichia coli gb AAC73865.1 (AE000180) dethiobiotin synthetase [Escherichia coli K12]	SEQ ID n-936
SEQ ID n° 7380	PL-1815.1	Contig9 from 1729731 to 1730498	m	69%	sp P36571 BIOC_SERMA BIOTIN SYNTHESIS PROTEIN BIOC dbj BAA04287.1 (D17468) the product of bioc [Serratia marcescens]	SEQ ID n-937
SEQ ID n° 7381	PL-1816.1	Contig9 from 1730482 to 1731633	m	79%	gb AAG60556.1 AF250768_1 (AF250768) KAPA- synthetase [uncultured bacterium pCosFS1]	SEQ ID n-938
SEQ ID n° 7382	PL-1817.1	Contig9 from 1731633 to 1732670	m	89%	sp P36569 BIOB_SERMA BIOTIN SYNTHASE (BIOTIN SYNTHETASE) dbj BAA04285.1 (D17468) biotin synthetase [Serratia marcescens]	SEQ ID n-939
SEQ ID n° 7383	PL-1818.1	Contig9 from 1732765 to 1734036	p	86%	gb AAF04396.1 AF191556_4 (AF191556) BioA [Xenorhabdus nematophilus]	SEQ ID n-940
SEQ ID n° 7384	PL-1819.1	Contig9 from 1734248 to 1734913	m	No Hits found		SEQ ID n-941
SEQ ID n° 7385	PL-6542.1	Contig9 from 1735015 to 1735272	p	No Hits found		#N/A
SEQ ID n° 7386	PL-6541.1	Contig9 from 1735737 to 1735904	p	48%	emb CAB41498.1 (AJ238399) hypothetical transposase [Escherichia coli]	#N/A
SEQ ID n° 7387	PL-1821.1	Contig9 from 1736133 to 1737119	m	67%	gb AAF04393.1 AF191556_1 (AF191556) Ybhe [Xenorhabdus nematophilus]	SEQ ID n-943

TABLEAU II

SEQ ID n° 7388	PL-1822.1	Contig9 from 1737265 to 1738083	p	72%	sp P21829 YBHA_ECOLI HYPOTHETICAL 30.2 KDA PROTEIN IN MODC-BIOA INTERGENIC REGION pir F64812 ybha protein - Escherichia coli (strain K-12) gb AAB60177.1 (U27192) unknown [Escherichia coli] gb AAC73853.1 (AE000179) putative phosphatase [Escherichia coli K12] dbj BAA35430.1 (D90715) Hypothetical 30.2 kd protein in modc 3'region. [Escherichia coli] prf 2204295E modc gene [Escherichia coli] SEQ ID n-944
SEQ ID n° 7389	PL-1823.1	Contig9 from 1738160 to 1739224	m	77%	pir BVECHD molybdenum transport protein modC - Escherichia coli gb AAB60173.1 (U27192) ModC [Escherichia coli] dbj BAA35429.1 (D90715) Molybdenum transport ATP-binding protein ModC. [Escherichia coli] gb AAC73852.1 (AE000179) ATP-binding component of molybdate transport [Escherichia coli K12] prf 2204295D modc gene [Escherichia coli] SEQ ID n-945
SEQ ID n° 7390	PL-1824.1	Contig9 from 1739218 to 1739916	m	85%	sp P09834 MODB_ECOLI MOLYBDENUM TRANSPORT SYSTEM PERMEASE PROTEIN MODB gb AAB00836.1 (L34009) hydrophobic membrane-bound protein [Escherichia coli] gb AAB60172.1 (U27192) ModB [Escherichia coli] gb AAB06894.1 (U07867) part of a molybdenum periplasmic binding protein dependent transport system [Escherichia coli] prf 2204295C modB gene [Escherichia coli] gb AAG55092.1 AE005254_4 (AE005254) molybdate- binding periplasmic protein; permease [Escherichia coli O157:H7] SEQ ID n-946
SEQ ID n° 7391	PL-1825.1	Contig9 from 1740053 to 1740823	m	72%	dbj BAA35426.1 (D90715) ORF_ID:0180#2 [Escherichia coli] SEQ ID n-947
SEQ ID n° 7392	PL-6540.1	Contig9 from 1741197 to 1741331	m	53%	pdb 1B9N A Chain A, Regulator From Escherichia Coli pdb 1B9N B Chain B, Regulator From Escherichia Coli #N/A
SEQ ID n° 7393	PL-1826.1	Contig9 from 1741514 to 1742305	p	72%	SEQ ID n-948

TABLEAU II

SEQ ID n° 7394	PL-1827.1	Contig9 from 1742482 to 1743957	p 80%	gb AAG5089.1 AE005254_1 (AE005254) ATP-binding component of molybdate transport system [Escherichia coli O157:H7] pir H83004 hypothetical protein PA5132 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG08517.1 AE004926_7 (AE004926) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-949
SEQ ID n° 7395	PL-1828.2	Contig9 from 1744362 to 1745189	p 65%	sp P31217 PMG1_ECOLI PHOSPHOGLYCERATE MUTASE 1 (PHOSPHOGLYCEROMUTASE 1) (PGAM 1) (BPG-DEPENDENT PGAM 1) pir C64811 phosphoglycerate mutase (EC 5.4.2.1) 1 - Escherichia coli gb AAC73842.1 (AE000178) phosphoglyceromutase 1 [Escherichia coli K12] dbj BAA35417.1 (D90714) phosphoglycerate mutase 1 (EC 5.4.2.1) (phosphoglyceromutase 1) (pgam 1) (bpg-dependent pgam 1). [Escherichia coli] gb AAG55084.1 AE005253_6 (AE005253) phosphoglyceromutase 1 [Escherichia coli O157:H7]	SEQ ID n-951
SEQ ID n° 7396	PL-1829.1	Contig9 from 1745349 to 1746101	p 90%		

TABLEAU II

SEQ ID n° 7397 PL-1830.1	Contig9 from 1746198 to 1747250	m	90%	sp P00886 AROG_ECOLI_PHOSPHO-2-DEHYDRO-3- DEOXYHEPTONATE ALDOLASE, PHE-SENSITIVE (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE) (DAHP SYNTHETASE) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7- PHOSPHATE SYNTHASE) pir ADECHF 2- dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) (Phe-sensitive) - Escherichia coli pdb 1GG1 A Chain A, Crystal Structure Analysis Of Dahp Synthase In Complex With Mn2+ And 2-Phosphoglycolate pdb 1GG1 B Chain B, Crystal-Structure Analysis Of Dahp Synthase In Complex With Mn2+ And 2- Phosphoglycolate pdb 1GG1 C Chain C, Crystal Structure Analysis Of Dahp Synthase In Complex With Mn2+ And 2-Phosphoglycolate pdb 1GG1 D Chain D, Crystal Structure Analysis Of Dahp Synthase In Complex With Mn2+ And 2- Phosphoglycolate pdb 1QR7 D Chain D, Crystal Structure Of Phenylalanine-Regulated 3-Deoxy-D- Arabino-Heptulosonate-7-Phosphate Synthase From Escherichia Coli Complexed With Pb2+ And Pep pdb 1QR7 A Chain A, Crystal Structure Of	SEQ ID n-953
				gb AAG55080.1 AE005253_2 (AE005253) required for NMN transport [Escherichia coli O157:H7]	
				sp P11458 NADA_ECOLI_QUINOLINATE SYNTHETASE A pir SYECQA quinolinate synthetase nada. [validated] - Escherichia coli dbj BAA35409.1 (D90713) Quinolinate synthetase A. [Escherichia coli] dbj BAA35412.1 (D90714) Quinolinate synthetase A. [Escherichia coli] gb AAC73837.1 (AE000177) quinolinate synthetase, A protein [Escherichia coli K12]	
				emb CBB88835.1 (AL353832) putative ABC- transport protein, ATP-binding component. [Streptomyces coelicolor A3(2)]	
SEQ ID n° 7398 PL-1831.1	Contig9 from 1747642 to 1748367	m	79%	gb AAG55080.1 AE005253_2 (AE005253) required for NMN transport [Escherichia coli O157:H7]	SEQ ID n-954
				sp P11458 NADA_ECOLI_QUINOLINATE SYNTHETASE A pir SYECQA quinolinate synthetase nada. [validated] - Escherichia coli dbj BAA35409.1 (D90713) Quinolinate synthetase A. [Escherichia coli] dbj BAA35412.1 (D90714) Quinolinate synthetase A. [Escherichia coli] gb AAC73837.1 (AE000177) quinolinate synthetase, A protein [Escherichia coli K12]	
SEQ ID n° 7399 PL-1832.1	Contig9 from 1748544 to 1749584	m	82%	gb AAG55080.1 AE005253_2 (AE005253) required for NMN transport [Escherichia coli O157:H7]	SEQ ID n-955
				sp P11458 NADA_ECOLI_QUINOLINATE SYNTHETASE A pir SYECQA quinolinate synthetase nada. [validated] - Escherichia coli dbj BAA35409.1 (D90713) Quinolinate synthetase A. [Escherichia coli] dbj BAA35412.1 (D90714) Quinolinate synthetase A. [Escherichia coli] gb AAC73837.1 (AE000177) quinolinate synthetase, A protein [Escherichia coli K12]	
SEQ ID n° 7400 PL-1833.1	Contig9 from 1750598 to 1751362	p	43%	gb AAG55080.1 AE005253_2 (AE005253) required for NMN transport [Escherichia coli O157:H7]	SEQ ID n-956
				sp P11458 NADA_ECOLI_QUINOLINATE SYNTHETASE A pir SYECQA quinolinate synthetase nada. [validated] - Escherichia coli dbj BAA35409.1 (D90713) Quinolinate synthetase A. [Escherichia coli] dbj BAA35412.1 (D90714) Quinolinate synthetase A. [Escherichia coli] gb AAC73837.1 (AE000177) quinolinate synthetase, A protein [Escherichia coli K12]	

TABLEAU II

SEQ ID n° 7401	PL-3932.2	Contig9 from 1751669 to 1752229	p	38%	pir H71196 hypothetical protein PH1846 - Pyrococcus horikoshii dbj BAA30967.1 (AP000007) 273aa long hypothetical protein [Pyrococcus horikoshii]	#N/A
SEQ ID n° 7402	PL-1834.2	Contig9 from 1752468 to 1752992	p	32%	pir H75377 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb AAFI1145.1 AE002002_3 (AE002002) conserved hypothetical protein [Deinococcus radiodurans]	#N/A
SEQ ID n° 7403	PL-1835.1	Contig9 from 1753150 to 1753968	m	32%	pir S18687 Sc/SvN protein - Escherichia coli plasmid p15B emb CAA44050.1 (X62121) DNA inversion product [Escherichia coli]	SEQ ID n-958
SEQ ID n° 7404	PL-1836.1	Contig9 from 1754385 to 1755299	m	32%	pir S18690 Sc/SvQ protein - Escherichia coli plasmid p15B emb CAA44053.1 (X62121) DNA inversion product [Escherichia coli]	SEQ ID n-959
SEQ ID n° 7405	PL-6538.1	Contig9 from 1755705 to 1756088	m	No Hits found		#N/A
SEQ ID n° 7406	PL-6537.1	Contig9 from 1756085 to 1756441	m	No Hits found		#N/A
SEQ ID n° 7407	PL-1837.1	Contig9 from 1756851 to 1757753	m	31%	pir S18690 Sc/SvQ protein - Escherichia coli plasmid p15B emb CAA44053.1 (X62121) DNA inversion product [Escherichia coli]	SEQ ID n-960
SEQ ID n° 7408	PL-6536.1	Contig9 from 1758000 to 1758146	m	No Hits found		#N/A
SEQ ID n° 7409	PL-1838.2	Contig9 from 1758557 to 1759408	p	49%	pir S25259 streptomycin resistance protein - Bacteroides sp. transposon Tn4551 gb AA227459.1 (M72415) streptomycin adenyltransferase [Transposon Tn4551]	#N/A
SEQ ID n° 7410	PL-6535.1	Contig9 from 1759488 to 1759646	p	No Hits found		#N/A

TABLEAU II

WO 02/094867

665

PCT/IB02/03040

SEQ ID n° 7411	PL-1839.2	Contig9 from 1761092 to 1761868	m	80%	sp P45955 YBGF_ECOLI_HYPOTHETICAL_28.2_KDA PROTEIN IN PAL-LYST INTERGENIC REGION PRECURSOR pir E64810 ybGF protein precursor - Escherichia coli gb AAC73836.1 (AE000177) orf, hypothetical protein [Escherichia coli K12] dbj BAA35408.1 (D90713) Hypothetical 28.2 kd protein in pal-lyst intergenic region. [Escherichia coli]	#N/A
SEQ ID n° 7412	PL-3931.2	Contig9 from 1761878 to 1762378	m	81%	sp P07176 PAL_ECOLI_PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN PRECURSOR pir LPECPG peptidoglycan- associated lipoprotein precursor - Escherichia coli emb CAA46673.1 (X65796) peptidoglycan- associated lipoprotein [Escherichia coli] emb CAA28771.1 (X05123) precursor polypeptide (AA-21 to -1) [Escherichia coli] dbj BAA35407.1 (D90713) Peptidoglycan- associated lipoprotein precursor. [Escherichia coli] gb AAC73835.1 (AE000177) peptidoglycan-associated lipoprotein [Escherichia coli K12] gb AAG55077.1 AE005252_13 (AE005252) peptidoglycan-associated lipoprotein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7413	PL-1840.1	Contig9 from 1762421 to 1763713	m	86%	pdb 1C5K A Chain A, The Structure Of Tolb, An Essential Component Of The Tol- Dependent Translocation System And Its Interactions With The Translocation Domain Of Colicin E9 gb AAG55075.1 AE005252_11 (AE005252) membrane spanning protein, required for outer membrane integrity [Escherichia coli O157:H7]	SEQ ID n-964 SEQ ID n-966
SEQ ID n° 7414	PL-1842.1	Contig9 from 1763927 to 1764997	m	71%		

TABLEAU II

SEQ ID n° 7415 PL-6533.1	Contig9 from 1765043 to 1765468	m 82%	sp P05829 TOLR_ECOLI TOLR PROTEIN pir BVECTR tolr protein - Escherichia coli gb AA83921.1 (M16489) ORF 3; putative [Escherichia coli] dbj BAA35404.1 (D90713) TolR protein [Escherichia coli] gb AAC73832.1 (AE000177) putative inner membrane protein, involved in the tonB-independent uptake of group A colicins [Escherichia coli K12]	#N/A
			gb AAG55074.1 AE005252_10 (AE005252) putative inner membrane protein, involved in the tonB-independent uptake of group A colicins [Escherichia coli O157:H7]	
SEQ ID n° 7416 PL-1843.1	Contig9 from 1765483 to 1766178	m 90%	sp P05828 TOLQ_ECOLI TOLQ PROTEIN pir BVECTR biopolymer transport protein tolQ - Escherichia coli gb AA83919.1 (M16489) ORF 2; putative [Escherichia coli] dbj BAA35403.1 (D90713) TOLQ protein. [Escherichia coli] gb AAC73831.1 (AE000177) inner membrane protein, membrane- spanning, maintains integrity of cell envelope; tolerance to group A colicins [Escherichia coli K12] gb AAG55073.1 AE005252_9 (AE005252) inner membrane protein, membrane-spanning, maintains integrity of cell envelope; tolerance to group A colicins [Escherichia coli O157:H7]	SEQ ID n-967
			sp P08999 YBGC_ECOLI 15.6 KDA PROTEIN IN CYDB- TOLQ INTERGENIC REGION pir WNEC15 ybgC protein - Escherichia coli gb AA83918.1 (M16489) ORF 1; putative [Escherichia coli] gb AAC73830.1 (AE000177) orf, hypothetical protein [Escherichia coli K12] dbj BAA35402.1 (D90713) 15.5k protein (tolAB operon 5' region). [Escherichia coli] gb AAG55072.1 AE005252_8 (AE005252) orf, hypothetical protein [Escherichia coli O157:H7]	
SEQ ID n° 7417 PL-3930.1	Contig9 from 1766175 to 1766579	m 66%		

SEQ ID n-9093

TABLEAU II

SEQ ID n° 7418	PL-1844.1	Contig9 from 1767125 to 1768264	m	83%	sp P11027 CYDB_ECOLI CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (CYTOCHROME BD-I OXIDASE SUBUNIT II) pir B28940 cytochrome d ubiquinol oxidase (EC 1.10.3.-) chain II - Escherichia coli gb AAA1805.1 (J03939) cytochrome oxidase d subunit II [Escherichia coli] dbj BAA35400.1 (D90713) Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-). [Escherichia coli] gb AAC73828.1 (AE000176) cytochrome d terminal oxidase polypeptide subunit II [Escherichia coli K12] gb AAG55070.1 AE005252_6 (AE005252) cytochrome d terminal oxidase polypeptide subunit II [Escherichia coli O157:H7]	SEQ ID n-968
SEQ ID n° 7419	PL-1845.1	Contig9 from 1768279 to 1769847	m	91%	gb AAA18804.1 (J03939) cytochrome oxidase d subunit I [Escherichia coli]	SEQ ID n-969
SEQ ID n° 7420	PL-6530.1	Contig9 from 1771168 to 1771311	m	No Hits found	#N/A	
SEQ ID n° 7421	PL-6529.1	Contig9 from 1771827 to 1772201	m	No Hits found	#N/A	
SEQ ID n° 7422	PL-1846.1	Contig9 from 1772222 to 1772860	m	46%	pir A83124 hypothetical protein PA4182 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07569.1 AE004834_9 (AE004834) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-970
SEQ ID n° 7423	PL-3928.1	Contig9 from 1772871 to 1773335	m	No Hits found		SEQ ID n-9090
SEQ ID n° 7424	PL-1847.1	Contig9 from 1773349 to 1774455	m	40%	sp Q9ZHR5 HIS8_BUCAP HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (IMIDAZOLE ACETOL-PHOSPHATE TRANSAMINASE) gb AAC97356.1 (AF067228) histidinolphosphate aminotransferase [Buchnera aphidicola]	SEQ ID n-971

TABLEAU II

SEQ ID n° 7425 PL-1848.1	Contig9 from 1774497 to 1775687	m	38%	pir [H72265 hypothetical protein TM1336 - Thermotoga maritima (strain MSB8) gb AAD36408.1 AE001788.3 (AE001788) permease, putative [Thermotoga maritima] emb CAB67718.1 (AJ2711405) putative carbamoyl- phosphate-synthetase [Streptomyces rochei]	SEQ ID n-972
SEQ ID n° 7426 PL-1849.1	Contig9 from 1775745 to 1778051	m	19%	emb CAB92560.1 (AL356812) putative carboxylase. [Streptomyces coelicolor A3(2)]	SEQ ID n-973
SEQ ID n° 7427 PL-1850.1	Contig9 from 1778207 to 1779460	m	26%	gb AAK02181.1 (AE006045) unknown [Pasteurella multocida]	SEQ ID n-975
SEQ ID n° 7428 PL-1851.1	Contig9 from 1779500 to 1780249	m	36%	sp O67733 ILVE_AQUAE PROBABLE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (BCAT) pir [C70463 branched-chain amino acid aminotransferase - Aquifex aeolicus gb AAC07697.1 (AE000762) branched-chain amino acid aminotransferase [Aquifex aeolicus] dbj BAA82878.1 (AB024335) 3-(3- hydroxyphenyl)propionate hydroxylase [Comamonas testosteroni]	SEQ ID n-976
SEQ ID n° 7429 PL-1852.1	Contig9 from 1780282 to 1781055	m	61%		SEQ ID n-977
SEQ ID n° 7430 PL-1853.1	Contig9 from 1781226 to 1782848	m	36%		SEQ ID n-978
SEQ ID n° 7431 PL-1854.1	Contig9 from 1782858 to 1784144	m	No Hits found		SEQ ID n-979
SEQ ID n° 7432 PL-1855.1	Contig9 from 1784193 to 1785335	m	46%	sp P42253 YCBU_BACSU HYPOTHETICAL 40.8 KD PROTEIN IN PCP-LMRB INTERGENIC REGION PRECURSOR (ORF21) pir [E69754 nifs protein homolog ycbu - Bacillus subtilis dbj BAA22227.1 (AB000617) ycbu [Bacillus subtilis] emb CAB12060.1 (Z99105) similar to Nifs protein homolog [Bacillus subtilis] pir [r36536 probable oxidoreductase - Streptomyces coelicolor emb CAB42033.1 (AL049754) putative oxidoreductase [Streptomyces coelicolor A3(2)]	SEQ ID n-980
SEQ ID n° 7433 PL-1856.1	Contig9 from 1785341 to 1786042	m	42%		SEQ ID n-981

TABLEAU II

SEQ ID n° 7434 PL-1857.1	Contig9 from 1786786 to 1787661	m	91%	sp P07459 SUCD_ECOLI SUCCINYL-COA SYNTHETASE
				ALPHA CHAIN (SCS-ALPHA) pir SYECSA succinate--
				CoA ligase (ADP-forming) (EC 6.2.1.5) alpha
				chain - Escherichia coli
				gb AA23900.1 (J01619) succinyl-CoA synthetase
				alpha-subunit [Escherichia coli]
				dbj BAA35395.1 (D90711) Succinate-CoA ligase
				(ADP-forming) (EC 6.2.1.5) alpha
				chain. [Escherichia coli] gb AAC73823.1
				(AE000176) succinyl-CoA synthetase, alpha
				subunit [Escherichia coli] K12]
				gb AAG55053.1 AE005251_2 (AE005251) succinyl-CoA
				synthetase, alpha subunit [Escherichia coli
				O157:H7]
				SEQ ID n-982

SEQ ID n° 7435 PL-1858.1 1787664 to 1788830 Contig9 from

sp|P07460|SUCC_ECOLI SUCCINYL-COA SYNTHETASE
BETA CHAIN (SCS-BETA) pir||SYECSB succinate--
CoA ligase (ADP-forming) (EC 6.2.1.5) beta chain
----- Escherichia coli pdb|1SCU|B Chain
- B, Succinyl-CoA Synthetase (Succinate-CoA
Ligase) (Adp-Forming) (E.C.6.2.1.5)
pdb|1SCU|E Chain E; Succinyl-CoA Synthetase
(Succinate-CoA Ligase) (Adp-Forming)
(E.C.6.2.1.5) pdb|2SCU|B Chain B, A Detailed
Description Of The Structure Of Succinyl-CoA
Synthetase From Escherichia Coli pdb|2SCU|E
Chain E, A Detailed Description Of The Structure
Of Succinyl-CoA Synthetase From
Escherichia Coli gb|AAA23899.1| (J01619)
succinyl-CoA synthetase beta-subunit
[Escherichia coli] dbj|BAA35394.1| (D90711)
Succinate-CoA ligase (ADP-forming) (EC 6.2.1.5)
beta chain. [Escherichia coli]
gb|AAC73822.1| (AE000176) succinyl-CoA
synthetase, beta subunit [Escherichia coli
K12] gb|AAG55052.1|AE005251_1 (AE005251)
succinyl-CoA synthetase, beta subunit
[Escherichia coli] O157:H7]

SEQ ID n-983

TABLEAU II

SEQ ID n° 7436 PL-1860.1	Contig9 from 1788997 to 1790217	m	87%	sp P07016 ODO2_ECOLI DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (E2) pir XUECSD dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) [validated] - Escherichia coli emb CAA25284.1 (X00664) E20 component [Escherichia coli] gb AA23898.1 (J01619) dihydrolipoamide succinyltransferase [Escherichia coli] dbj BAA35393.1 (D90711) Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61). [Escherichia coli] gb AAC73821.1 (AE000175) 2-oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase E2 component) [Escherichia coli K12] gb AAG55051.1 AE005250_10 (AE005250) 2- oxoglutarate dehydrogenase (dihydrolipoyltranssuccinase E2 component) [Escherichia coli O157:H7] sp P07015 ODO1_ECOLI 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE) pir DEECOG oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - Escherichia coli dbj BAA35392.1 (D90711) Oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) [Escherichia coli] gb AAC73820.1 (AE000175) 2-oxoglutarate dehydrogenase (decarboxylase component) [Escherichia coli K12] gb AAG55048.1 AE005250_7 (AE005250) succinate dehydrogenase, iron sulfur protein [Escherichia coli O157:H7]
				SEQ ID n-985
SEQ ID n° 7437 PL-1861.1	Contig9 from 1790232 to 1793039	m	90%	SEQ ID n-986
				SEQ ID n-987
SEQ ID n° 7438 PL-1862.1	Contig9 from 1793306 to 1794022	m	95%	

TABLEAU II

SEQ ID n° 7439 PL-1863.1	Contig9 from 1794059 to 1795825	m 96%	sp P10444 DHSA_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT pir DECSF succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Escherichia coli dbj BAA35390.1 (D90711) Succinate dehydrogenase (EC 1.3.99.1) flavoprotein [Escherichia coli] gb AAC73817.1 (AE000175) succinate dehydrogenase, flavoprotein subunit [Escherichia coli K12]	SEQ ID n-988
SEQ ID n° 7440 PL-6520.1	Contig9 from 1795826 to 1796173	m 75%	sp P10445 DHSD_ECOLI SUCCINATE DEHYDROGENASE HYDROPHOBIC MEMBRANE ANCHOR PROTEIN pir DECS2 succinate dehydrogenase (EC 1.3.99.1) 13K protein - Escherichia coli emb CAA25486.1 (X00980) succinate dehydrogenase hydrophobic subunit (sdhD) (aa 1-114) [Escherichia coli] gb AA23894.1 (J01619) ... succinate dehydrogenase [Escherichia coli] dbj BAA35389.1 (D90711) succinate dehydrogenase (EC 1.3.99.1) 13k hydrophobic protein [Escherichia coli] gb AAC73816.1 (AE000175) succinate dehydrogenase, hydrophobic subunit [Escherichia coli K12]	#N/A

TABLEAU II

sp P10446 DHSC_ECOLI SUCCINATE DEHYDROGENASE CYTOCHROME B-556 SUBUNIT pir DECS4 succinate dehydrogenase [EC 1.3.99.1] cytochrome b556 - Escherichia coli emb CAA25485.1 (X00980) succinate dehydrogenase (sdhc) hydrophobic subunit (aa 1-128) [Escherichia coli] gb AAA23893.1 (J01619) succinate dehydrogenase [Escherichia coli] gb AAA24616.1 (M28989) succinate dehydrogenase [Escherichia coli] dbj BAA35388.1 (D90711) Succinate dehydrogenase cytochrome b-556 subunit. [Escherichia coli] gb AAC73815.1 (AE000175) succinate dehydrogenase, cytochrome b556 [Escherichia coli K12] gb AAG5045.1 AE005250_4 (AE005250) succinate dehydrogenase, cytochrome b556 [Escherichia coli O157:H7]	#N/A		
Contig9 from 1796167 to 1796499	m	64%	
SEQ ID n° 7441 PL-6519.1			
Contig9 from 1796436 to 1796612	p	No Hits found	#N/A
SEQ ID n° 7442 PL-6518.1			
Contig9 from 1797426 to 1798709	p	86%	
SEQ ID n° 7443 PL-1864.1			
Contig9 from 1799062 to 1799805	m	75%	
SEQ ID n° 7444 PL-1865.1			

TABLEAU II

SEQ ID n° 7445 PL-6517.1	Contig9 from 1799872 to 1800081	m	52%	sp P28913 YBFA_ECOLI HYPOTHETICAL 8.3 KDA PROTEIN IN KOPA-RHSC INTERGENIC REGION PRECURSOR pir B64805 ybfa protein - Escherichia coli gb AAC63071.1 (L02373) unknown [Escherichia coli] gb AAC73793.1 (AE000173) orf, hypothetical protein [Escherichia coli K12] dbj BA35358.1 (D90709) Hypothetical 8.3 kd protein in rhsc 5' region precursor. [Escherichia coli] gb AGS5020.1 AE005248_1 (AE005248) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
					SEQ ID n-3089
SEQ ID n° 7446 PL-3926.1	Contig9 from 1800600 to 1800980	p	No Hits found	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-991
SEQ ID n° 7447 PL-1866.1	Contig9 from 1801073 to 1802134	p	21%	sp P03959 ATKA_ECOLI POTASSIUM-TRANSPORTING ATPASE A CHAIN (POTASSIUM-TRANSLCATING ATPASE A CHAIN) (ATP PHOSPHOHYDROLASE [POTASSIUM-TRANSPORTING] A CHAIN) (POTASSIUM BINDING AND TRANSLCATING SUBUNIT A) pir PWECAK H+/K+-exchanging ATPase (EC 3.6.1.36) chain A [validated] - Escherichia coli gb AAB96335.1 (K02670) kdpA [Escherichia coli] dbj BA35356.1 (D90709) Potassium-transporting ATPase (EC 3.6.1.36), a chain (ATP phosphohydrolase (potassium-transporting), A chain). [Escherichia coli] gb AAC73792.1 (AE000173) ATPase of high-affinity potassium transport system, A chain [Escherichia coli K12]	SEQ ID n-992
SEQ ID n° 7448 PL-1867.1	Contig9 from 1802635 to 1804341	p	82%	gb AAB96336.1 (K02670) kdpB [Escherichia coli]	SEQ ID n-993
SEQ ID n° 7449 PL-1869.1	Contig9 from 1804362 to 1806428	p	86%		

TABLEAU II

Contig9 from SEQ ID n° 7450 PL-3925.1 1806440 to 1807021	p 62%	gb AAC55017.1 AE005247_8 (AE005247) high-affinity potassium transport system [Escherichia coli O157:H7] sp P21865 KDPD_ECOLI_SENSOR_PROTEIN_KDPD pir B42372 histidine kinase kdpD (EC 2.7.3.-) [validated] - Escherichia coli gb AA2404.1.1 (M36066) transmembrane protein (kdpD) [Escherichia coli] dbj BAA35352.1 (D90708) Regulatory protein kdpD. [Escherichia coli] gb AAC73789.1 (AE000173) sensor for high-affinity potassium transport system [Escherichia coli K12] SEQ ID n-9088
Contig9 from SEQ ID n° 7451 PL-1870.1 1807030 to 1809723	p 77%	sp P21866 KDPD_ECOLI_KDP_OPERON_TRANSCRIPTIONAL_REGULATORY_PROTEIN_KDPE pir E64804 transcription regulator kdpE [validated] - Escherichia coli gb AAC73788.1 (AE000173) regulator of kdp operon (transcriptional effector) [Escherichia coli K12] SEQ ID n-995
Contig9 from SEQ ID n° 7452 PL-1871.1 1809720 to 1810412	p 81%	SEQ ID n-996
Contig9 from SEQ ID n° 7453 PL-1872.1 1810678 to 1812210	m No Hits found	SEQ ID n-997
Contig9 from SEQ ID n° 7454 PL-1873.1 1812643 to 1813470	m 59%	pir E82358 conserved hypothetical protein VC0134 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93311.1 (AE004104) conserved hypothetical protein [Vibrio cholerae] SEQ ID n-998
Contig9 from SEQ ID n° 7455 PL-1874.1 1813478 to 1814158	m 27%	pir A75275 methionyl-tRNA formyltransferase - Deinococcus radiodurans (strain R1) gb AAF11976.1 AE002073_6 (AE002073) methionyl-tRNA formyltransferase [Deinococcus radiodurans] SEQ ID n-999
Contig9 from SEQ ID n° 7456 PL-1875.1 1814149 to 1816005	m 55%	gb AAC05838.1 (AF052516) hemolysin erythrocyte lysis protein 2 [Prevotella intermedia] SEQ ID n-2000

TABLEAU II

SEQ ID n° 7457 PL-1876.1	Contig9 from 1816242 to m 18% 1817444	pir E71622 probable membrane associated protein PFB0125c - malaria parasite (Plasmodium falciparum) gb AAC71815.1 (AE001374) predicted membrane associated protein [Plasmodium falciparum] SEQ ID n-2001
SEQ ID n° 7458 PL-6513.1	Contig9 from 1817431 to m 45% 1817688	gb AAG45728.1 AF229440.1 (AF229440) y4y8 [Sinorhizobium fredii] #N/A
SEQ ID n° 7459 PL-1877.1	Contig9 from 1817792 to m 55% 1819024	pir C82395 conserved hypothetical protein VCA0972 [imported] - Vibrio cholerae (group O1 strain NI961) gb AAF96868.1 (AE004423) conserved hypothetical protein [Vibrio cholerae] SEQ ID n-2002
SEQ ID n° 7460 PL-6512.1	Contig9 from 1819784 to p 65% 1820212	pir B75075 hypothetical protein PAB0665 - Pyrococcus abyssi (strain Orsay) emb CAB49903.1 (AJ248286) hypothetical protein [Pyrococcus abyssi] #N/A
SEQ ID n° 7461 PL-1878.1	Contig9 from 1820276 to m 84% 1821916	sp P36938 PGMU_ECOLI PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM) pir G64803 phosphoglucumutase (EC 5.4.2.2) - Escherichia coli gb AAA57067.1 (U08369) phosphoglucumutase [Escherichia coli] dbj BAA35337.1 (D90707) phosphoglucumutase (EC 5.4.2.2) (glucose phosphomutase) (pgm). [Escherichia coli] dbj BAA35345.1 (D90708) phosphoglucumutase (EC 5.4.2.2) (glucose phosphomutase) (pgm). [Escherichia coli] gb AAC73782.1 (AE000172) phosphoglucumutase [Escherichia coli KL2] SEQ ID n-2003

TABLEAU II

SEQ ID n° 7462 PL-3924.1	Contig9 from 1821978 to 1822502	m	77%	sp P36658 SEQA_ECOLI_SEQA_PROTEIN_pir A54296 seqA protein - Escherichia coli gb AA19855.1 (U07651) SeqA [Escherichia coli] dbj BAA35336.1 (D90707) SeqA protein. [Escherichia coli] dbj BAA35344.1 (D90708) SeqA protein. [Escherichia coli] gb AAC73781.1 (AE000172) negative modulator of initiation of replication [Escherichia coli K12] SEQ ID n-3087 sp P46880 HXKG_ECOLI_GLUCOKINASE (GLUCOSE KINASE) pir A65013 glucokinase (EC 2.7.1.2) - Escherichia coli (strain K-12) gb AAC75447.1 (AE000327) glucokinase [Escherichia coli K12] dbj BA16258.1 (D90868) GLUCOKINASE (EC 2.7.1.2). [Escherichia coli] dbj BA16261.1 (D90869) GLUCOKINASE (EC 2.7.1.2). [Escherichia coli] gb AAG57514.1 AE005470_1 (AE005470) glucokinase [Escherichia coli O157:H7] SEQ ID n-3004
SEQ ID n° 7463 PL-1879.1	Contig9 from 1823289 to 1824254	m	76%	
SEQ ID n° 7464 PL-6510.1	Contig9 from 1825140 to 1825247	m	No Hits found	#N/A
SEQ ID n° 7465 PL-6509.1	Contig9 from 1825578 to 1825745	p	No Hits found	#N/A
SEQ ID n° 7466 PL-6508.1	Contig9 from 1825736 to 1825909	p	No Hits found	#N/A
SEQ ID n° 7467 PL-6507.1	Contig9 from 1825911 to 1826195	p	50%	pir E82455 conserved hypothetical protein VCA0469 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96373.1 (AE004379) conserved hypothetical protein [Vibrio cholerae] #N/A
SEQ ID n° 7468 PL-3923.1	Contig9 from 1826365 to 1826877	m	No Hits found	SEQ ID n-3086

TABLEAU II

SEQ ID n° 7469 PL-1880.1	Contig9 from 1827248 to 1828666	p	89%	sp P04805 SYE_ECOLI GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS) pir SYECET glutamate--trna_ligase (EC 6.1.1.17) - Escherichia coli emb CAA45391.1 (X63976) glutamyl-trna synthetase [Escherichia coli] gb AA65715.1 (M13687) glutamyl-trna synthetase [Escherichia coli] gb AAC75457.1 (AE000328) glutamate trna synthetase, catalytic subunit [Escherichia coli K12] dbj BAAL6272.1 (D90869) glutamate--trna ligase (EC 6.1.1.17) [Escherichia coli]	SEQ ID n-1006
SEQ ID n° 7470 PL-6504.1	Contig9 from 1829016 to 1829138	p	No Hits found	sp P56604 YPER_ECOLI HYPOTHETICAL 8.4 KD PROTEIN IN XAPB-LIG INTERGENIC REGION gb AAG57529.1 AE005471_6 (AE005471) Z3676 gene product [Escherichia coli O157:H7] sp P33031 NUPC_ECOLI NUCLEOSIDE PERMEASE NUPC (NUCLEOSIDE-TRANSPORT SYSTEM PROTEIN NUPC) pir F65013 nucleoside transport protein nupC - Escherichia coli gb AAC75452.1 (AE000327) permease of transport system for 3 nucleosides [Escherichia coli K12] dbj BAA16263.1 (D90869) NUCLEOSIDE PERMEASE NUPC (NUCLEOSIDE-TRANSPORT SYSTEM PROTEIN NUPC) . [Escherichia coli]	#N/A
SEQ ID n° 7471 PL-6502.1	Contig9 from 1829343 to 1829558	m	46%	sp P15042 DNLJ_ECOLI DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [NAD+]) pir LQEC6 DNA ligase (NAD+) (EC 6.5.1.2) - Escherichia coli gb AA24070.1 (M24278) DNA ligase (EC 6.5.1.2) [Escherichia coli] gb AAC75464.1 (AE000328) DNA ligase [Escherichia coli K12]	SEQ ID n-1007
SEQ ID n° 7472 PL-1881.1	Contig9 from 1829642 to 1830826	m	85%		
SEQ ID n° 7473 PL-1882.1	Contig9 from 1831187 to 1833205	m	88%		

TABLEAU II

SEQ ID n° 7474 PL-1883.1	Contig9 from 1833267 to 1834178	m 64%	sp P77173 ZIPA_ECOLI CELL DIVISION PROTEIN ZIPA gb AAB42061.1 (U74650) Zipa [Escherichia coli] sp P12610 CYSZ_ECOLI CYSZ PROTEIN pir [BVECCZ probable sulfate transport protein Cysz - Escherichia coli (strain K-12) gb AAC75466.1 (AE000329) required for sulfate transport [Escherichia coli K12] gb AAG57532.1 AE005471.9 (AE005471) required for sulfate transport [Escherichia coli O157:H7]	SEQ ID n-2009
SEQ ID n° 7475 PL-1884.1	Contig9 from 1834399 to 1835169	p 72%	pdb 1FCJ A Chain A, Crystal Structure Of Oass Complexed With Chloride And Sulfate pdb 1FCJ B Chain B, Crystal Structure Of Oass Complexed With Chloride And Sulfate pdb 1FCJ C Chain C, Crystal Structure Of Oass Complexed With Chloride And Sulfate pdb 1FCJ D Chain D, Crystal Structure Of Oass Complexed With Chloride And Sulfate pdb 1OAS A Chain A, O-Acetylserine Sulphydrylase From Salmonella Typhimurium pdb 1OAS B Chain B, O-Acetylserine Sulphydrylase From Salmonella Typhimurium	SEQ ID n-2010
SEQ ID n° 7476 PL-1885.1	Contig9 from 1835284 to 1836237	p 89%		SEQ ID n-2011

TABLEAU II

sp P07006 PTHP_ECOLI PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN) pir WQBCPH phosphotransferase system phosphohistidine- containing protein [validated] -					
Escherichia coli pir WQEBPH phosphotransferase system phosphohistidine-containing protein - Salmonella typhimurium pdb 1GGR B Chain B, Complex Of Enzyme Iiaglc And The Histidine- Containing PhosphocARRIER Protein Hpr From Escherichia Coli Nmr, Restrained Regularized Mean Structure pdb 1POH					
Phosphotransferase (Histidine-Containing PhosphocARRIER Protein) pdb 2JEL P Chain P, JEL42 FabHPR COMPLEX pdb 3EZE B Chain B, Complex Of The Amino Terminal Domain Of Enzyme I And The Histidine-Containing PhosphocARRIER Protein Hpr From Escherichia Coli Nmr, Restrained Regularized Mean Structure pdb 3EZA B Chain B, Complex Of The Amino Terminal Domain Of Enzyme I And The Histidine-Containing PhosphocARRIER Protein Hpr From Escherichia Coli Nmr, Restrained Regularized sp P12654 PTI_SALTY PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I) pir WQEBPI phosphotransferase system enzyme I (EC 2.7.3.9) Salmonella typhimurium gb AAA27060.1 (M76176) enzyme I [Salmonella typhimurium]					#N/A
Contig9 from SEQ ID n° 7477 PL-6500.1 1836791 to 1837048	p	92%			
Contig9 from SEQ ID n° 7478 PL-1886.1 1837233 to 1838960	p	87%			

SEQ ID n° 1012

TABLEAU II

sp P08837 PTGA_ECOLI PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (BIIA-GLC)					
(GLUCOSE-PERMEASE IIA COMPONENT)					
(PHOSPHOTRANSFERASE					ENZYME II, A
COMPONENT) (BIII-GLC) pir WQPCP3					
phosphotransferase system enzyme II (EC 2.7.1.69),					glucose-specific, factor
III - Escherichia coli gb AA23602.1 (M93578)					
PTS enzyme III glc [Escherichia coli]					
gb AA23603.1 (M93580) PTS enzyme III glc					
[Escherichia coli] gb AA23604.1 (M93582) PTS					
enzyme III glc [Escherichia coli]					
gb AA23605.1 (M93579) PTS enzyme III glc					
[Escherichia coli] gb AA23606.1 (M93581) PTS					
enzyme III glc [Escherichia coli]					
gb AA23607.1 (M93594) PTS enzyme III glc					
[Escherichia coli] gb AA23608.1 (M93595) PTS					
enzyme III glc [Escherichia coli]					
gb AA23609.1 (M93597) PTS enzyme III glc					
[Escherichia coli] gb AA23610.1 (M93584) PTS					
enzyme III glc [Escherichia coli]					
gb AA23611.1 (M93596) PTS enzyme III glc					
[Escherichia coli] gb AA23612.1 (M93587) PTS					
enzyme III glc [Escherichia coli]					
gb AA23613.1 (M93598) PTS enzyme III glc					SEQ ID n-3085
gb AAG57539.1 AE005472_6 (AE005472) cysteine					
synthase B, O-acetylserine sulphydrolase B					
[Escherichia coli O157:H7]					SEQ ID n-3877
Contig9 from					
SEQ ID n° 7479 PL-3921.1	1839009 to	p	928		
	1839518				
Contig9 from					
SEQ ID n° 7480 PL-2680.2	1839761 to	m	748		
	1840642				

TABLEAU II

SEQ ID n° 7481	PL-2679.1	Contig9 from 1840781 to 1841869	m	82%	sp P16676 CYSA_ECOLI SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA pir QRECSA sulfate transport ATP-binding protein cysA - Escherichia coli gb AAC75475.1 (AE000329) ATP-binding component of sulfate permease A protein; chromate resistance [Escherichia coli K12] dbj BAA16296.1 (D90871) sulfate/thiosulfate transport protein cysA [Escherichia coli] dbj BAA16305.1 (D90872) sulfate/thiosulfate transport protein cysA [Escherichia coli]	SEQ ID n° 1875
SEQ ID n° 7482	PL-2678.1	Contig9 from 1841884 to 1842729	m	84%	sp P16702 CYSW_ECOLI SULFATE TRANSPORT SYSTEM PERMEASE PROTEIN CYSW gb AAA23638.1 (M32101) sulfate permease [Escherichia coli] dbj BAA16297.1 (D90871) sulfate/thiosulfate transport protein cysW [Escherichia coli] dbj BAA16306.1 (D90872) sulfate/thiosulfate transport protein cysW [Escherichia coli]	SEQ ID n° 1874
SEQ ID n° 7483	PL-2677.1	Contig9 from 1842729 to 1843562	m	91%	gb AAG57542.1 AE005472_9 (AE005472) sulfate, thiosulfate transport system permease T protein [Escherichia coli O157:H7] sp P16700 CYSW_ECOLI THIOSULFATE-BINDING PROTEIN PRECURSOR pir JGECT thiosulfate-binding protein cysP precursor - Escherichia coli gb AAA23636.1 (M32101) thiosulfate binding protein [Escherichia coli] gb AAC75478.1 (AE000330) thiosulfate binding protein [Escherichia coli K12] dbj BAA16299.1 (D90871) thiosulfate-binding protein cysP precursor [Escherichia coli] dbj BAA16308.1 (D90872) thiosulfate-binding protein cysP precursor [Escherichia coli]	SEQ ID n° 1873
SEQ ID n° 7484	PL-2676.1	Contig9 from 1843562 to 1844584	m	79%	sp P16700 CYSW_ECOLI THIOSULFATE-BINDING PROTEIN PRECURSOR pir JGECT thiosulfate-binding protein cysP precursor - Escherichia coli gb AAA23636.1 (M32101) thiosulfate binding protein [Escherichia coli] gb AAC75478.1 (AE000330) thiosulfate binding protein [Escherichia coli K12] dbj BAA16299.1 (D90871) thiosulfate-binding protein cysP precursor [Escherichia coli] dbj BAA16308.1 (D90872) thiosulfate-binding protein cysP precursor [Escherichia coli]	SEQ ID n° 1872

TABLEAU II

SEQ ID n° 7485	PL-2675.1	Contig9 from 1844952 to 1845560	m	60%	sp P76537 YFEY_ECOLI_HYPOTHETICAL_20.9_KDA PROTEIN IN UCFA-AMIA INTERGENIC REGION PRECURSOR pir G65017_hypothetical protein b2432 - Escherichia coli (strain K-12) gb AAC75485.1 (AE000330) orf, hypothetical protein [Escherichia coli K12] sp P52083 YGIW_ECOLI_PROTEIN_YGIW_PRECURSOR pir F65089_ygiw protein precursor - Escherichia coli gb AAA69192.1 (U28377) ORF_f130 [Escherichia coli] gb AAC76060.1 (AE000384) orf, hypothetical protein [Escherichia coli K12] gb AAG58158.1 AE005532_2 (AE005532) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-1871
SEQ ID n° 7486	PL-3919.1	Contig9 from 1845732 to 1846151	p	57%	gb AAG57552.1 AE005473_7 (AE005473) Z3699 gene product [Escherichia coli O157:H7] gb AAG57554.1 AE005474_2 (AE005474) coproporphyrinogen III oxidase [Escherichia coli O157:H7] sp Q99132 PRT1_ERWCA_EXTRACELLULAR METALLOPROTEINASE PRECURSOR pir A41048 extracellular metalloproteinase (EC 3.4.24.-) precursor - Erwinia carotovora subsp. carotovora gb AAA24858.1 (M36651) extracellular protease (prt) [Pectobacterium carotovorum] SEQ ID n-1869
SEQ ID n° 7487	PL-3918.1	Contig9 from 1846276 to 1846707	m	74%	sp P77254 ENGA_ECOLI_PROBABLE_GTP-BINDING PROTEIN ENGA SEQ ID n-1868
SEQ ID n° 7488	PL-2674.1	Contig9 from 1846845 to 1847753	p	81%	gb AAG31169.1 (AF314961) unknown [Salmonella typhimurium] SEQ ID n-1867
SEQ ID n° 7489	PL-2673.1	Contig9 from 1847986 to 1849083	p	64%	
SEQ ID n° 7490	PL-6497.1	Contig9 from 1849244 to 1849561	p	No Hits found	
SEQ ID n° 7491	PL-2672.1	Contig9 from 1849586 to 1851067	m	89%	
SEQ ID n° 7492	PL-2671.1	Contig9 from 1851358 to 1852530	m	81%	

TABLEAU II

SEQ ID n° 7493	PL-2670.1	Contig9 from 1852545 to 1853165	m 66%	gb AAG57623.1 AE005480_10 (AE005480) orf, hypothetical protein [Escherichia coli O157:H7] sp P04804 SYH_ECOLI HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS) pir SYECH histidine--trna ligase (EC 6.1.1.21) [validated] - Escherichia coli pdb 1KMM C Chain C, Histidyl- Trna Synthetase Complexed With Histidyl- Adenylate pdb 1KMM A Chain A, Histidyl-Trna Synthetase Complexed With Histidyl-Adenylate pdb 1KMM C Chain C, Histidyl-Trna Synthetase Complexed With Histidinol And Atp pdb 1KMM A Chain A, Histidyl-Trna Synthetase Complexed With Histidinol And Atp pdb 1KMM B Chain B, Histidyl- Trna Synthetase Complexed With Histidyl- Adenylate pdb 1KMM D Chain D, Histidyl-Trna Synthetase Complexed With Histidyl-Adenylate pdb 1KMM B Chain B, Histidyl-Trna Synthetase Complexed With Histidinol And Atp pdb 1KMM D Chain D, Histidyl-Trna Synthetase Complexed With Histidinol And Atp gb AAA03226.1 (M11843) histidine-trna synthetase [Escherichia coli] gb AAC75567.1 (AE000337) histidine trna synthetase [Escherichia coli K12] dbj BAA16401.1 (D90880) histidine--trna ligase (EC 6.1.1.21) [Escherichia coli] sp P72241 GCPE_PROST GCPE PROTEIN HOMOLOG gb AAB51469.1 (U67933) Aarc [Providencia stuartii]	SEQ ID n-1866
SEQ ID n° 7494	PL-2669.1	Contig9 from 1853177 to 1854454	m 86%	gb AAG57626.1 AE005481_2 (AE005481) putative membrane protein [Escherichia coli O157:H7]	SEQ ID n-1862
SEQ ID n° 7495	PL-2668.1	Contig9 from 1854573 to 1855694	m 84%		SEQ ID n-1863
SEQ ID n° 7496	PL-2667.1	Contig9 from 1855768 to 1856808	m 59%		SEQ ID n-1862

TABLEAU II

SEQ ID n° 7497 PL-3917.1	Contig9 from 1856930 to 1857331	m 42%	pir [P82178 probable fimbrial biogenesis and twitching motility protein VC1612 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94766.1 (AE004238) fimbrial biogenesis and twitching motility protein, putative [Vibrio cholerae] sp P36979 YFGB ECOLI HYPOTHETICAL 43.1 KDA PROTEIN IN NDK-GCPE INTERGENIC REGION SEQ ID n-3081
SEQ ID n° 7498 PL-2666.1	Contig9 from 1857448 to 1858626	m 86%	pir [D65028 hypothetical 43.1 kD protein in ndk- gcpe intergenic region - Escherichia coli (strain K-12) gb AAZ1359.1 (U02965) unknown [Escherichia coli] gb AAC75570.1 (AE000338) orf, hypothetical protein [Escherichia coli K12] dbj BAAL6404.1 (D90881) similar to [SwissProt Accession Number P36979] [Escherichia coli] dbj BAAL6408.1 (D90882) similar to [SwissProt Accession Number P36979] [Escherichia coli] gb AA93513.1 (L37442) thymidylate:zeocin resistance protein:NDP kinase fusion protein [Cloning vector pZEO-SG4] sp P76577 PBPC_ECOLI BIFUNCTIONAL PENICILLIN- BINDING PROTEIN 1C PRECURSOR (PBP-1C) SEQ ID n-2861
SEQ ID n° 7499 PL-3916.1	Contig9 from 1858809 to 1859234	m 74%	pir [F65028 hypothetical protein b2519 - Escherichia coli (strain K-12) gb AAC75572.1 (AE000338) putative peptidoglycan enzyme [Escherichia coli K12] gb AAB48052.1 (U88571) bifunctional penicillin-binding protein 1C [Escherichia coli] gb AAG57634.1 AE005482_1 (AE005482) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3080
SEQ ID n° 7500 PL-2664.1	Contig9 from 1859454 to 1861775	m 72%	pir [G75120 hypothetical protein PAB0518 - Pyrococcus abyssi (strain Orsay) emb CAB49680.1 (AJ248285) hypothetical protein [Pyrococcus abyssi] SEQ ID n-2860
SEQ ID n° 7501 PL-2663.1	Contig9 from 1861832 to 1866862	m 72%	SEQ ID n-2859
SEQ ID n° 7502 PL-2662.1	Contig9 from 1868104 to 1868904	m 49%	SEQ ID n-2858

TABLEAU II

SEQ ID n° 7503	PL-2661.1	Contig9 from 1870488 to 1872152	p 56%	pir F82543 outer membrane hemolysin activator protein XF2550 [imported] - Xylella fastidiososa (strain 9a5c) gb AAF85347.1 AE004062_2 (AE004062) outer membrane hemolysin activator protein [Xylella fastidiososa] SEQ ID n° 2857
SEQ ID n° 7504	PL-2660.1	Contig9 from 1872201 to 1881086	p 46%	pir E82589 hemagglutinin-like secreted protein XF2196 [imported] - Xylella fastidiososa (strain 9a5c) gb AAF84995.1 AE004032_14 (AE004032) hemagglutinin-like secreted protein [Xylella fastidiososa] SEQ ID n° 2856
SEQ ID n° 7505	PL-6921.1	Contig9 from 1881788 to 1882600	p No Hits found	#N/A
SEQ ID n° 7506	PL-7430.1	Contig9 from 1882597 to 1882914	p No Hits found	#N/A
SEQ ID n° 7507	PL-7429.1	Contig9 from 1882959 to 1883201	m 38%	sp P39394 YJW_ECOLI_HYPOTHETICAL 14.6 KDA PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132) pir S56573 hypothetical 14.6K protein (mcrB-hsdS intergenic region) - Escherichia coli gb AA97244.1 (U14003) ORF_f132 [Escherichia coli] gb AAC77303.1 (AE000505) orf, hypothetical protein [Escherichia coli K12] #N/A
SEQ ID n° 7508	PL-6485.1	Contig9 from 1883294 to 1883665	m 48%	sp O34419 RSR1_VIBCH_CRYPTIC PHAGE CTXPHI TRANSCRIPTIONAL REPRESSOR RSTR pir H82197 transcription repressor Rstr VC1464 VC1455 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAB81724.1 (U83795) Rstr [Vibrio cholerae] gb AAB81728.1 (U83796) Rstr [Vibrio cholerae] gb AAF94612.1 (AE004224) transcriptional repressor Rstr [Vibrio cholerae] gb AAF94621.1 (AE004224) transcriptional repressor Rstr [Vibrio cholerae] #N/A

TABLEAU II

SEQ ID n° 7509	PL-4048.2	Contig9 from 1883765 to 1884193	p	37%	dbj BAB05094.1 (AP001511) DNA primase [Bacillus halodurans]	#N/A
SEQ ID n° 7510	PL-3161.1	Contig9 from 1884204 to 1885586	p	57%	pdb 1F3I A Chain A, Crystal Structure Of Tn5 Transposase Complexed With End Dna	SEQ ID n-2408
SEQ ID n° 7511	PL-3160.2	Contig9 from 1885620 to 1888583	p	11%	sp 067465 PRIM_AQUAE DNA PRIMASE pir [G70429 DNA primase - Aquifex aeolicus gb AAC07430.1 (AEC000743) DNA primase [Aquifex aeolicus]	#N/A
SEQ ID n° 7512	PL-3158.1	Contig9 from 1888570 to 1889700	p	31%	gb AAF89876.1 (AF173869) putative site-specific recombinase XerD [Staphylococcus aureus]	SEQ ID n-2404
SEQ ID n° 7513	PL-6926.1	Contig9 from 1890255 to 1890521	p	No Hits found		#N/A
SEQ ID n° 7514	PL-4051.1	Contig9 from 1890543 to 1891010	p	No Hits found		SEQ ID n-3197
SEQ ID n° 7515	PL-6474.1	Contig9 from 1891060 to 1891371	p	No Hits found		#N/A
SEQ ID n° 7516	PL-4052.1	Contig9 from 1891368 to 1891823	p	No Hits found		SEQ ID n-3198
SEQ ID n° 7517	PL-6473.1	Contig9 from 1891864 to 1891995	p	No Hits found		#N/A
SEQ ID n° 7518	PL-3188.1	Contig9 from 1892043 to 1892699	p	No Hits found		SEQ ID n-2437
SEQ ID n° 7519	PL-6471.1	Contig9 from 1892973 to 1893320	p	41%	pir [B81207 hypothetical protein NMB0372 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF40814.1 (AE002393) hypothetical protein [Neisseria meningitidis MC58]	#N/A

TABLEAU II

SEQ ID n° 7520	PL-4053.2	Contig9 from 1893324 to 1893779	p	No Hits found	#N/A
SEQ ID n° 7521	PL-7004.1	Contig9 from 1893815 to 1893970	p	No Hits found	#N/A
SEQ ID n° 7522	PL-6820.2	Contig9 from 1894538 to 1894660	p	No Hits found	#N/A
SEQ ID n° 7523	PL-6819.2	Contig9 from 1894648 to 1894992	p	No Hits found	#N/A
SEQ ID n° 7524	PL-4010.2	Contig9 from 1895179 to 1895691	p	No Hits found	#N/A
SEQ ID n° 7525	PL-2599.1	Contig9 from 1896176 to 1897060	m	59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] SEQ ID n-1790
SEQ ID n° 7526	PL-2598.1	Contig9 from 1897260 to 1909475	m	34%	pir C82199 RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] SEQ ID n-1789
SEQ ID n° 7527	PL-2597.1	Contig9 from 1910252 to 1920670	m	38%	pir C82199 RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] SEQ ID n-1788
SEQ ID n° 7528	PL-2594.1	Contig9 from 1920633 to 1921286	m	69%	pir C82199 RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] SEQ ID n-1786
SEQ ID n° 7529	PL-2593.1	Contig9 from 1922076 to 1933094	m	41%	pir C82199 RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae] SEQ ID n-1785

THIS PAGE BLANK (USPTO)

TABLEAU II

SEQ ID n° 7530	PL-2590.1	Contig9 from 1933706 to 1938832	m	52%	gb AAD21057.1 (AF119150) RtxA protein [Vibrio cholerae]	SEQ ID n-2783
SEQ ID n° 7531	PL-2588.1	Contig9 from 1938888 to 1944743	m	78%	pir C82199 RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae]	SEQ ID n-2780
SEQ ID n° 7532	PL-4003.1	Contig9 from 1945353 to 1945781	m	62%	pir F75337 transposase - Deinococcus radiodurans (strain R1) gb AAF11477.1 AE002031.6 (AE002031) transposase [Deinococcus radiodurans]	SEQ ID n-3158
SEQ ID n° 7533	PL-3038.3	Contig9 from 1946045 to 1956109	m	38%	pir C82199 RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae]	#N/A
SEQ ID n° 7534	PL-3039.1	Contig9 from 1956110 to 1957099	m	64%	pir C82199 RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae]	SEQ ID n-2272
SEQ ID n° 7535	PL-3888.1	Contig9 from 1957217 to 1957678	m	84%	sp Q9X4W3 RTXC_VIBCH CYTOLYSIN-ACTIVATING LYSINE ACYLTRANSFERASE RTXC pir B82199 RTX toxin activating protein VC1450 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAD21058.1 (AF119150) RtxC protein [Vibrio cholerae] gb AAF94607.1 (AE004223) RTX toxin activating protein [Vibrio cholerae]	SEQ ID n-3057
SEQ ID n° 7536	PL-6805.1	Contig9 from 1957700 to 1958065	m	66%	pir A82199 hypothetical protein VC1449 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94606.1 (AE004223) hypothetical protein [Vibrio cholerae]	#N/A
SEQ ID n° 7537	PL-3040.1	Contig9 from 1958373 to 1960478	p	83%	pir H82198 RTX toxin transporter VC1448 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94605.1 (AE004223) RTX toxin transporter [Vibrio cholerae]	SEQ ID n-2274

TABLEAU II

Contig9 from SEQ ID n° 7538-PL-3041.1 1960471 to 1961826	p	79%	pir [G82198 RTX toxin transporter VC1447 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAD21060.1 (AF119150) RtxD protein [Vibrio cholerae] gb AAF94604.1 (AE004223) RTX toxin transporter [Vibrio cholerae] SEQ ID n-2275
Contig9 from SEQ ID n° 7539 PL-3042.1 1961829 to 1963979	p	83%	pir [F82198 probable toxin secretion transporter VC1446 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94603.1 (AE004223) toxin secretion transporter, putative [Vibrio cholerae] SEQ ID n-2276
Contig9 from SEQ ID n° 7540 PL-3043.1 1964329 to 1965135	p	43%	pir [F83090 probable transcription regulator PA4436 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07824.1 AE004858.2 (AE004858) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-2277
Contig9 from SEQ ID n° 7541 PL-6803.1 1965274 to 1965561	p	67%	sp P75735 YBFE_ECOLI HYPOTHETICAL 13.9 KDA PROTEIN IN FLDA-SEA INTERGENIC REGION pir [D64803 ybfe protein - Escherichia coli gb AAC73779.1 (AE000172) orf, hypothetical protein [Escherichia coli K12] dbj BAA35334.1 (D90707) ORF_ID:0173#3 [Escherichia coli] dbj BAA35342.1 (D90708) ORF_ID:0173#3 [Escherichia coli] gb AAG55008.1 AE005246_8 (AE005246) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
Contig9 from SEQ ID n° 7542 PL-3887.1 1965736 to 1966266	p	85%	sp P23243 FLAV_ECOLI FLAVODOXIN 1 pir [A37319 flavodoxin A - Escherichia coli gb AA23789.1 (M59426) flavodoxin [Escherichia coli] dbj BAA35333.1 (D90707) Flavodoxin. [Escherichia coli] dbj BAA35341.1 (D90708) Flavodoxin. [Escherichia coli] gb AAC73778.1 (AE000172) flavodoxin 1 [Escherichia coli K12] gb AAG55007.1 AB005246_7 (AB005246) flavodoxin 1 [Escherichia coli O157:H7] SEQ ID n-3056

TABLEAU II

SEQ ID n° 7543	PL-6800.1	Contig9 from 1966632 to 1967078	p	92%	gb AAD01582.1 (AF016035) ferric uptake regulation protein [Pectobacterium chrysanthemi] #N/A
SEQ ID n° 7544	PL-6799.1	Contig9 from 1967177 to 1967458	m	71%	pir [c82603 conserved hypothetical protein XF2080 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84879.1 AE004023_15 (AE004023) conserved hypothetical protein [Xylella fastidiosa] #N/A
SEQ ID n° 7545	PL-6798.1	Contig9 from 1967445 to 1967708	m	72%	pir [H82603 DNA-damage-inducible protein XF2081 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84880.1 AE004023_16 (AE004023) DNA-damage-inducible protein [Xylella fastidiosa] #N/A
SEQ ID n° 7546	PL-3044.1	Contig9 from 1968029 to 1970704	m	78%	sp Q54468 CHB_SERMA CHITOBIASE PRECURSOR (N- ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) pir [JC4732 beta-N- acetylhexosaminidase (EC 3.2.1.52) - Serratia marcescens gb AAB03808.1 (L43594) N-acetyl- beta-D-glucosaminidase [Serratia marcescens] SEQ ID n-2278
SEQ ID n° 7547	PL-3886.1	Contig9 from 1971398 to 1971847	m	30%	dbj BAB05723.1 (AP001514) gentisate 1,2- dioxygenase [Bacillus halodurans] SEQ ID n-3055
SEQ ID n° 7548	PL-3045.1	Contig9 from 1972465 to 1974132	m	53%	emb CAA51370.1 (X72850) 2,4-dihydroxybenzoate monooxygenase [Sphingomonas sp.] SEQ ID n-2279
SEQ ID n° 7549	PL-6795.1	Contig9 from 1974698 to 1975054	m	No Hits found	#N/A
SEQ ID n° 7550	PL-2971.2	Contig9 from 1975675 to 1976439	m	No Hits found	SEQ ID n-2197

TABLEAU II

SEQ ID n° 7551	PL-2970.1	Contig9 from 1976889 to 1977782	P	68%	pir D83357 probable transcription regulator PA2316 [imported] - Pseudomonas aeruginosa (strain PA01) gb AA05704.1 AE004657.11 (AE004657) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-2196
SEQ ID n° 7552	PL-2969.1	Contig9 from 1977952 to 1979619	m	87%	sp P00962 SYQ_ECOLI GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) pir SYECQT glutamine--trna ligase (EC 6.1.1.18) [validated] - Escherichia coli emb CAA24894.1 (V01575) glutaminy1-trna synthetase precursor [Escherichia coli] gb AAC73774.1 (AE000171) glutamine trna synthetase [Escherichia coli K12] dbj BAA35328.1 (D90707) Glutaminy1-trna synthetase (EC 6.1.1.18) (glutamine-trna ligase) (GlnRS). [Escherichia coli] pir F82254 PTS system, N-acetylglucosamine- specific IIABC component VC0995 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94156.1 (AE004181) PTS system, N- acetylglucosamine-specific IIABC component [Vibrio cholerae] SEQ ID n-2194
SEQ ID n° 7553	PL-2968.1	Contig9 from 1980670 to 1982184	p	67%	acetylglucosamine-specific IIABC component [Vibrio cholerae] SEQ ID n-2193

TABLEAU II

SEQ ID n° 7554 PL-2967.2	Contig9 from 1982462 to 1983274	p 854	sp P09375 NAGB_ECOLI GLUCOSAMINE-6-PHOSPHATE ISOMERASE (GLUCOSAMINE-6-PHOSPHATE DEAMINASE) (GNPDA) (GLC6P DEAMINASE) pir MUECNG glucosamine-6-phosphate isomerase (EC 5.3.1.10) - Escherichia coli pdb IDEA A Chain A, Mol id: 1; Molecule: Glucosamine 6- Phosphate Deaminase; Chain: A, B; Ec: 5.3.1.10; Engineered: Yes; Heterogen: Inorganic Phosphate pdb IDEA B Chain B, Mol_id: 1; Molecule: Glucosamine 6-Phosphate Deaminase; Chain: A, B; Ec: 5.3.1.10; Engineered: Yes; Heterogen: Inorganic Phosphate pdb ICD5 A Chain A, Glucosamine-6-Phosphate Deaminase From E.Coli, T Conformer pdb IHOT A Chain A, Glucosamine 6-Phosphate Deaminase Complexed With The Allosteric Activator N-Acetyl-Glucosamine-6-Phosphate pdb IHOT B Chain B, Glucosamine 6-Phosphate Deaminase Complexed With The Allosteric Activator N-Acetyl-Glucosamine-6- Phosphate pdb IHOR A Chain A, Mol_id: 1; Molecule: Glucosamine 6-Phosphate Deaminase; Chain: A, B; Ec: 5.3.1.10; Engineered: Yes;
			SEQ ID n-2192

TABLEAU II

SEQ ID n° 7555 PL-2966.2	Contig9 from 1983359 to 1984519	p 77%	sp P15300 NAGA_ECOLI N-ACETYLGLUCOSAMINE-6- PHOSPHATE DEACETYLASE (GLCNAC 6-P phosphate deacetylase (EC 3.5.1.25) - Escherichia coli emb CAA32353.1 (X14135) naga gene product (AA 1-382) [Escherichia coli] dbj BAA35320.1 (D90706) N-acetylglucosamine-6- phosphate deacetylase (EC 3.5.1.25) (Naga) [Escherichia coli] dbj BAA35325.1 (D90707) N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (Naga) [Escherichia coli] gb AAC73771.1 (AE000171) N- acetylglucosamine-6-phosphate deacetylase [Escherichia coli K12] gb AAC09325.1 (AF052007) N-acetylglucosamine-6- phosphate deacetylase [Escherichia coli] gb AAG54999.1 (AE005245_8 (AE005245) N- acetylglucosamine-6-phosphate deacetylase [Escherichia coli O157:H7] sp P15301 NAGC_ECOLI N-ACETYLGLUCOSAMINE REPRESSOR pir C64802 N-acetylglucosamine repressor - Escherichia coli dbj BAA35319.1 (D90706) N-acetylglucosamine repressor. [Escherichia coli] dbj BAA35324.1 (D90707) N- acetylglucosamine repressor. [Escherichia coli] gb AAC73770.1 (AE000171) transcriptional repressor of nag (N-acetylglucosamine) operon [Escherichia coli K12] gb AAC09326.1 (AF052007) N-acetylglucosamine repressor [Escherichia coli] gb AAG54998.1 (AE005245_7 (AE005245) transcriptional repressor of nag (N- acetylglucosamine) operon [Escherichia coli O157:H7] pir E64801 hypothetical protein b0663 - Escherichia coli gb AAC73764.1 (AE000170) putative RNA [Escherichia coli K12]
			SEQ ID n~2191
SEQ ID n° 7556 PL-2965.1	Contig9 from 1984535 to 1985758	p 85%	
SEQ ID n° 7557 PL-6789.1	Contig9 from 1986096 to 1986260	m 33%	

#N/A

TABLEAU II

SEQ ID n° 7558	PL-2964.1	Contig9 from 1986755 to 1987936	m	63%	gb AAG54995.1 AE005245_4 (AE005245) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2189
SEQ ID n° 7559	PL-2963.1	Contig9 from 1988135 to 1989565	p	91%	emb CAB62263.1 (AJ249116) MiaB protein [Salmonella typhimurium]	SEQ ID n-2188
SEQ ID n° 7560	PL-2962.1	Contig9 from 1989581 to 1990630	p	90%	emb CAB62264.1 (AJ249116) Ybez protein [Salmonella typhimurium]	SEQ ID n-2187
SEQ ID n° 7561	PL-3885.1	Contig9 from 1990627 to 1991094	p	83%	sp P77385 YBEY_ECOLI HYPOTHETICAL 17.5 KDA PROTEIN IN CUTE-CORC INTERGENIC REGION pir A64801 ybez protein - Escherichia coli gb AAB40861.1 (U82598) HI0004 homolog [Escherichia coli] gb AAC73760.1 (AE000170) orf, hypothetical protein [Escherichia coli K12] dbj BAA35314.1 (D90706) Hypothetical protein HI0004 [Escherichia coli]	SEQ ID n-3054
SEQ ID n° 7562	PL-2961.1	Contig9 from 1991167 to 1992048	p	91%	sp P77392 YBEX_ECOLI HYPOTHETICAL 33.3 KDA PROTEIN IN CUTE-ASNB INTERGENIC REGION pir H64800 ybez protein - Escherichia coli gb AAB40860.1 (U82598) similar to H. influenzae [Escherichia coli] gb AAC73759.1 (AE000170) putative transport protein [Escherichia coli K12] gb AAG54991.1 AE005244_9 (AE005244) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-2186
SEQ ID n° 7563	PL-2960.1	Contig9 from 1992056 to 1993585	p	77%	gb AAD09824.1 (AF116773) apolipoprotein N- acyltransferase [Salmonella typhimurium]	SEQ ID n-2185
SEQ ID n° 7564	PL-2959.1	Contig9 from 1994148 to 1995041	p	75%	dbj BAA35307.1 (D90705) Hypothetical protein in glutJ 5' region . [Escherichia coli]	SEQ ID n-2183

TABLEAU II

SEQ ID n° 7565 PL-2958.1	Contig9 from 1995174 to 1995914	p 79%	sp P41074 GLTJ_ECOLI GLUTAMATE/ASPARTATE TRANSPORT SYSTEM PERMEASE PROTEIN GLTJ pir D64800 glutamate/aspartate transport protein gltJ - Escherichia coli gb AAA60980.1 (U10981) gltJ [Escherichia coli] dbj BAA35306.1 (D90705) Glutamate/aspartate transport system permease protein gltJ. [Escherichia coli] gb AAB40855.1 (U82598) glutamate/aspartate transport system permease protein [Escherichia coli] gb AAC73755.1 (AE000169) glutamate/aspartate transport system permease [Escherichia coli K12]	SEQ ID n-2182
			sp P41075 GLTK_ECOLI GLUTAMATE/ASPARTATE TRANSPORT SYSTEM PERMEASE PROTEIN GLTK pir C64800 glutamate/aspartate transport protein gltK - Escherichia coli gb AAA60981.1 (U10981) gltK [Escherichia coli] dbj BAA35305.1 (D90705) Glutamate/aspartate transport system permease protein gltK. [Escherichia coli] gb AAB40854.1 (U82598) glutamate/aspartate transport system permease protein [Escherichia coli] gb AAC73754.1 (AE000169) glutamate/aspartate transport system permease [Escherichia coli K12] gb AAC54987.1 AE005244_5 (AE005244) glutamate/aspartate transport system permease [Escherichia coli O157:H7]	
SEQ ID n° 7566 PL-2957.1	Contig9 from 1995915 to 1996589	p 91%	sp P41074 GLTJ_ECOLI GLUTAMATE/ASPARTATE TRANSPORT SYSTEM PERMEASE PROTEIN GLTJ pir D64800 glutamate/aspartate transport protein gltJ - Escherichia coli gb AAA60980.1 (U10981) gltJ [Escherichia coli] dbj BAA35306.1 (D90705) Glutamate/aspartate transport system permease protein gltJ. [Escherichia coli] gb AAB40855.1 (U82598) glutamate/aspartate transport system permease protein [Escherichia coli] gb AAC73755.1 (AE000169) glutamate/aspartate transport system permease [Escherichia coli K12]	SEQ ID n-2182
			sp P41075 GLTK_ECOLI GLUTAMATE/ASPARTATE TRANSPORT SYSTEM PERMEASE PROTEIN GLTK pir C64800 glutamate/aspartate transport protein gltK - Escherichia coli gb AAA60981.1 (U10981) gltK [Escherichia coli] dbj BAA35305.1 (D90705) Glutamate/aspartate transport system permease protein gltK. [Escherichia coli] gb AAB40854.1 (U82598) glutamate/aspartate transport system permease protein [Escherichia coli] gb AAC73754.1 (AE000169) glutamate/aspartate transport system permease [Escherichia coli K12] gb AAC54987.1 AE005244_5 (AE005244) glutamate/aspartate transport system permease [Escherichia coli O157:H7]	

TABLEAU II

SEQ ID n° 7567 PL-2956.1	Contig9 from 1996589 to 1997314	p 90%	sp P41076 GLTL_ECOLI GLUTAMATE/ASPARTATE TRANSPORT ATP-BINDING PROTEIN GLTL pir B64800 glutamate/aspartate transport protein gltl - Escherichia coli gb AAAG0982.1 (U10981) GltL [Escherichia coli] dbj BAA35304.1 (D90705) Glutamate/aspartate transport atp-binding protein gltl. [Escherichia coli] gb AAB40853.1 (U82598) glutamate/aspartate transport ATP-binding protein [Escherichia coli] gb AAC73753.1 (AE000169) ATP-binding protein of glutamate/aspartate transport system [Escherichia coli K12] gb AAG54986.1 AE005244_4 (AE005244) ATP- binding protein of glutamate/aspartate transport system [Escherichia coli O157:H7]	SEQ ID n-2180
			gb AAG54976.1 AE005243_5 (AE005243) leucine tRNA synthetase [Escherichia coli O157:H7]	
SEQ ID n° 7568 PL-2955.1	Contig9 from 1997477 to 2000059	p 88%	sp P10101 RLPB_ECOLI RARE LIPOPROTEIN B PRECURSOR pir LPECRB lipoprotein rlpB precursor - Escherichia coli dbj BAA35288.1 (D90704) Lipoprotein rlpB precursor. [Escherichia coli] gb AAB40842.1 (U82598) lipoprotein B precursor [Escherichia coli] gb AAC73742.1 (AE000168) a minor lipoprotein [Escherichia coli K12]	SEQ ID n-2179
SEQ ID n° 7569 PL-3883.1	Contig9 from 2000073 to 2000621	p 63%		SEQ ID n-3053

TABLEAU II

SEQ ID n° 7570 PL-2954.1	Contig9 from 2000618 to 2001658	p 72%	sp P28630 HOLA_ECOLI DNA POLYMERASE III, DELTA SUBUNIT pir A45251 DNA-directed DNA polymerase (EC 2.7.7.7) III delta chain - Escherichia coli gb AA23675.1 (U04576) DNA polymerase III delta subunit [Escherichia coli] gb AB59047.1 (M94267) DNA polymerase III delta subunit [Escherichia coli] dbj BA35287.1 (D90704) DNA-directed DNA polymerase (EC 2.7.7.7) III delta chain [Escherichia coli] gb AB40841.1 (U82598) DNA-directed DNA polymerase III delta chain [Escherichia coli] gb AAC73741.1 (AE000168) DNA polymerase III, delta subunit [Escherichia coli K12] SEQ ID n-2178
			gb AGS4973.1 AE005243_2 (AE005243) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2177
			sp P05848 YBEB_ECOLI HYPOTHETICAL 11.6 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION gb AB40837.1 (U82598) HI0034 homolog [Escherichia coli] #N/A
SEQ ID n° 7571 PL-2953.1	Contig9 from 2001642 to 2002319	p 63%	sp P05850 YBEA_ECOLI HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION pir QOECPI ybeA protein - Escherichia coli emb CA28200.1 (X04516) ORF2 (AA 1-155) [Escherichia coli] gb AB40836.1 (U82598) hypothetical protein [Escherichia coli] gb AAC73737.1 (AE000168) orf, hypothetical protein [Escherichia coli K12] dbj BA35283.1 (D90704) Hypothetical 17k protein (pbpa 5' region) [Escherichia coli] gb AGS4970.1 AE005242_14 (AE005242) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3052
SEQ ID n° 7572 PL-6782.1	Contig9 from 2002427 to 2002744	p 86%	
SEQ ID n° 7573 PL-3882.1	Contig9 from 2002747 to 2003217	p 81%	

TABLEAU II

SEQ ID n° 7574 PL-2952.1	Contig9 from 2003258 to 2005153	p 84%	sp P08150 PBP2_ECOLI PENICILLIN-BINDING PROTEIN 2 (PBP-2) pir ZPBCP2 penicillin-binding protein 2 - Escherichia coli emb CAA28201.1 (X04516) penicillin-binding protein 2 (PBP2) [Escherichia coli] dbj BAA35282.1 (D90704)
			Penicillin-binding protein 2 (pbp-2). [Escherichia coli] gb AAB40835.1 (U82598)
			penicillin-binding protein 2 [Escherichia coli] gb AAC73736.1 (AE000168) cell elongation, e phase; peptidoglycan synthetase; penicillin-binding protein 2 [Escherichia coli K12] gb AAG54969.1 AE005242_13 (AE005242) cell elongation, e phase; peptidoglycan synthetase; penicillin-binding protein 2 [Escherichia coli O157:H7]
SEQ ID n° 7575 PL-2951.1	Contig9 from 2005162 to 2006274	p 90%	sp P15035 RODA_ECOLI ROD SHAPE-DETERMINING PROTEIN RODA pir BVECRD rod shape-determining protein mrdB - Escherichia coli gb AAA24571.1 (M22857) rod-shape-determining protein [Escherichia coli] dbj BAA35277.1 (D90703) Rod shape-determining protein MrdB. [Escherichia coli] gb AAB40834.1 (U82598) rod-shape- determining protein [Escherichia coli] gb AAC73735.1 (AE000168) rod shape-determining membrane protein; sensitivity to radiation and drugs [Escherichia coli K12] dbj BAA35281.1 (D90704) Rod shape-determining protein MrdB. [Escherichia coli] gb AAG54968.1 AE005242_12 (AE005242) rod shape- determining membrane protein; sensitivity to radiation and drugs [Escherichia coli O157:H7]
			gb AAG54967.1 AE005242_11 (AE005242) a minor lipoprotein [Escherichia coli O157:H7]
SEQ ID n° 7576 PL-2950.2	Contig9 from 2006288 to 2007286	p 64%	

SEQ ID n-2176

SEQ ID n-2175

SEQ ID n-2174

TABLEAU II

SEQ ID n° 7577 PL-2949.2	Contig9 from 2007491 to 2008660	p 82%	gb AAB40832.1 (U82598) penicillin-binding protein 5 [Escherichia coli] sp P30977 YBED_ECOLI HYPOTHETICAL 9.8 KDA PROTEIN IN LIPB-DACA INTERGENIC REGION (ORF1) pir E64797 ybed protein - Escherichia coli gb AAA66341.1 (L07636) ORF 1 [Escherichia coli] gb AAB40831.1 (U82598) hypothetical protein [Escherichia coli] gb AAC73732.1 (AE000168) orf, hypothetical protein [Escherichia coli K12] dbj BAA35274.1 (D90703) Hypothetical 9.8 kd protein in lipB-dacA intergenic region (orf1). [Escherichia coli] gb AAG54965.1 AE005242_9 (AE005242) orf, hypothetical protein [Escherichia coli O157:H7] #N/A	SEQ ID n-2172
SEQ ID n° 7578 PL-6780.1	Contig9 from 2008801 to 2009064	p 72%	sp P30976 LIPB_ECOLI LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS PROTEIN B) sp P25945 LIPA_ECOLI LIPOIC ACID SYNTHETASE (LIP- SYN) (LIPOATE SYNTHASE) pir E64797 lipolic acid synthase (EC 2.8.1.-) [validated] - Escherichia coli dbj BAA35271.1 (D90703) Lipolic acid synthetase (lip-syn). [Escherichia coli] gb AAB40828.1 (U82598) lipolic acid synthetase [Escherichia coli] gb AAC73729.1 (AE000167) lipoate synthesis, sulfur insertion? [Escherichia coli K12] sp P37002 CRCB_ECOLI CRCB PROTEIN pir F64796 crcB protein - Escherichia coli gb AAB40824.1 (U82598) hypothetical protein [Escherichia coli] gb AAC73725.1 (AE000167) orf, hypothetical protein [Escherichia coli K12] dbj BAA35267.1 (D90703) Hypothetical 13.8 kd protein in cspB- lipA intergenic region. [Escherichia coli]	SEQ ID n-2170
SEQ ID n° 7579 PL-2948.1	Contig9 from 2009172 to 2009837	p 68%	Contig9 from 2009948 to 2010913	SEQ ID n-2171
SEQ ID n° 7580 PL-2947.1	Contig9 from 2011053 to 2011427	p 60%		

TABLEAU II

SEQ ID n° 7582 PL-6778.1	Contig9 from 2011504 to 2011716	m	65%	gb AAB40823.1 (U82598) cold shock-like protein [Escherichia coli]	#N/A
SEQ ID n° 7583 PL-3880.1	Contig9 from 2011932 to 2012393	m	60%	pir P82390 methylated-DNA--protein-cysteine S- methyltransferase (EC 2.1.1.63) VCA1017 [similarity] - Vibrio cholerae (group O1 strain N16961) gb AAF96913.1 (AE004427) methylated-DNA--protein-cysteine S- methyltransferase [Vibrio cholerae] pir P70648 probable NrdH protein - Mycobacterium tuberculosis (strain H37RV) emb CAB06243.1 (Z83866) nrdH [Mycobacterium tuberculosis]	SEQ ID n-3050 #N/A
SEQ ID n° 7584 PL-6777.1	Contig9 from 2012725 to 2012955	p	51%	dbj BAAL6538.1 (D90891) similar to [SwissProt Accession Number P47472] coll	#N/A
SEQ ID n° 7585 PL-6776.1	Contig9 from 2012963 to 2013385	p	68%	gb AAA64444.1 (I34407) ribonucleotide reductase R1 subunit [Mycobacterium tuberculosis]	SEQ ID n-2169
SEQ ID n° 7586 PL-2946.1	Contig9 from 2013388 to 2015517	p	85%	sp P17424 R1A4_SALTY RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 2 BETA CHAIN (RIBONUCLEOTIDE REDUCTASE 2) (R2F PROTEIN) pir S34272 ribonucleoside-diphosphate reductase (EC 1.17.4.1) - Salmonella typhimurium pdb 2R2F A Chain A, Ribonucleotide Reductase R2f Protein From Salmonella Typhimurium (Oxidized) pdb 2R2F B Chain B, Ribonucleotide Reductase R2f Protein From Salmonella Typhimurium (Oxidized) pdb 1R2F A Chain A, Ribonucleotide Reductase R2f Protein From Salmonella Typhimurium pdb 1R2F B Chain B, Ribonucleotide Reductase R2f Protein From Salmonella Typhimurium emb CAA51695.1 (X73226) ribonucleoside- diphosphate reductase [Salmonella typhimurium]	SEQ ID n-2168
SEQ ID n° 7587 PL-2945.1	Contig9 from 2015538 to 2016497	p	84%		

TABLEAU II

SEQ ID n° 7588 PL-2944.1	Contig9 from 2017095 to 2018294	p 84%	sp P14175 PROV_ECOLI GLYCINE BETAINES/L-PROLINE TRANSPORT ATP-BINDING PROTEIN PROV pir BVECPV glycine betaine/L-proline transport ATP-binding protein prov - Escherichia coli gb AA24427.1 (M24856) prov peptide [Escherichia coli] gb AAC75724.1 (AE000352) ATP-binding component of transport system for glycine, betaine and proline [Escherichia coli K12] dbj BA16542.1 (D90891) GLYCINE BETAINES/L-PROLINE TRANSPORT ATP-BINDING PROTEIN PROV. [Escherichia coli] SEQ ID n-2167
			sp P14176 PROV_ECOLI GLYCINE BETAINES/L-PROLINE TRANSPORT SYSTEM PERMEASE PROTEIN PROV pir MMECPW glycine betaine/L-proline transport system permease protein P - Escherichia coli gb AA24428.1 (M24856) prov peptide [Escherichia coli] gb AAC75725.1 (AE000352) high-affinity transport system for glycine betaine and proline [Escherichia coli K12] dbj BA16543.1 (D90891) glycine betaine/proline transport system protein prov [Escherichia coli] SEQ ID n-2166
SEQ ID n° 7590 PL-2942.1	Contig9 from 2019442 to 2020440	p 77%	sp P14177 PROX_ECOLI GLYCINE BETAINES-BINDING PERIPLASMIC PROTEIN PRECURSOR pir BLECGP glycine betaine/proline transport system binding protein prox precursor - Escherichia coli gb AA24429.1 (M24856) prox peptide precursor [Escherichia coli] gb AAC75726.1 (AE000352) high-affinity transport system for glycine betaine and proline [Escherichia coli K12] dbj BA16544.1 (D90891) GLYCINE BETAINES-BINDING PERIPLASMIC PROTEIN PRECURSOR. [Escherichia coli] SEQ ID n-2165
			gb AGS7790.1 AE005497_1 (AE005497) putative transport protein [Escherichia coli O157:H7] SEQ ID n-2164

TABLEAU II

SEQ ID n° 7592	PL-2940.1	Contig9 from 2022132 to 2022890	P	72%	sp P76630 YGAZ_ECOLI HYPOTHETICAL 26.1 KD PROTEIN IN PROX-MPRA INTERGENIC REGION pir [C65048 hypothetical protein b2682 - Escherichia coli (strain K-12) gb AAC75729.1 (AE000353) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-2163
SEQ ID n° 7593	PL-6772.1	Contig9 from 2022887 to 2023225	P	63%	sp P43667 YGAH_ECOLI HYPOTHETICAL 12.0 KDA PROTEIN IN PROX-EMMR INTERGENIC REGION pir [D65048 hypothetical protein (emrR 5' region) - Escherichia coli (strain K- 12) gb AAC75730.1 (AE000353) orf, hypothetical protein [Escherichia coli K12] dbj BAAL6545.1 (D90891) similar to [SwissProt Accession Number P43667] [Escherichia coli] #N/A
SEQ ID n° 7594	PL-3879.1	Contig9 from 2023355 to 2023882	P	79%	sp P24201 MPRA_ECOLI TRANSCRIPTIONAL REPRESSOR MPRA (EMMR PROTEIN) pir [S14473 regulatory protein mprA - Escherichia coli emb CAA38090.1 (X54151) mprA [Escherichia coli] gb AAC75731.1 (AE000353) regulator of plasmid mcrB operon (microcin B17 synthesis) [Escherichia coli K12] dbj BAAL6546.1 (D90891) EMMR PROTEIN. [Escherichia coli] SEQ ID n-3048
SEQ ID n° 7595	PL-2939.1	Contig9 from 2024116 to 2025300	P	75%	gb AAG57794.1 AE005497_5 (AE005497) multidrug resistance secretion protein [Escherichia coli O157:H7] SEQ ID n-2161
SEQ ID n° 7596	PL-2938.1	Contig9 from 2025315 to 2026856	P	87%	sp P27304 EMRB_ECOLI MULTIDRUG RESISTANCE PROTEIN B pir [G65048 multidrug resistance protein B - Escherichia coli gb AAC75733.1 (AE000353) multidrug resistance; probably membrane translocase [Escherichia coli K12] dbj BAAL6548.1 (D90891) multidrug resistant protein emrB [Escherichia coli] dbj BAAL6553.1 (D90892) multidrug resistant protein emrB [Escherichia coli] SEQ ID n-2160

TABLEAU II

SEQ ID n° 7597	PL-2937.1	Contig9 from 2026906 to 2027922	m	73%	sp P33635 YFIY_ECOLI HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE YFIY pir D65036 hypothetical 37.8 kD protein in ung 3' region - Escherichia coli (strain K-12) gb AAC75634.1 (AE000344) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-2159
SEQ ID n° 7598	PL-6766.1	Contig9 from 2028022 to 2028264	p	No Hits found	#N/A	
SEQ ID n° 7599	PL-2936.1	Contig9 from 2028245 to 2030887	p	82%	sp P76594 YFIQ_ECOLI HYPOTHETICAL 98.0 kD PROTEIN IN UNG-P89A INTERGENIC REGION pir G65036 hypothetical protein b2584 - Escherichia coli (strain K-12) gb AAC75637.1 (AE000344) orf, hypothetical protein [Escherichia coli K12] dbj BAAL6470.1 (D90886) CDP-DIACYLGLYCEROL-- SERINE O-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.8) (PHOSPHATIDYLTRANSFERASE) [Escherichia coli] dbj BAAL6473.1 (D90887) CDP-DIACYLGLYCEROL--SERINE O- PHOSPHATIDYLTRANSFERASE (EC 2.7.8.8) (PHOSPHATIDYLTRANSFERASE). [Escherichia coli]	SEQ ID n-2158
SEQ ID n° 7600	PL-2935.1	Contig9 from 2031048 to 2032406	p	81%		SEQ ID n-2157
SEQ ID n° 7601	PL-7426.1	Contig9 from 2033324 to 2033479	m	No Hits found	#N/A	
SEQ ID n° 7602	PL-7424.1	Contig9 from 2034879 to 2034911	p	No Hits found	#N/A	
SEQ ID n° 7603	PL-1786.1	Contig9 from 2038549 to 2041122	m	91%	gb AAG57705.1 AE005489_4 (AE005489) heat shock protein [Escherichia coli O157:H7]	SEQ ID n-905

TABLEAU II

SEQ ID n° 7604 PL-1785.1	Contig9 from 2041256 to 2041987	m	72%	sp P33644 YFIIH_ECOLI HYPOTHETICAL 26.3 KDA PROTEIN IN SFHB-CLPB INTERGENIC REGION pir D65037 hypothetical 26.3 kD protein in clpb 5'region - Escherichia coli (strain K-12) gb AAC75642.1 (AE000346) orf, hypothetical protein [Escherichia coli K12] dbj BAA16477.1 (D90887) similar to [SwissProt Accession Number P33644] [Escherichia coli] SEQ ID n-904
SEQ ID n° 7605 PL-1784.1	Contig9 from 2041988 to 2042965	m	88%	gb AAF78056.1 AF263561_1 (AF263561) 23S rRNA pseudouridine synthase [secondary endosymbiont of Glycaspis brimblecombei] sp P77146 YFIO_ECOLI HYPOTHETICAL 27.8 KDA LIPOPROTEIN IN RLUD-PHEL INTERGENIC REGION PRECURSOR pir P65037 hypothetical protein b2595 - Escherichia coli (strain K-12) gb AAC75644.1 (AE000346) orf, hypothetical protein [Escherichia coli K12] dbj BAA16480.1 (D90887) similar to [SwissProt Accession Number P44553] [Escherichia coli] SEQ ID n-903
SEQ ID n° 7606 PL-1783.1	Contig9 from 2043101 to 2043835	p	76%	gb AAG57708.1 AE005490_3 (AE005490) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-902 sp P11285 YFIA_ECOLI PROTEIN YFIA pir Q5ECPA hypothetical 13K protein (phea 5' region) - Escherichia coli gb AA24328.1 (M10431) 12,785 MW protein (ORF1) [Escherichia coli] emb CAA94436.1 (Z70523) URP1 (ORF554) [Escherichia coli] gb AAC75646.1 (AE000346) putative yhbH sigma 54 modulator [Escherichia coli K12] dbj BAA16481.1 (D90887) similar to [PIR Accession Number A30275] [Escherichia coli] dbj BAA16483.1 (D90888) similar to [PIR Accession Number A30275] [Escherichia coli] gb AAG57709.1 AE005490_4 (AE005490) putative yhbH sigma 54 modulator [Escherichia coli O157:H7] #N/A
SEQ ID n° 7607 PL-6740.1	Contig9 from 2044123 to 2044485	p	68%	

TABLEAU II

SEQ ID n° 7608	PL-1782.1	Contig9 from 2044755 to 2045912	p	78%	sp P07022 PHEA_ECOLI P-PROTEIN [INCLUDES: CHORISMATE MUTASE (CM); PREPHENATE DEHYDRATASE (PDT)] pir KMECPW chorismate mutase (EC 5.4.99.5) / prephenate dehydratase (EC 4.2.1.51) pheA [validated] - Escherichia coli gb AA24330.1 (M10431) chorismate mutase/prephenate dehydratase [Escherichia coli] gb AAC75648.1 (AE000346) chorismate mutase-P and prephenate dehydratase [Escherichia coli K12] dbj BAAL6484.1 (D90888) chorismate mutase (EC 5.4.99.5) P / prephenate dehydratase (EC 4.2.1.51) [Escherichia coli]	SEQ ID n-901
SEQ ID n° 7609	PL-3878.1	Contig9 from 2046381 to 2046827	p	45%	pir E82237 DNA-binding protein H-NS VC1130 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94289.1 (AE004193) DNA- binding protein H-NS [Vibrio cholerae] sp Q02287 TYRA_ERWHE T-PROTEIN [INCLUDES: CHORISMATE MUTASE (CM); PREPHENATE DEHYDROGENASE (PDH)] pir S29934 chorismate mutase (EC 5.4.99.5) T / prephenate dehydrogenase (EC 1.3.1.12) - Erwinia herbicola emb CAA42950.1 (X60420) chorismate mutase [Erwinia herbicola] gb AAG57712.1 AE005490_7 (AE005490) 3-deoxy-D- arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tyrosine repressible) [Escherichia coli O157:H7] pir A82313 probable beta-ketoacidate enol- lactone hydrolase VC0522 [imported] Vibrio cholerae (group O1 strain N16961) gb AAF93690.1 (AE004138) beta-ketoacidate enol- lactone hydrolase, putative [Vibrio cholerae]	SEQ ID n-9047
SEQ ID n° 7610	PL-1781.1	Contig9 from 2048728 to 2049849	m	81%	sp Q02287 TYRA_ERWHE T-PROTEIN [INCLUDES: CHORISMATE MUTASE (CM); PREPHENATE DEHYDROGENASE (PDH)] pir S29934 chorismate mutase (EC 5.4.99.5) T / prephenate dehydrogenase (EC 1.3.1.12) - Erwinia herbicola emb CAA42950.1 (X60420) chorismate mutase [Erwinia herbicola] gb AAG57712.1 AE005490_7 (AE005490) 3-deoxy-D- arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tyrosine repressible) [Escherichia coli O157:H7] pir A82313 probable beta-ketoacidate enol- lactone hydrolase VC0522 [imported] Vibrio cholerae (group O1 strain N16961) gb AAF93690.1 (AE004138) beta-ketoacidate enol- lactone hydrolase, putative [Vibrio cholerae]	SEQ ID n-900
SEQ ID n° 7611	PL-1780.2	Contig9 from 2049855 to 2050949	m	84%	sp Q02287 TYRA_ERWHE T-PROTEIN [INCLUDES: CHORISMATE MUTASE (CM); PREPHENATE DEHYDROGENASE (PDH)] pir S29934 chorismate mutase (EC 5.4.99.5) T / prephenate dehydrogenase (EC 1.3.1.12) - Erwinia herbicola emb CAA42950.1 (X60420) chorismate mutase [Erwinia herbicola] gb AAG57712.1 AE005490_7 (AE005490) 3-deoxy-D- arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tyrosine repressible) [Escherichia coli O157:H7] pir A82313 probable beta-ketoacidate enol- lactone hydrolase VC0522 [imported] Vibrio cholerae (group O1 strain N16961) gb AAF93690.1 (AE004138) beta-ketoacidate enol- lactone hydrolase, putative [Vibrio cholerae]	SEQ ID n-899
SEQ ID n° 7612	PL-1779.1	Contig9 from 2051490 to 2052296	m	62%	sp Q02287 TYRA_ERWHE T-PROTEIN [INCLUDES: CHORISMATE MUTASE (CM); PREPHENATE DEHYDROGENASE (PDH)] pir S29934 chorismate mutase (EC 5.4.99.5) T / prephenate dehydrogenase (EC 1.3.1.12) - Erwinia herbicola emb CAA42950.1 (X60420) chorismate mutase [Erwinia herbicola] gb AAG57712.1 AE005490_7 (AE005490) 3-deoxy-D- arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tyrosine repressible) [Escherichia coli O157:H7] pir A82313 probable beta-ketoacidate enol- lactone hydrolase VC0522 [imported] Vibrio cholerae (group O1 strain N16961) gb AAF93690.1 (AE004138) beta-ketoacidate enol- lactone hydrolase, putative [Vibrio cholerae]	SEQ ID n-897

TABLEAU II

SEQ ID n° 7613 PL-6738.1	Contig9 from 2052800 to 2053153	m 93%	sp P02420 RL19_ECOLI 50S RIBOSOMAL PROTEIN L19 pir R5EC19 ribosomal protein L19 [validated] - Escherichia coli emb CAA25960.1 (X01818) ribosomal protein L19 (rplS gene) (aa 1-115) [Escherichia coli] gb AAC75655.1 (AE000346) 50S ribosomal subunit protein L19 [Escherichia coli K12] dbj BAI6491.1 (D90888) ribosomal protein L19 [Escherichia coli] gb AAG57717.1 AE005490_12 (AE005490) 50S ribosomal subunit protein L19 [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7614 PL-1778.1	Contig9 from 2053218 to 2053970	m 92%	sp P36244 TRMD_SERMA TRNA (GUANINE-N1) - METHYLTRANSFERASE (M1G-METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE) gb AAA50783.1 (L233334) m1G-methyltransferase [Serratia marcescens]	SEQ ID n-896
SEQ ID n° 7615 PL-3877.1	Contig9 from 2054010 to 2054567	m 88%	pir C65039 hypothetical 21K protein (timD-rpsp intergenic region) - Escherichia coli gb AAC75657.1 (AE000346) orf, hypothetical protein [Escherichia coli K12] dbj BAAL6493.1 (D90888) similar to [SwissProt Accession Number P21504] [Escherichia coli] gb AAG57719.1 AE005490_14 (AE005490) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3046	
SEQ ID n° 7616 PL-6737.1	Contig9 from 2054577 to 2054825	m 78%	sp P44382 RS16_HAETIN 30S RIBOSOMAL PROTEIN S16 pir D64054 ribosomal protein S16 - Haemophilus influenzae (strain Rd KW20) gb AAC21873.1 (U32705) ribosomal protein S16 (rps16) [Haemophilus influenzae Rd]	#N/A

TABLEAU II

SEQ ID n° 7617	PL-1777.2	Contig9 from 2054962 to 2056323	m	92%	sp P07019 SR54_ECOLI SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) (P48) pir [E65039 signal recognition particle protein - Escherichia coli gb AAC75659.1 (AE000347) GTP- binding export factor binds to signal sequence, and RNA [Escherichia coli K12] GTP gb AAG57721.1 AE005491_1 (AE005491) GTP-binding export factor binds to signal sequence, GTP and RNA [Escherichia coli O157:H7] #N/A	SEQ ID n-894
SEQ ID n° 7618	PL-1776.1	Contig9 from 2056508 to 2057299	p	80%	gb AAD31437.1 AF130857_1 (AF130857)-CorH [Salmonella typhimurium]	SEQ ID n-893
SEQ ID n° 7619	PL-1775.1	Contig9 from 2057339 to 2058631	p	86%	sp P37908 YFUD_ECOLI HYPOTHETICAL 46.4 KDA PROTEIN IN FFH-GRPE INTERGENIC REGION	SEQ ID n-9045
SEQ ID n° 7620	PL-3875.1	Contig9 from 2058730 to 2059245	m	86%	gb AAF73475.1 AF268390_2 (AF268390) LuxS [Salmonella typhimurium]	SEQ ID n-892
SEQ ID n° 7621	PL-1774.1	Contig9 from 2059398 to 2060957	m	76%	sp O68838 GSH1_SALTY GLUTAMATE--CYSTEINE LIGASE (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) gb AAC09345.1 (AF055352) gamma-glutamylcysteine synthetase [Salmonella typhimurium]	#N/A
SEQ ID n° 7622	PL-6732.1	Contig9 from 2062170 to 2062355	m	89%	emb CAB46440.1 (AJ238885) RsmA protein [Erwinia carotovora]	SEQ ID n-891
SEQ ID n° 7623	PL-1773.1	Contig9 from 2062602 to 2065232	m	87%	sp P00957 SYA_ECOLI ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) pir [SYECAT alanine--trna ligase (EC 6.1.1.7) [validated] - Escherichia coli gb AAC75739.1 (AE000353) alanyl-trna synthetase [Escherichia coli K12] dbj BAA16559.1 (D90892) ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE--TRNA LIGASE) (ALARS). [Escherichia coli]	

TABLEAU II

SEQ ID n° 7624	PL-1772.1	Contig9 from 2065623 to 2066690	m	94%	sp P96185 RECA_XENBV RECA PROTEIN (RECOMBINASE A) gb AAD12585.1 (U87924) RECA [Xenorhabdus bovienii] sp P51967 YQAD_ENTAG HYPOTHETICAL 17.2 KD PROTEIN 1 IN RECA 5'REGION pir S31480 hypothetical protein 1 - Enterobacter agglomerans gb AA91765.1 (L03291) unnamed protein [Pantoea agglomerans] sp P39196 YGED_ECOLI HYPOTHETICAL 41.7 KD PROTEIN IN MUTH-AAS INTERGENIC REGION pir D65066 hypothetical protein in muth-aas intergenic region - Escherichia coli (strain K-12) gb AAB40482.1 (U29581) ORF_F397 [Escherichia coli] gb AAC75874.1 (AE000367) putative resistance proteins [Escherichia coli K12]	SEQ ID n-890
SEQ ID n° 7625	PL-1771.1	Contig9 from 2066813 to 2067355	m	63%	sp P31119 AAS_ECOLI AAS BIFUNCTIONAL PROTEIN [INCLUDES: 2- ACYLGLYCEROPHOSPHOETHANOLAMINE ACYLTRANSFERASE (2-ACYL-GPE ACYLTRANSFERASE); ACYL-ACYL CARRIER PROTEIN SYNTHETASE (ACYL-ACP SYNTHETASE)] pir E65066 2- acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase - Escherichia coli (strain K-12) gb AAB40483.1 (U29581) 2- acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase [Escherichia coli] gb AAC75875.1 (AE000367) 2-acyl-glycerophospho-ethanolamine acyltransferase; acyl-acyl-carrier protein synthetase [Escherichia coli K12]	SEQ ID n-889
SEQ ID n° 7626	PL-1770.1	Contig9 from 2067381 to 2068577	m	78%	sp P31119 AAS_ECOLI AAS BIFUNCTIONAL PROTEIN [INCLUDES: 2- ACYLGLYCEROPHOSPHOETHANOLAMINE ACYLTRANSFERASE (2-ACYL-GPE ACYLTRANSFERASE); ACYL-ACYL CARRIER PROTEIN SYNTHETASE (ACYL-ACP SYNTHETASE)] pir E65066 2- acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase - Escherichia coli (strain K-12) gb AAB40483.1 (U29581) 2- acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase [Escherichia coli] gb AAC75875.1 (AE000367) 2-acyl-glycerophospho-ethanolamine acyltransferase; acyl-acyl-carrier protein synthetase [Escherichia coli K12]	SEQ ID n-888
SEQ ID n° 7627	PL-1769.1	Contig9 from 2068590 to 2070509	m	74%	sp P31119 AAS_ECOLI AAS BIFUNCTIONAL PROTEIN [INCLUDES: 2- ACYLGLYCEROPHOSPHOETHANOLAMINE ACYLTRANSFERASE (2-ACYL-GPE ACYLTRANSFERASE); ACYL-ACYL CARRIER PROTEIN SYNTHETASE (ACYL-ACP SYNTHETASE)] pir E65066 2- acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase - Escherichia coli (strain K-12) gb AAB40483.1 (U29581) 2- acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase [Escherichia coli] gb AAC75875.1 (AE000367) 2-acyl-glycerophospho-ethanolamine acyltransferase; acyl-acyl-carrier protein synthetase [Escherichia coli K12]	SEQ ID n-886

TABLEAU II

SEQ ID n° 7628	PL-3872.1	Contig9 from 2070609 to 2071133	m	61%	sp P10880 AROL_ERWCH_SHIKIMATE_KINASE (SK) pir S09613 shikimate kinase (EC 2.7.1.71) - Erwinia chrysanthemi pdb 1SHK A Chain A, The Three-Dimensional Structure Of Shikimate Kinase From Erwinia Chrysanthemi pdb 2SHK A Chain A, The Three-Dimensional Structure Of Shikimate Kinase From Erwinia Chrysanthemi Complexed With Adp emb CAA32883.1 (X14777) shikimate kinase [Erwinia chrysanthemi] SEQ ID n-9044 sp P17857 PROA_SERMA_GAMMA-GLUTAMYL_PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE) pir RDSSEM glutamate-5- semialdehyde dehydrogenase (EC 1.2.1.41) - Serratia marcescens emb CAA37255.1 (X53086) gamma-glutamyl phosphate reductase [Serratia marcescens] dbj BAAL4365.1 (D90351) gamma-glutamyl phosphate reductase [Serratia marcescens]	SEQ ID n-885
SEQ ID n° 7630	PL-1767.1	Contig9 from 2072697 to 2073803	m	89%	sp P17856 PROB_SERMA GLUTAMATE 5-KINASE (GAMMA- GLUTAMYL KINASE) (GK) pir KISEEM glutamate 5- kinase (EC 2.7.2.11) - Serratia marcescens emb CAA37254.1 (X53086) gamma-glutamyl kinase [Serratia marcescens]	SEQ ID n-884
SEQ ID n° 7631	PL-1766.2	Contig9 from 2074001 to 2075248	m	72%	gb AAG54564.1 AE005202_2 (AE005202) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-883
SEQ ID n° 7632	PL-3871.1	Contig9 from 2075263 to 2075724	m	89%	prf 1102210A protein gpt [Escherichia coli]	SEQ ID n-9043
SEQ ID n° 7633	PL-1765.2	Contig9 from 2075949 to 2077409	p	82%	gb AAG54562.1 AE005201_15 (AE005201) aminocacetyl- histidine dipeptidase (peptidase D) [Escherichia coli O157:H7]	SEQ ID n-882

TABLEAU II

SEQ ID n° 7634	PL-1764.1	Contig9 from 2077445 to 2078500	m	83%	sp Q47155 DINP_ECOLI DNA-DAMAGE-INDUCIBLE PROTEIN P pir H64747 DNA-damage-inducible protein dinp - Escherichia coli dbj BAA07593.1 (D38582) DinP [Escherichia coli] gb AAB08651.1 (U70214) DinP [Escherichia coli] gb AAC73335.1 (AE000131) damage-inducible protein P; putative trna synthetase [Escherichia coli K12] dbj BAA77901.1 (D83536) DNA-damage- inducible protein p. [Escherichia coli] sp P44523 HXCI_HAEIN HEME-HEMOPEXIN UTILIZATION PROTEIN C PRECURSOR pir B64049 outer membrane protein hxuc homolog - Haemophilus influenzae (strain Rd KW20) gb AAC21789.1 (U32696) hemin receptor (hemR) [Haemophilus influenzae Rd] SEQ ID n-881
SEQ ID n° 7635	PL-1763.1	Contig9 from 2078761 to 2081061	p	61%	ref NP_053218.1 pXO2-63 [Bacillus anthracis] gb AAF13668.1 AF188935_66 (AF188935) pXO2-63 [Bacillus anthracis] pir F83158 probable sigma-70 factor, ECF subfamily PA3899 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07286.1 AE004807_5 (AE004807) probable sigma-70 factor, ECF subfamily [Pseudomonas aeruginosa] pir F83047 conserved hypothetical protein PA4792 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08178.1 AE004892_9 (AE004892) conserved hypothetical protein [Pseudomonas aeruginosa] dbj BAA16380.1 (D90878) FORMATE HYDROGENLYASE TRANSCRIPTIONAL ACTIVATOR. [Escherichia coli] SEQ ID n-877
SEQ ID n° 7636	PL-1762.1	Contig9 from 2081434 to 2081631	p	50%	ref NP_053218.1 pXO2-63 [Bacillus anthracis] gb AAF13668.1 AF188935_66 (AF188935) pXO2-63 [Bacillus anthracis] pir F83158 probable sigma-70 factor, ECF subfamily PA3899 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07286.1 AE004807_5 (AE004807) probable sigma-70 factor, ECF subfamily [Pseudomonas aeruginosa] pir F83047 conserved hypothetical protein PA4792 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08178.1 AE004892_9 (AE004892) conserved hypothetical protein [Pseudomonas aeruginosa] dbj BAA16380.1 (D90878) FORMATE HYDROGENLYASE TRANSCRIPTIONAL ACTIVATOR. [Escherichia coli] SEQ ID n-877
SEQ ID n° 7637	PL-1762.1	Contig9 from 2081636 to 2082271	p	53%	ref NP_053218.1 pXO2-63 [Bacillus anthracis] gb AAF13668.1 AF188935_66 (AF188935) pXO2-63 [Bacillus anthracis] pir F83158 probable sigma-70 factor, ECF subfamily PA3899 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07286.1 AE004807_5 (AE004807) probable sigma-70 factor, ECF subfamily [Pseudomonas aeruginosa] pir F83047 conserved hypothetical protein PA4792 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08178.1 AE004892_9 (AE004892) conserved hypothetical protein [Pseudomonas aeruginosa] dbj BAA16380.1 (D90878) FORMATE HYDROGENLYASE TRANSCRIPTIONAL ACTIVATOR. [Escherichia coli] SEQ ID n-877
SEQ ID n° 7638	PL-3870.1	Contig9 from 2082840 to 2083340	p	55%	ref NP_053218.1 pXO2-63 [Bacillus anthracis] gb AAF13668.1 AF188935_66 (AF188935) pXO2-63 [Bacillus anthracis] pir F83158 probable sigma-70 factor, ECF subfamily PA3899 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07286.1 AE004807_5 (AE004807) probable sigma-70 factor, ECF subfamily [Pseudomonas aeruginosa] pir F83047 conserved hypothetical protein PA4792 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08178.1 AE004892_9 (AE004892) conserved hypothetical protein [Pseudomonas aeruginosa] dbj BAA16380.1 (D90878) FORMATE HYDROGENLYASE TRANSCRIPTIONAL ACTIVATOR. [Escherichia coli] SEQ ID n-877
SEQ ID n° 7639	PL-1761.1	Contig9 from 2083422 to 2084318	p	37%	ref NP_053218.1 pXO2-63 [Bacillus anthracis] gb AAF13668.1 AF188935_66 (AF188935) pXO2-63 [Bacillus anthracis] pir F83158 probable sigma-70 factor, ECF subfamily PA3899 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07286.1 AE004807_5 (AE004807) probable sigma-70 factor, ECF subfamily [Pseudomonas aeruginosa] pir F83047 conserved hypothetical protein PA4792 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08178.1 AE004892_9 (AE004892) conserved hypothetical protein [Pseudomonas aeruginosa] dbj BAA16380.1 (D90878) FORMATE HYDROGENLYASE TRANSCRIPTIONAL ACTIVATOR. [Escherichia coli] SEQ ID n-877
SEQ ID n° 7640	PL-1760.1	Contig9 from 2084485 to 2086416	m	37%	ref NP_053218.1 pXO2-63 [Bacillus anthracis] gb AAF13668.1 AF188935_66 (AF188935) pXO2-63 [Bacillus anthracis] pir F83158 probable sigma-70 factor, ECF subfamily PA3899 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07286.1 AE004807_5 (AE004807) probable sigma-70 factor, ECF subfamily [Pseudomonas aeruginosa] pir F83047 conserved hypothetical protein PA4792 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08178.1 AE004892_9 (AE004892) conserved hypothetical protein [Pseudomonas aeruginosa] dbj BAA16380.1 (D90878) FORMATE HYDROGENLYASE TRANSCRIPTIONAL ACTIVATOR. [Escherichia coli] SEQ ID n-877

TABLEAU II

SEQ ID n° 7641	PL-3869.1	Contig9 from 2086694 to 2087176	P	71%	pir S77026 hypothetical protein sl10783 - Synecocystis sp. (strain PCC 6803) dbj BAA10718.1 (D64005) hypothetical protein [Synecocystis sp.]	SEQ ID n-3040
SEQ ID n° 7642	PL-1759.1	Contig9 from 2087206 to 2088213	P	65%	pir S77025 nitrilase (EC 3.5.5.1) - Synecocystis sp. (strain PCC 6803) dbj BAA10717.1 (D64005) nitrilase [Synecocystis sp.]	SEQ ID n-875
SEQ ID n° 7643	PL-1758.1	Contig9 from 2088237 to 2089334	P	67%	pir S77024 hypothetical protein sl10785 - Synecocystis sp. (strain PCC 6803) dbj BAA10716.1 (D64005) hypothetical protein [Synecocystis sp.]	SEQ ID n-874
SEQ ID n° 7644	PL-3868.1	Contig9 from 2089347 to 2089910	P	41%	pir S77023 hypothetical protein sl10786 - Synecocystis sp. (strain PCC 6803) dbj BAA10715.1 (D64005) hypothetical protein [Synecocystis sp.]	SEQ ID n-3039
SEQ ID n° 7645	PL-1757.1	Contig9 from 2089910 to 2090962	P	41%	sp Q55946 Y787_SYNY3 HYPOTHETICAL 34.7 KD PROTEIN SL10787 pir S77022 hypothetical protein sl10787 - Synecocystis sp. (strain PCC 6803) dbj BAA10714.1 (D64005) hypothetical protein [Synecocystis sp.]	SEQ ID n-873
SEQ ID n° 7646	PL-6725.1	Contig9 from 2090950 to 2091240	P	50%	pir S77021 hypothetical protein sl1464 - Synecocystis sp. (strain PCC 6803) dbj BAA10713.1 (D64005) hypothetical protein [Synecocystis sp.]	#N/A
SEQ ID n° 7647	PL-1756.1	Contig9 from 2091253 to 2092590	P	61%	pir S77027 hypothetical protein slr0801 - Synecocystis sp. (strain PCC 6803) dbj BAA10719.1 (D64005) hypothetical protein [Synecocystis sp.]	SEQ ID n-872
SEQ ID n° 7648	PL-1755.1	Contig9 from 2092858 to 2093862	M	84%	ref NP_044235.1 TnpA [Enterobacter aerogenes] pir T08494 probable transposase - Enterobacter aerogenes plasmid R751 gb AA03489.1 (U60777) transposase [Plasmid R751] gb AAC64438.1 (U67194) TnpA [Enterobacter aerogenes]	SEQ ID n-871

TABLEAU II

SEQ ID n° 7649	PL-3867.1	Contig9 from 2094147 to 2094527	p	61%	ref NP_061690.1 conserved hypothetical protein [Xylella fastidiosa] pir B82865 conserved hypothetical protein XFA0034 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85603.1 AE003851_34 (AE003851) conserved hypothetical protein [Xylella fastidiosa] SEQ ID n-9038
SEQ ID n° 7650	PL-6724.1	Contig9 from 2094559 to 2094846	p	26%	ref NP_061691.1 hypothetical protein [Xylella fastidiosa] pir C82865 hypothetical protein XFA0035 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85604.1 AE003851_35 (AE003851) hypothetical protein [Xylella fastidiosa] #N/A
SEQ ID n° 7651	PL-1754.1	Contig9 from 2095175 to 2096179	m	84%	ref NP_044235.1 TnpA [Enterobacter aerogenes] pir T08494 probable transposase - Enterobacter aerogenes plasmid R751 gb AAB03489.1 (U60777) transposase [Plasmid R751] gb AAC64438.1 (U67194) TnpA [Enterobacter aerogenes] SEQ ID n-870
SEQ ID n° 7652	PL-7200.1	Contig9 from 2096227 to 2096379	m	No Hits found	#N/A
SEQ ID n° 7653	PL-6722.1	Contig9 from 2096486 to 2096836	m	68%	pir H82412 diaminobutyrate--pyruvate aminotransferase VCA0824 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96722.1 (AE004410) diaminobutyrate-- pyruvate aminotransferase [Vibrio cholerae] #N/A
SEQ ID n° 7654	PL-1753.1	Contig9 from 2097009 to 2100191	m	47%	pir T17468 peptide-synthetase - Amycolatopsis mediterranei (fragment) emb CAA66454.1 (X97860) peptide-synthetase [Amycolatopsis mediterranei] SEQ ID n-869
SEQ ID n° 7655	PL-1752.1	Contig9 from 2100201 to 2101436	m	60%	gb AAG34185.1 AF321122_4 (AF321122) Sim-nI [Streptomyces antibioticus] SEQ ID n-868

TABLEAU II

SEQ ID n° 7656	PL-1751.1	Contig9 from 2101433 to 2102956	m	26%	sp P39641 YWFE_BACSU HYPOTHETICAL 52.3 KD PROTEIN IN ROCC-PTA INTERGENIC REGION pir S39738 yWE protein - Bacillus subtilis emb CAA51639.1 (X73124) ipa-83d [Bacillus subtilis] emb CAB15798.1 (Z99123) alternate gene name: ipa-83d [Bacillus subtilis] pir T17413 thioesterase II (EC 3.1.2.-) - Streptomyces venezuelae gb AAC69333.1 (AF079138) thioesterase II PIKAV [Streptomyces venezuelae] SEQ ID n-867
SEQ ID n° 7657	PL-1750.1	Contig9 from 2102956 to 2103720	m	46%	emb CAB93682.1 (Y17268) hypothetical protein [Streptomyces viridochromogenes] pir S74461 ABC transporter slr1494 - Synecocystis sp. (strain PCC 6803) dbj BA16613.1 (D90899) ABC transporter [Synecocystis sp.] SEQ ID n-866
SEQ ID n° 7658	PL-6721.1	Contig9 from 2103717 to 2103896	m	43%	emb CAB93682.1 (Y17268) hypothetical protein [Streptomyces viridochromogenes] pir S74461 ABC transporter slr1494 - Synecocystis sp. (strain PCC 6803) dbj BA16613.1 (D90899) ABC transporter [Synecocystis sp.] SEQ ID n-865
SEQ ID n° 7659	PL-1749.1	Contig9 from 2103893 to 2105539	m	50%	pir S74455 ABC-type transport protein slr1488 - Synecocystis sp. (strain PCC 6803) dbj BA16607.1 (D90899) ABC transporter [Synecocystis sp.] SEQ ID n-864
SEQ ID n° 7660	PL-1748.1	Contig9 from 2105536 to 2107290	m	48%	pir S74455 ABC-type transport protein slr1488 - Synecocystis sp. (strain PCC 6803) dbj BA16607.1 (D90899) ABC transporter [Synecocystis sp.] SEQ ID n-863
SEQ ID n° 7661	PL-1747.1	Contig9 from 2107292 to 2112301	m	42%	pir F83345 probable non-ribosomal peptide synthetase PA2402 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05790.1 AE004667.1 (AE004667) probable non- ribosomal peptide synthetase [Pseudomonas aeruginosa] SEQ ID n-862
SEQ ID n° 7662	PL-1746.1	Contig9 from 2112304 to 2116107	m	26%	emb CAB36627.1 (AL035480) putative polyketide synthase [Mycobacterium leprae] SEQ ID n-861
SEQ ID n° 7663	PL-1745.2	Contig9 from 2116104 to 2117888	m	47%	gb AAD04758.1 (U95370) lichenysin synthetase B; LicB [Bacillus licheniformis] SEQ ID n-860

SEQ ID n°	Contig9 from	PL-XXXX.X	m	No Hits found	SEQ ID n-859
2117867 to 2118658	Contig9 from 2117867 to 2118658	PL-1744.2	50%		
2119915 to 2120931	Contig9 from 2119915 to 2120931	PL-1743.2	16%		
2121360 to 2121761	Contig9 from 2121360 to 2121761	PL-3865.1			
2122386 to 2123240	Contig9 from 2122386 to 2123240	PL-1742.1			
2123883 to 2124107	Contig9 from 2123883 to 2124107	PL-6714.1	54%		
2124124 to 2125152	Contig9 from 2124124 to 2125152	PL-1741.1	72%		
2125232 to 2126458	Contig9 from 2125232 to 2126458	PL-1740.1	89%		

pir||A83358 hypothetical protein PA2303
 [imported] - Pseudomonas aeruginosa
 (strain PAO1) gb|AAG05691.1|AE004656.3
 (AE004656) hypothetical protein [Pseudomonas
 aeruginosa]
 sp|P77354|YAFU_ECOLI_HYPOTHETICAL 12.1 KD
 PROTEIN IN DNAQ-GMHA INTERGENIC REGION
 pir||C64746 yafu protein - Escherichia coli
 gb|AAB08640.1| (U70214) hypothetical protein
 [Escherichia coli] gb|AAC73322.1| (AE000130)
 orf, hypothetical protein [Escherichia coli K12]

SEQ ID n-859
 SEQ ID n-9036
 SEQ ID n-857
 #N/A
 SEQ ID n-856

pir||H82093 conserved hypothetical protein
 VC2288 [imported] - Vibrio cholerae
 (group O1 strain N16961) gb|AAF95432.1|
 (AE004300) conserved hypothetical protein
 [Vibrio cholerae]
 pir||A82094 thiamin biosynthesis lipoprotein
 ApbE VC2289 [imported] - Vibrio
 cholerae (group O1 strain N16961)
 gb|AAF95433.1| (AE004300) thiamin biosynthesis
 lipoprotein ApbE [Vibrio cholerae]
 pir||D64052 Na+-translocating NADH-ubiquinone
 oxidoreductase (EC 1.-.-.-) beta
 chain - Haemophilus influenzae (strain Rd KW20)
 gb|AAC21841.1| (U32702) Nqr6 subunit of Na-
 translocating NADH-quinone reductase
 complex beta-subunit (nqr6) [Haemophilus
 influenzae Rd]

SEQ ID n-855

TABLEAU II

SEQ ID n° 7671	PL-3864.1	Contig9 from 2126474 to 2127070	m	90%	sp Q56589 NQRE_VTBAL NA(+)-TRANSLOCATING NADH- QUINONE REDUCTASE SUBUNIT E (NA-NQR COMPLEX SUBUNIT 5) pir S65530 sodium- translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) nqrB chain - Vibrio alginolyticus dbj BAA22914.1 (AB008030) Nqr5 subunit of Na-translocating NADH-quinone reductase complex [Vibrio alginolyticus] prf 2111280C Na-translocating NADH quinone reductase [Vibrio alginolyticus]	SEQ ID n-9035
SEQ ID n° 7672	PL-1739.1	Contig9 from 2127079 to 2127708	m	90%	gb AAK03415.1 (AE006171) unknown [Pasteurella multocida]	SEQ ID n-853
SEQ ID n° 7673	PL-1738.1	Contig9 from 2127701 to 2128498	m	67%	pir S65528 sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) nqrC chain - Vibrio alginolyticus dbj BAA22912.1 (AB008030) Nqr3 subunit of Na- translocating NADH-quinone reductase complex gamma-subunit [Vibrio alginolyticus] prf 2111280A Na-translocating NADH quinone reductase [Vibrio alginolyticus]	SEQ ID n-852
SEQ ID n° 7674	PL-1737.1	Contig9 from 2128491 to 2129729	m	86%	dbj BAA22911.1 (AB008030) Nqr2 subunit of Na- translocating NADH-quinone reductase complex [Vibrio alginolyticus] pir A81919 probable sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) chain A NMA0752 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB84035.1 (AL162754) putative Na(+)- translocating NADH-ubiquinone reductase subunit A [Neisseria meningitidis Z2491]	SEQ ID n-851
SEQ ID n° 7675	PL-1736.1	Contig9 from 2129734 to 2131077	m	77%		SEQ ID n-850

TABLEAU II

SEQ ID n° 7676	PL-1735.1	Contig9 from 2131497 to 2132240	p	63%	sp Q47148 YAFK_ECOLI HYPOTHETICAL 28.0 KD PROTEIN IN GMHA-DINJ INTERGENIC REGION PRECUSOR pir A64747 probable membrane protein yafK - Escherichia coli dbj BAA07586.1 (D38582) yafK [Escherichia coli] gb AAB08646.1 (U70214) hypothetical [Escherichia coli] gb AAC73328.1 [AE000131] orf, hypothetical protein [Escherichia coli K12] dbj BAA77894.1 (D83536) Hypothetical 28.0 kd protein in gmha- dinJ intergenic region precursor. [Escherichia coli] gb AAG54549.1 AE005201_2 (AE005201) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-849
SEQ ID n° 7677	PL-1734.1	Contig9 from 2132211 to 2132978	m	83%	sp Q47147 YAFU_ECOLI HYPOTHETICAL 28.6 KD PROTEIN IN GMHA-DINJ INTERGENIC REGION pir H64746 yafJ protein - Escherichia coli dbj BAA07585.1 (D38582) yafJ [Escherichia coli] gb AAB08645.1 (U70214) hypothetical [Escherichia coli] gb AAC73327.1 (AE000131) putative amidotransferase [Escherichia coli K12] dbj BAA77893.1 (D83536) Hypothetical protein H11037 [Escherichia coli] SEQ ID n-848
SEQ ID n° 7678	PL-1733.1	Contig9 from 2133128 to 2133709	m	89%	gb AAB08644.1 (U70214) hypothetical [Escherichia coli] SEQ ID n-847
SEQ ID n° 7679	PL-1732.1	Contig9 from 2133969 to 2136404	p	87%	dbj BAA77891.1 (D83536) Acyl-CoA dehydrogenase (EC 1.3.99.-). [Escherichia coli] gb AAG57950.1 AE005512_9 (AE005512) diaminopimelate decarboxylase [Escherichia coli O157:H7] SEQ ID n-846
SEQ ID n° 7680	PL-1731.1	Contig9 from 2136477 to 2137787	m	74%	gb AAG57951.1 AE005512_10 (AE005512) positive regulator for lys [Escherichia coli O157:H7] SEQ ID n-845
SEQ ID n° 7681	PL-1730.1	Contig9 from 2137901 to 2138836	p	76%	gb AAG57951.1 AE005512_10 (AE005512) positive regulator for lys [Escherichia coli O157:H7] SEQ ID n-844

TABLEAU II

SEQ ID n° 7682	PL-1729.1	Contig9 from 2138819 to 2139733	m	70%	pir F83638 probable transcription regulator PA0056 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG03446.1 AE004445_7 (AE004445) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-842
SEQ ID n° 7683	PL-1728.1	Contig9 from 2139839 to 2140723	p	57%	pir G83638 hypothetical protein PA0057 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG03447.1 AE004445_8 (AE004445) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-841
SEQ ID n° 7684	PL-1727.1	Contig9 from 2140755 to 2141396	p	55%	pir H83638 hypothetical protein PA0058 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG03448.1 AE004445_9 (AE004445) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-840
SEQ ID n° 7685	PL-1726.1	Contig9 from 2141445 to 2142056	m	49%	sp O68964 LEP4_AERSA TYPE 4 PREPILIN-LIKE PROTEINS LEADER PEPTIDE PROCESSING ENZYME [INCLUDES: LEADER PEPTIDASE (PREPILIN PEPTIDASE); N-METHYLTRANSFERASE] gb AAC33569.1 (AF059249) type IV prepilin peptidase TapD [Aeromonas salmonicida] pir A65080 hypothetical protein in endA-gshB intergenic region - Escherichia coli (strain K-12) gb AAA69113.1 (U28377) ORF_0252 [Escherichia coli] gb AAC75983.1 (AE000377) orf, hypothetical protein [Escherichia coli K12] gb AAG58077.1 AE005525_3 (AE005525) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-839
SEQ ID n° 7686	PL-1725.1	Contig9 from 2142382 to 2143113	p	74%	

TABLEAU II

SEQ ID n° 7687	PL-1724.1	Contig9 from 2143123 to 2144073	p	88%	sp P04425 GSHB_ECOLI GLUTATHIONE SYNTHETASE (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) (GSHASE) pir SYECGS glutathione synthase (EC 6.3.2.3) - Escherichia coli pdb 1GSA Structure Of Glutathione Synthetase Complexed With Adp And Glutathione pdb 1GSH Structure Of Escherichia Coli Glutathione Synthetase At Ph 7.5 pdb 2GLT Structure Of Escherichia Coli Glutathione Synthetase At Ph 6.0. emb CAA25826.1 (X01666) GSH-II [Escherichia coli] gb AA69114.1 (U28377) glutathione synthetase [Escherichia coli] gb AAC75984.1 (AE000377) glutathione synthetase [Escherichia coli K12]	SEQ ID n-837
SEQ ID n° 7688	PL-1723.1	Contig9 from 2144183 to 2144746	p	69%	sp P52049 YQGE_ECOLI PROTEIN YQGE	SEQ ID n-836
SEQ ID n° 7689	PL-6707.1	Contig9 from 2144747 to 2145166	p	81%	gb AAK03954.1 (AE006224) unknown [Pasteurella multocida]	#N/A
SEQ ID n° 7690	PL-1722.1	Contig9 from 2145221 to 2146258	m	69%	gb AAG58081.1 AE005525_7 (AE005525) putative protein transport [Escherichia coli O157:H7] sp P52054 YGGG_ECOLI HYPOTHETICAL 25.8 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION pir F65080 hypothetical protein b2951 - Escherichia coli (strain K-12) gb AA69118.1 (U28377) ORF_0234 [Escherichia coli] gb AAC75988.1 (AE000378) orf, hypothetical protein [Escherichia coli K12] gb AAG58082.1 AE005525_8 (AE005525) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-835
SEQ ID n° 7691	PL-1721.1	Contig9 from 2146280 to 2146975	p	77%		SEQ ID n-834

TABLEAU II

SEQ ID n° 7692	PL-1720.1	Contig9 from 2147001 to 2147822	p 71%	pir B82321 pyrroline-5-carboxylate reductase VC0460 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93633.1 (AE004132) pyrroline-5-carboxylate reductase [Vibrio cholerae] SEQ ID n-833
SEQ ID n° 7693	PL-3863.1	Contig9 from 2147841 to 2148389	p 75%	pir C82321 conserved hypothetical protein VC0459 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93632.1 (AE004132) conserved hypothetical protein [Vibrio cholerae] SEQ ID n-3034
SEQ ID n° 7694	PL-3862.1	Contig9 from 2148416 to 2149009	p 89%	gb AAG58085.1 AE005525_11 (AE005525) putative ribosomal protein [Escherichia coli O157:H7] SEQ ID n-3033
SEQ ID n° 7695	PL-1719.1	Contig9 from 2149002 to 2150132	p 86%	sp P52062 YGGW_ECOLI HYPOTHETICAL 42.6 KDA PROTEIN IN GSHB-ANSE INTERGENIC REGION pir B65081 hypothetical protein b2955 - Escherichia coli (strain K-12) gb AAA69123.1 (U28377) ORF_0378 [Escherichia coli] gb AAC75992.1 (AE000378) putative oxidase [Escherichia coli K12] SEQ ID n-831
SEQ ID n° 7696	PL-1718.1	Contig9 from 2150753 to 2151415	p No Hits found	SEQ ID n-830
SEQ ID n° 7697	PL-1717.1	Contig9 from 2152100 to 2153050	m 51%	pir B69763 probable ferrichrome ABC transporter yqlQ - Bacillus subtilis dbj BAA09015.1 (D50453) ferric anguibactin-binding protein precursor FatB of V. anguillarum [Bacillus subtilis] emb CAB12191.1 (Z99106) similar to ferrichrome ABC transporter (binding protein) [Bacillus subtilis] SEQ ID n-829
SEQ ID n° 7698	PL-1716.1	Contig9 from 2153168 to 2153890	m 66%	gb AAG58089.1 AE005526_2 (AE005526) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-828

TABLEAU II

SEQ ID n° 7699	PL-1715.1	Contig9 from 2153938 to 2154864	m	79%	<p>sp P77470 GLS2_ECOLI PROBABLE GLUTAMINASE YNEH pir G64906 glutaminase homolog yneh - Escherichia coli dbj BAAL5206.1 (D90795) Glutaminase, kidney isoform precursor [EC 3.5.1.2) (GLS). [Escherichia coli] dbj BAA15214.1 (D90796) Glutaminase, kidney isoform precursor [EC 3.5.1.2) (GLS). [Escherichia coli] gb AAC74597.1 (AE000250) putative glutaminase [Escherichia coli K12] gb AAC56241.1 AE005352_7 (AE005352) putative glutaminase [Escherichia coli O157:H7]</p>	SEQ ID n-827
SEQ ID n° 7700	PL-6704.1	Contig9 from 2154944 to 2155270	m	81%	<p>gb AAG58090.1 AE005526_3 (AE005526) orf, hypothetical protein [Escherichia coli O157:H7] sp P32049 YGGH_ECOLI HYPOTHETICAL 27.3 KD PROTEIN IN ANSB-MUTY INTERGENIC REGION (F239) pir G65081 hypothetical 27.3 kd protein in muty 5' region - Escherichia coli (strain K-12) gb AAA69127.1 (U28377) ORF_f239; alternate name yggH; orf of M59471 [Escherichia coli] gb AAC75997.1 (AE000378) orf, hypothetical protein [Escherichia coli K12] sp P17802 MUTY_ECOLI A/G-SPECIFIC ADENINE GLYCOSYLASE pir B38535 A/G-specific adenine glycosylase (EC 3.2.2.-) [validated] - Escherichia coli emb CAA36624.1 (X52391) adenine glycosylase (AA 1-350) [Escherichia coli] gb AAA72957.1 (M59471) A/G-specific adenine glycosylase [Escherichia coli] gb AAA69128.1 (U28377) CG Site No. 18130; alternate name mica [Escherichia coli] gb AAC75998.1 (AE000378) adenine glycosylase; G.C --> T.A transversions [Escherichia coli K12]</p>	#N/A
SEQ ID n° 7701	PL-1714.1	Contig9 from 2155270 to 2155989	m	82%		SEQ ID n-826
SEQ ID n° 7702	PL-1713.1	Contig9 from 2156362 to 2157399	p	80%		SEQ ID n-825

TABLEAU II

SEQ ID n° 7703	PL-6700.1	Contig9 from 2157430 to 2157702	P	84%	sp P52065 YGGX_BCOLI PROTEIN YGGX pir A65082 hypothetical protein b2962 - Escherichia coli (strain K-12) gb AAA69129.1 (U28377) ORF_091 [Escherichia coli] gb AAC75999.1 (AE000378) orf, hypothetical protein [Escherichia coli K12] gb AAG58093.1 AE005526_6 (AE005526) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG58094.1 AE005526_7 (AE005526) membrane- bound lytic murein transglycosylase C [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7704	PL-1712.2	Contig9 from 2157766 to 2158839	P	81%		SEQ ID n-824
SEQ ID n° 7705	PL-6699.1	Contig9 from 2158961 to 2159101	P	No Hits found		#N/A
SEQ ID n° 7706	PL-1711.1	Contig9 from 2159462 to 2160463	M	47%	gb AAG02084.1 AF285416_2 (AF285416) XerC [Pseudomonas aeruginosa] pir C82641 hypothetical protein XF1753 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84562.1 AE003998_4 (AE003998) hypothetical protein [Xylella fastidiosa]	SEQ ID n-823
SEQ ID n° 7707	PL-1710.1	Contig9 from 2160558 to 2162078	M	22%		SEQ ID n-822
SEQ ID n° 7708	PL-6697.1	Contig9 from 2162161 to 2162340	M	No Hits found		#N/A
SEQ ID n° 7709	PL-1709.1	Contig9 from 2162474 to 2163196	M	No Hits found		SEQ ID n-820
SEQ ID n° 7710	PL-1708.1	Contig9 from 2163344 to 2164264	M	47%	ref NP_052478.1 yccB [Plasmid Colib-P9] dbj BAW5117.1 (AB021078) yccb [Plasmid Colib- P9]	SEQ ID n-819
SEQ ID n° 7711	PL-6696.1	Contig9 from 2164394 to 2164582	M	No Hits found		#N/A

TABLEAU II

SEQ ID n° 7712	PL-6694.1	Contig9 from 2164671 to 2165003	m	54%	pir E82639 hypothetical protein XF1764 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84573.1 AE003999_1 (AE003999) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 7713	PL-1707.1	Contig9 from 2165069 to 2165980	m	No Hits found		SEQ ID n-818
SEQ ID n° 7714	PL-1706.1	Contig9 from 2166080 to 2168053	m	19%	ref NP_066681.1 similar to ardC gene in psa(IncW plasmid) [Agrobacterium rhizogenes] dbj BAB16219.1 (AP002086) similar to ardC gene in psa(IncW plasmid) [Agrobacterium rhizogenes]	SEQ ID n-817
SEQ ID n° 7715	PL-3860.1	Contig9 from 2168121 to 2168666	m	No Hits found		SEQ ID n-3032
SEQ ID n° 7716	PL-6691.1	Contig9 from 2168672 to 2168968	m	No Hits found		#N/A
SEQ ID n° 7717	PL-6689.1	Contig9 from 2168968 to 2169354	m	No Hits found		#N/A
SEQ ID n° 7718	PL-6687.1	Contig9 from 2169367 to 2169588	m	No Hits found		#N/A
SEQ ID n° 7719	PL-6686.1	Contig9 from 2169601 to 2169765	m	No Hits found		#N/A
SEQ ID n° 7720	PL-1705.1	Contig9 from 2170208 to 2171185	m	36%	gb AAK02039.1 AF261825_8 (AF261825) hypothetical protein [Salmonella enterica subsp. enterica serovar Typhimurium]	SEQ ID n-816
SEQ ID n° 7721	PL-6683.1	Contig9 from 2171488 to 2171745	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 7722	PL-1704.1	Contig9 from 2172577 to 2174241	p	56%	pir F82543 outer membrane hemolysin activator protein XF2550 [imported] - Xylella fastidiosia (strain 9a5c) gb AAF85347.1 AE004062_2 (AE004062) outer membrane hemolysin activator protein [Xylella fastidiosia] SEQ ID n-815
SEQ ID n° 7723	PL-1703.1	Contig9 from 2174290 to 2183103	p	37%	pir F81045 hemagglutinin/hemolysin-related protein NMB1768 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF42109.1 (AE002526) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58] pir A82955 hypothetical protein PA5527 (strain PAO1) gb AAG08912.1 AE004965_4 (AE004965) hypothetical protein [Pseudomonas aeruginosa] #N/A
SEQ ID n° 7724	PL-7420.1	Contig9 from 2183112 to 2183531	p	56%	sp P39394 YJTW_ECOLI HYPOTHETICAL 14.6 KDA PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132) pir S56573 hypothetical 14.6K protein (mcrB-hsdS intergenic region) - Escherichia coli gb AA97244.1 (U14003) ORF_f132 [Escherichia coli] gb AAC77303.1 (AE000505) orf, hypothetical protein [Escherichia coli K12] #N/A
SEQ ID n° 7726	PL-7417.1	Contig9 from 2183918 to 2184253	m	29%	emb CAB53822.1 (AJ242593) putative repressor protein [Bacteriophage A118] #N/A
SEQ ID n° 7727	PL-3.3	Contig9 from 2184441 to 2187755	p	16%	sp P47762 PRIM_LISMO DNA PRIMASE gb AAC43305.1 (U13165) DNA primase [Listeria monocytogenes] prf 2104269B DNA primase [Listeria monocytogenes] #N/A
SEQ ID n° 7728	PL-7415.1	Contig9 from 2187742 to 2188872	p	33%	gb AAF89876.1 (AF173869) putative site-specific recombinase XerD [Staphylococcus aureus] #N/A

TABLEAU II

SEQ ID n° 7729	PL-7412.1	Contig9 from 2189065 to 2189196	p	No Hits found	#N/A
SEQ ID n° 7730	PL-6918.2	Contig9 from 2189424 to 2189690	p	No Hits found	#N/A
SEQ ID n° 7731	PL-3195.1	Contig9 from 2189712 to 2190398	p	30%	gb AAK05486.1 AE006370_11 (AE006370) prophage pi3 protein 14 [Lactococcus lactis subsp. lactis]
SEQ ID n° 7732	PL-5715.1	Contig9 from 2190388 to 2190651	p	No Hits found	SEQ ID n-2445
SEQ ID n° 7733	PL-3194.1	Contig9 from 2190726 to 2191346	p	22%	#N/A
SEQ ID n° 7734	PL-6930.1	Contig9 from 2191811 to 2192722	p	No Hits found	SEQ ID n-2444
SEQ ID n° 7735	PL-7411.1	Contig9 from 2192719 to 2193036	p	No Hits found	#N/A
SEQ ID n° 7736	PL-7410.1	Contig9 from 2193081 to 2193323	m	38%	sp P39394 YJTW_ECOLI_HYPOTHETICAL 14.6 KDA PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132) pir S56573 hypothetical 14.6K protein (mcrB-hsdS intergenic region) - Escherichia coli gb AAA97244.1 (U14003) ORP_f132 [Escherichia coli] gb AAC77303.1 (AE000505) orf, hypothetical protein [Escherichia coli K12]

TABLEAU II

SEQ ID n° 7737	PL-7409.1	Contig9 from 2193416 to 2193787	m	48%	sp O34419 RSR1_VIBCH_CRYPTIC_PHAGE_CTXPHI TRANSCRIPTIONAL REPRESSOR RSTR pir H82197 transcriptional repressor Rstr VC1464 VC1455 [imported] - Vibrio cholerae (group O1 strain N16961) gb AA881724.1 (U83795) RSTR [Vibrio cholerae] gb AA881728.1 (U83796) RSTR [Vibrio cholerae] gb AAF94612.1 (AE004224) transcriptional repressor Rstr [Vibrio cholerae] gb AAF94621.1 (AE004224) transcriptional repressor Rstr [Vibrio cholerae] sp P47762 PRIM_LISMO_DNA_PRIMASE gb AAC43305.1 (U13165) DNA primase [Listeria monocytogenes] prf 2104269B DNA primase [Listeria monocytogenes] #N/A	#N/A
SEQ ID n° 7738	PL-7408.1	Contig9 from 2193887 to 2197201	p	17%	pir F83177 integrase/recombinase XerD PA3738 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07125.1 AE004793_2 (AE004793) integrase/recombinase XerD [Pseudomonas aeruginosa] #N/A	#N/A
SEQ ID n° 7739	PL-6943.3	Contig9 from 2197188 to 2198300	p	38%	emb CAB65124.1 (AJ007421) spalt-like zinc finger protein [Homo sapiens] #N/A	SEQ ID n-2728
SEQ ID n° 7740	PL-3517.1	Contig9 from 2198676 to 2199131	p	29%		SEQ ID n-3223
SEQ ID n° 7741	PL-417.1	Contig9 from 2199153 to 2200007	p	No Hits found		#N/A
SEQ ID n° 7742	PL-5725.1	Contig9 from 2200004 to 2200309	p	No Hits found		SEQ ID n-3224
SEQ ID n° 7743	PL-418.1	Contig9 from 2200451 to 2201326	p	No Hits found		SEQ ID n-3225
SEQ ID n° 7744	PL-419.1	Contig9 from 2201691 to 2202488	p	No Hits found		

727

ref NP_047570.1 unknown [Yersinia pestis] pir T42852 hypothetical protein Y0012 - Yersinia pestis plasmid pCD1 gb AAC69767.1 (AF074612) unknown [Yersinia pestis] emb CAB54945.1 (AL117189) YPCD1.68c, Y0012, hypothetical protein, len: 68 aa; identical to corresponding CDS from Y.pestis KIM5 pCD1 (EMBL:AF074612) (68 aa), fasta scores, opt: 453 z-score: 678.5 E(): 2e-30 98.5% identity in 68 aa overlap. Similar to parts of hypothe>	Contig9 from 2202674 to 2202841	p	38%	#N/A
gb AAG61082.1 AF322013_201 (AF322013) ID930 [Bradyrhizobium japonicum]	Contig9 from 2202949 to 2203218	m	33%	SEQ ID n-9227
gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]	Contig9 from 2203330 to 2204214	p	59%	SEQ ID n-9228
gb AAG61082.1 AF322013_201 (AF322013) ID930 [Bradyrhizobium japonicum]	Contig9 from 2204227 to 2209602	m	65%	SEQ ID n-9229
pdb 1F3I A Chain A, Crystal Structure Of Tn5 Transposase Complexed With End Dna pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae]	Contig9 from 2210996 to 2225947	m	54%	SEQ ID n-9230
gb AAC82519.1 (AF027768) Reta [Serratia marcescens]	Contig9 from 2226513 to 2227115	m	31%	SEQ ID n-9231
gb AAG61023.1 AF322013_142 (AF322013) ID776 [Bradyrhizobium japonicum]	Contig9 from 2227070 to 2228479	m	62%	SEQ ID n-9232

TABLEAU II

SEQ ID n° 7753	PL-5745.1	Contig9 from 2228476 to 2228676	m	No Hits found			#N/A
SEQ ID n° 7754	PL-426.1	Contig9 from 2228857 to 2229330	m	58%	gb AAC82519.1 (AF027768) Reta [Serratia marcescens]	SEQ ID n-9233	
SEQ ID n° 7755	PL-5748.1	Contig9 from 2229477 to 2229746	m	52%	gb AAG60892.1 AF322013_11 (AF322013) ID459 [Bradyrhizobium japonicum]	#N/A	
SEQ ID n° 7756	PL-427.1	Contig9 from 2230262 to 2230837	p	40%	dbj BAB16031.1 (AB030747). transposase [Streptococcus pyogenes]	SEQ ID n-9234	
SEQ ID n° 7757	PL-428.1	Contig9 from 2230991 to 2232139	m	67%	sp P20932 MDLB_PSEPU L(+)-MANDELATE DEHYDROGENASE (S-MANDELATE DEHYDROGENASE) (MDH) pir B44767 L-mandelate dehydrogenase (EC 1.1.1.2...) - Pseudomonas putida gb AAC15503.1 (J05293) S-mandelate dehydrogenase [Pseudomonas putida] pir T36319 probable aminotransferase - Streptomyces coelicolor (fragment) emb CAB38598.1 (AL035654) putative aminotransferase [Streptomyces coelicolor A3(2)]	SEQ ID n-9235	
SEQ ID n° 7758	PL-429.1	Contig9 from 2232383 to 2233675	m	54%	pir E75215 glyoxalase I related protein PAB2438 [imported] - Pyrococcus abyssi (strain Orsay) emb CAB49172.1 (AJ248283) LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) METHYLGLYOXALASE) (ALDOXETOMUTASE) (GLYOXALASE I). [Pyrococcus abyssi]	SEQ ID n-9236	
SEQ ID n° 7759	PL-3526.1	Contig9 from 2233697 to 2234287	m	37%	gb AAG02359.1 AF210249_18 (AF210249) peptide synthetase NRPS-4-3 [Streptomyces verticillus]		
SEQ ID n° 7760	PL-7190.1	Contig9 from 2234340 to 2234543	m	46%		#N/A	
SEQ ID n° 7761	PL-5752.1	Contig9 from 2234568 to 2234705	p	No Hits found		#N/A	

TABLEAU II

SEQ ID n° 7762	PL-5753.1	Contig9 from 2234750 to 2235010	p	44%	sp Q51649 T408_BURCE PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS408 gb AA25863.1 (L09108) IS408 transposase; putative [Burkholderia cepacia] prf 2113421C transposase [Burkholderia cepacia] sp P55379 Y4BL_RHISN PUTATIVE TRANSPOSASE Y4BL/Y4KJ/Y4TB pir T47075 hypothetical protein Y4KJ [Imported] - Rhizobium sp. (NGR234) plasmid pNGR234a gb AAB91627.1 (AE000066) Y4BL [Rhizobium sp. NGR234] gb AAB91741.1 ... (AE000081) Y4KJ [Rhizobium sp. NGR234] gb AAB91856.1 (AE000097) Y4TB [Rhizobium sp. NGR234]	#N/A
SEQ ID n° 7763	PL-5754.1	Contig9 from 2234962 to 2235246	p	47%		#N/A
SEQ ID n° 7764	PL-5756.1	Contig9 from 2235297 to 2235530	p	No Hits found		#N/A
SEQ ID n° 7765	PL-5757.1	Contig9 from 2235531 to 2235659	p	No Hits found		#N/A
SEQ ID n° 7766	PL-5758.1	Contig9 from 2235703 to 2236065	m	No Hits found		#N/A
SEQ ID n° 7767	PL-5759.1	Contig9 from 2236297 to 2236545	m	63%	gb AAF22961.1 AF157489_1 (AF157489) Pln [Photorhabdus luminescens]	#N/A
SEQ ID n° 7768	PL-3527.1	Contig9 from 2236819 to 2237385	p	No Hits found		SEQ ID n° 2732
SEQ ID n° 7769	PL-5760.1	Contig9 from 2237432 to 2237575	p	No Hits found		#N/A
SEQ ID n° 7770	PL-5761.1	Contig9 from 2237543 to 2237653	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 7771	PL-3528.1	Contig9 from 2237664 to 2238158	m	No Hits found	SEQ ID n-2733
SEQ ID n° 7772	PL-5762.1	Contig9 from 2238544 to 2238924	p	No Hits found	#N/A
SEQ ID n° 7773	PL-430.1	Contig9 from 2238974 to 2240488	m	No Hits found	SEQ ID n-3238
SEQ ID n° 7774	PL-5763.1	Contig9 from 2240485 to 2240859	m	No Hits found	#N/A
SEQ ID n° 7775	PL-432.1	Contig9 from 2240859 to 2242121	m	No Hits found	SEQ ID n-3239
SEQ ID n° 7776	PL-434.1	Contig9 from 2242302 to 2243300	m	No Hits found	SEQ ID n-3241
SEQ ID n° 7777	PL-5765.1	Contig9 from 2243297 to 2243707	m	No Hits found	#N/A
SEQ ID n° 7778	PL-435.1	Contig9 from 2243704 to 2246586	m	18%	ref NP_049162.1 sex pilus assembly and synthesis protein [Sphingomonas aromaticivorans] pir T31234 traC protein homolog - Sphingomonas aromaticivorans plasmid pNL1 gb AAD03958.1 (AF079317) sex pilus assembly and synthesis protein [Sphingomonas aromaticivorans]
SEQ ID n° 7779	PL-5767.1	Contig9 from 2246583 to 2247011	m	No Hits found	SEQ ID n-3242
SEQ ID n° 7780	PL-436.1	Contig9 from 2246998 to 2248476	m	No Hits found	#N/A
					SEQ ID n-3243

TABLEAU II

SEQ ID n° 7781	PL-437.1	Contig9 from 2248466 to 2249389	m	No Hits found	SEQ ID n-9244
SEQ ID n° 7782	PL-5770.1	Contig9 from 2250039 to 2250416	m	No Hits found	#N/A
SEQ ID n° 7783	PL-5771.1	Contig9 from 2250435 to 2250821	m	No Hits found	#N/A
SEQ ID n° 7784	PL-5772.1	Contig9 from 2250861 to 2251097	m	No Hits found	#N/A
SEQ ID n° 7785	PL-5773.1	Contig9 from 2251094 to 2251369	m	No Hits found	#N/A
SEQ ID n° 7786	PL-5775.1	Contig9 from 2251651 to 2251884	p	38%	ref NP_054630.1 transposon gamma-delta resolvase (transposon TN1000).homolog [Yersinia pestis] ref NP_047634.1 putative resolvase [Yersinia pestis] pir T43611 probable resolvase tnpR - Yersinia pestis plasmid pCD1 gb AAC62593.1 (AF053946) transposon gamma-delta resolvase (transposon TN1000) homolog [Yersinia pestis] gb AAC69824.1 (AF074612) putative resolvase [Yersinia pestis] emb CAB54968.1 (AL117189) putative resolvase [Yersinia pestis] dbj BA089622.1 (AB036665) similar to E.coli hypothetical protein o375 [bacteriophage WO]
SEQ ID n° 7787	PL-439.1	Contig9 from 2251887 to 2252957	p	66%	SEQ ID n-9245
SEQ ID n° 7788	PL-440.1	Contig9 from 2253167 to 2253919	m	No Hits found	SEQ ID n-9247
SEQ ID n° 7789	PL-5776.1	Contig9 from 2253900 to 2254109	m	No Hits found	#N/A

TABLEAU II

SEQ ID n° 7790	PL-441.1	Contig9 from 2254239 to 2255621	p	57%	pdb 1P3I A Chain A, Crystal Structure Of Tn5 Transposase Complexed With End Dna	SEQ ID n-9248
SEQ ID n° 7791	PL-442.1	Contig9 from 2255596 to 2257554	m	37%	ref NP_058332.1 orf; hypothetical protein [Salmonella typhi] gb AAF69957.1 AF250878_118 (AF250878) orf; hypothetical protein [Salmonella typhi]	SEQ ID n-9249
SEQ ID n° 7792	PL-3531.1	Contig9 from 2257658 to 2258104	m	No Hits found		SEQ ID n-9235
SEQ ID n° 7793	PL-443.1	Contig9 from 2258200 to 2258772	m	35%	pir [G7I704 hypothetical protein RP457 - Rickettsia prowazekii emb CA14913.1 (AJ235271) unknown [Rickettsia prowazekii]	SEQ ID n-9250
SEQ ID n° 7794	PL-444.1	Contig9 from 2258802 to 2259539	m	No Hits found		SEQ ID n-9251
SEQ ID n° 7795	PL-445.1	Contig9 from 2259542 to 2260342	m	No Hits found		SEQ ID n-9252
SEQ ID n° 7796	PL-5780.1	Contig9 from 2260726 to 2260911	m	No Hits found		#N/A
SEQ ID n° 7797	PL-5781.1	Contig9 from 2260994 to 2261311	p	64%	ref NP_061700.1 conserved hypothetical protein [Xylella fastidiosa] pir D82866 conserved hypothetical protein XFa0045 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85613.1 AE003851_44 (AE003851) conserved hypothetical protein [Xylella fastidiosa] ref NP_061701.1 hypothetical protein [Xylella fastidiosa] pir S82866 hypothetical protein XFa0046 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85614.1 AE003851_45 (AE003851) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 7798	PL-5782.1	Contig9 from 2261314 to 2261625	p	51%		#N/A

TABLEAU II

SEQ ID n° 7799	PL-5785.1	Contig9 from 2261768 to 2262013	m	No Hits found	#N/A
SEQ ID n° 7800	PL-5786.1	Contig9 from 2262234 to 2262461	m	No Hits found	#N/A
SEQ ID n° 7801	PL-446.1	Contig9 from 2262494 to 2263999	m	53%	ref NP_053113.1 orf51 [Escherichia coli] dbj BAA84886.1 (AB024946) orf51 [Escherichia coli] SEQ ID n-3253
SEQ ID n° 7802	PL-5788.1	Contig9 from 2264063 to 2264398	m	73%	gb AAG55308.1 AE005273_1 (AE005273) unknown in ISEC8 [Escherichia coli O157:H7] gb AAG55717.1 AB005309_7 (AE005309) unknown in ISEC8 [Escherichia coli O157:H7] #N/A
SEQ ID n° 7803	PL-5789.1	Contig9 from 2264392 to 2264757	m	No Hits found	#N/A
SEQ ID n° 7804	PL-447.1	Contig9 from 2265051 to 2266229	m	64%	sp P09750 SHU6_ECOLI_SHUFFLON PROTEIN C' pir P26421 shufflon C' - Escherichia coli plasmid R64 SEQ ID n-3254
SEQ ID n° 7805	PL-448.1	Contig9 from 2266295 to 2266960	m	60%	dbj BAA77981.1 (AB027308) prepilin peptidase [Plasmid R64] SEQ ID n-3255
SEQ ID n° 7806	PL-449.1	Contig9 from 2266961 to 2267563	m	66%	dbj BAA77979.1 (AB027308) type IV prepilin [Plasmid R64] ref NP_052542.1 integral membrane protein [Plasmid Colib-P9] dbj BAA75181.1 (AB021078) integral membrane protein [Plasmid Colib-P9] dbj BAA77978.1 (AB027308) integral membrane protein [Plasmid R64] SEQ ID n-3256
SEQ ID n° 7807	PL-450.1	Contig9 from 2267632 to 2268717	m	69%	gb AAF81213.1 AF247502_8 (AF247502) PilQ [Salmonella dublin] gb AAF14816.1 (AF000001) PilP [Salmonella typhi] gb AAF81212.1 AF247502_7 (AF247502) PilP [Salmonella dublin] SEQ ID n-2737
SEQ ID n° 7808	PL-451.1	Contig9 from 2268710 to 2270263	m	72%	
SEQ ID n° 7809	PL-3535.1	Contig9 from 2270277 to 2270741	m	42%	

TABLEAU II

SEQ ID n° 7810	PL-452.1	Contig9 from 2270749 to 2272065	m	52%	gb AAF14815.2 (AF000001) Pilo [Salmonella typhi] gb AAF81211.1 AF247502_6 (AF247502) Pilo [Salmonella dublin] ref NP_052546.1 lipoprotein [Plasmid Colib-P9] dbj BAA75185.1 (AB021078) lipoprotein [Plasmid Colib-P9] dbj BAA77974.1 (AB027308) lipoprotein [Plasmid R64] SEQ ID n-3260
SEQ ID n° 7811	PL-453.1	Contig9 from 2272089 to 2273792	m	72%	gb AAF81208.1 AF247502_3 (AF247502) Pilm [Salmonella dublin] #N/A
SEQ ID n° 7813	PL-454.1	Contig9 from 2274255 to 2275304	m	65%	gb AAF14812.2 (AF000001) Pilo [Salmonella typhi] gb AAF81207.1 AF247502_2 (AF247502) Pilo [Salmonella dublin] SEQ ID n-3262
SEQ ID n° 7814	PL-5800.1	Contig9 from 2275452 to 2275661	m	No Hits found	#N/A
SEQ ID n° 7815	PL-5801.1	Contig9 from 2275685 to 2276014	m	No Hits found	#N/A
SEQ ID n° 7816	PL-5802.1	Contig9 from 2276318 to 2276506	p	75%	pir G82648 conserved hypothetical protein XF1702 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84511.1 AE003994_10 (AE003994) conserved hypothetical protein [Xylella fastidiosa] #N/A
SEQ ID n° 7817	PL-5803.1	Contig9 from 2276585 to 2276833	m	No Hits found	#N/A
SEQ ID n° 7818	PL-7184.1	Contig9 from 2277367 to 2277603	m	No Hits found	#N/A
SEQ ID n° 7819	PL-455.1	Contig9 from 2277739 to 2278632	p	No Hits found	#N/A
SEQ ID n° 7820	PL-456.1	Contig9 from 2278750 to 2279532	p	No Hits found	SEQ ID n-3263
					SEQ ID n-3264

TABLEAU II

SEQ ID n° 7821	PL-457.1	Contig9 from 2279519 to 2280187	p	33%	pir A83438 serine/threonine phosphoprotein phosphatase Stp1 PA1570 [imported] Pseudomonas aeruginosa (strain PA01) gb AAG05059.1 AE004594_11 (AE004594) serine/threonine phosphoprotein phosphatase Stp1 [Pseudomonas aeruginosa] SEQ ID n-9265
SEQ ID n° 7822	PL-3536.1	Contig9 from 2280912 to 2281376	m	82%	sp P28046 SSB_PROMI_SINGLE-STRAND BINDING PROTEIN (SSB) (HELIX-DESTABILIZING PROTEIN) pir S19955 single-stranded DNA-binding protein Proteus mirabilis emb CAA46206.1 (X65079) single-stranded DNA-binding protein [Proteus mirabilis] SEQ ID n-2738
SEQ ID n° 7823	PL-3537.1	Contig9 from 2281450 to 2281908	m	39%	pir C82642 hypothetical protein XF1761 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84570.1 AE003998_12 (AE003998) hypothetical protein [Xylella fastidiosa] SEQ ID n-2739
SEQ ID n° 7824	PL-459.1	Contig9 from 2282568 to 2284598	m	76%	gb AAF14809.1 (AF000001) topoisomerase B [Salmonella typhi] SEQ ID n-3267
SEQ ID n° 7825	PL-460.1	Contig9 from 2284602 to 2285300	m	46%	pir E82638 hypothetical protein XF1780 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84588.1 AE004000_5 (AE004000) hypothetical protein [Xylella fastidiosa] SEQ ID n-3269
SEQ ID n° 7826	PL-461.1	Contig9 from 2285569 to 2286804	m	43%	pir F82638 hypothetical protein XF1781 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84589.1 AE004000_6 (AE004000) hypothetical protein [Xylella fastidiosa] SEQ ID n-3270
SEQ ID n° 7827	PL-5815.1	Contig9 from 2286821 to 2287084	m	No Hits found	#N/A

TABLEAU II

SEQ ID n° 7828	PL-3538.1	Contig9 from 2287081 to 2287671	m	52%	<p>pir T17449 hypothetical 21.9K protein [imported] - Yersinia pestis gb AAC69594.1 (AF091251) unknown [Yersinia pestis] emb CAA21400.1 (AL031866) ORF 77, len=192 aa, unknown [Yersinia pestis] ref NP_052955.1 100% identical to gp:AF005044_3 [Trar of plasmid R100-1, function unknown] [Plasmid R100] gb AAB61930.1 (AF005044) Trar [Escherichia coli] dbj BAA79859.1 (AP000342) 100% identical to gp:AF005044_3 [Trar of plasmid R100-1, function unknown] [Plasmid R100] pir A82639 hypothetical protein XF1784 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84592.1 AE004000_9 (AE004000) hypothetical protein [Xylella fastidiosa]</p>	SEQ ID n-2740
SEQ ID n° 7829	PL-5817.1	Contig9 from 2287735 to 2287986	m	42%		#N/A
SEQ ID n° 7830	PL-462.1	Contig9 from 2287979 to 2289709	m	23%		SEQ ID n-9271
SEQ ID n° 7831	PL-463.1	Contig9 from 2289706 to 2291085	m	67%	<p>sp P10338 DNAB_SALTY REPLICATIVE DNA HELICASE pir B82639 chromosome partitioning related protein XF1785 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84593.1 AE004000_10 (AE004000) chromosome partitioning related protein [Xylella fastidiosa]</p>	SEQ ID n-9272
SEQ ID n° 7832	PL-464.1	Contig9 from 2291078 to 2291962	m	57%		SEQ ID n-9273
SEQ ID n° 7833	PL-465.1	Contig9 from 2292497 to 2293498	m	47%	<p>gb AAG02084.1 AF285416_2 (AF285416) XerC [Pseudomonas aeruginosa] pir C82641 hypothetical protein XF1753 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84562.1 AE003998_4 (AE003998) hypothetical protein [Xylella fastidiosa]</p>	SEQ ID n-9274
SEQ ID n° 7834	PL-466.1	Contig9 from 2293576 to 2295117	m	20%		SEQ ID n-9275

TABLEAU II

SEQ ID n° 7835	PL-5820.1	Contig9 from 2295620 to 2295724	m	No Hits found		#N/A...
SEQ ID n° 7836	PL-467.1	Contig9 from 2295817 to 2296740	m	47%	ref NP_052478.1 yccB [Plasmid Colib-P9] dbj BAA75117.1 (AB021078) yccb [Plasmid Colib-P9]	SEQ ID n-9276
SEQ ID n° 7837	PL-5823.1	Contig9 from 2296870 to 2297118	m	No Hits found		#N/A
SEQ ID n° 7838	PL-468.1	Contig9 from 2297168 to 2298181	m	No Hits found		SEQ ID n-9277
SEQ ID n° 7839	PL-469.1	Contig9 from 2298015 to 2298842	m	63%	pir T00225 hypothetical protein - Escherichia coli plasmid pO157	SEQ ID n-9278
SEQ ID n° 7840	PL-5824.1	Contig9 from 2298869 to 2299171	m	80%	sp P39213 YI91_SHIDY INSERTION ELEMENT IS911 HYPOTHETICAL 12.7 KD PROTEIN	#N/A
SEQ ID n° 7841	PL-5825.1	Contig9 from 2299226 to 2299414	m	No Hits found		#N/A
SEQ ID n° 7842	PL-5827.1	Contig9 from 2299906 to 2300175	p	52%	gb AAG60892.1 AF322013_11 (AF322013) ID459 [Bradyrhizobium japonicum]	#N/A
SEQ ID n° 7843	PL-470.1	Contig9 from 2300323 to 2301102	p	69%	gb AAC82519.1 (AF027768) Reta [Serratia marcescens]	SEQ ID n-9280
SEQ ID n° 7844	PL-471.1	Contig9 from 2301099 to 2301683	p	14%	gb AAG60892.1 AF322013_11 (AF322013) ID459 [Bradyrhizobium japonicum]	SEQ ID n-9281
SEQ ID n° 7845	PL-473.1	Contig9 from 2302258 to 2302992	p	49%	sp P55606 Y4OU_RHIEN HYPOTHETICAL PROTEIN Y4OU PRECURSOR gb AAB91807.1 (AE000089) Y4OU [Rhizobium sp. NGR234]	SEQ ID n-9283
SEQ ID n° 7846	PL-5830.1	Contig9 from 2303602 to 2303820	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 7847	PL-5832.1	Contig9 from 2304342 to 2304434	m	66%	ref NP_053113.1 orf51 [Escherichia coli] dbj BAAB4886.1 (AB024946) orf51 [Escherichia coli]	#N/A
SEQ ID n° 7848	PL-474.1	Contig9 from 2304722 to 2305342	m	No Hits found		SEQ ID n-9284
SEQ ID n° 7849	PL-475.1	Contig9 from 2305483 to 2306727	p	60%	sp P55606 Y4OU_RHISN HYPOTHETICAL PROTEIN Y4OU PRECURSOR gb AAB91807.1 (AE000089) Y4OU [Rhizobium sp. NGR234]	SEQ ID n-9285
SEQ ID n° 7850	PL-476.1	Contig9 from 2306711 to 2307541	p	72%	sp P55607 Y4OV_RHISN HYPOTHETICAL 30.2 KD PROTEIN Y4OV gb AAB91808.1 (AE000089) Y4OV [Rhizobium sp. NGR234]	SEQ ID n-9286
SEQ ID n° 7851	PL-5835.1	Contig9 from 2307592 to 2307840	p	No Hits found		#N/A
SEQ ID n° 7852	PL-3540.1	Contig9 from 2307998 to 2308456	m	No Hits found		SEQ ID n-2742
SEQ ID n° 7853	PL-5838.1	Contig9 from 2308566 to 2308790	m	67%	gb AAF22961.1 AF157489_1 (AF157489) Pln [Photorhabdus luminescens]	#N/A
SEQ ID n° 7854	PL-5839.1	Contig9 from 2309050 to 2309190	m	No Hits found		#N/A
SEQ ID n° 7855	PL-3541.1	Contig9 from 2309381 to 2309908	m	No Hits found		SEQ ID n-2743
SEQ ID n° 7856	PL-5841.1	Contig9 from 2310044 to 2310247	p	No Hits found		#N/A
SEQ ID n° 7857	PL-477.1	Contig9 from 2310806 to 2312158	m	60%	pir G83616 4-hydroxybenzoate transporter PcaK PA0235 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG03624.1 AE004461_7 (AE004461) 4- hydroxybenzoate transporter PcaK [Pseudomonas aeruginosa]	SEQ ID n-9287

TABLEAU II

SEQ ID n° 7858	PL-478.1	Contig9 from 2312213 to 2313160	m	50%	sp P37610 TAUD_ECOLI_ALPHA-KETOGLUTARATE- DEPENDENT TAURINE DIOXYGENASE (SULFATE STARVATION-INDUCED PROTEIN 3) (SSI3) pir H64764 probable taurine dioxygenase (EC 1.- .-.-) - Escherichia coli dbj BAAL2841.1 (D85613) dioxygenase [Escherichia coli] gb AAB18091.1 (U73857) dioxygenase [Escherichia coli] gb AAC73471.1 (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli K12]	SEQ ID n-3288
SEQ ID n° 7859	PL-479.1	Contig9 from 2313195 to 2314406	m	41%	gb AAB18065.1 (U73857) cyanate transport protein [Escherichia coli] pir C83589 conserved hypothetical protein PA0446 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG03835.1 AE004482_2 (AE004482) conserved hypothetical protein [Pseudomonas aeruginosa] gb AAD12608.1 (AF036940) salicylate-5- hydroxylase small oxygenase component [Ralstonia sp. U2] gb AAD12607.1 (AF036940) salicylate-5- hydroxylase large oxygenase component [Ralstonia sp. U2] pir C71664 hypothetical protein RP592 - Rickettsia prowazekii emb CAA15037.1 (AJ235272) unknown [Rickettsia prowazekii] gb AAG02168.1 AF212041_24 (AF212041) 3-oxoacyl- (acylcarrier protein) reductase [Zymomonas mobilis]	SEQ ID n-3289
SEQ ID n° 7860	PL-480.1	Contig9 from 2314531 to 2315715	m	56%	gb AAG03835.1 AE004482_2 (AE004482) conserved hypothetical protein [Pseudomonas aeruginosa] gb AAD12608.1 (AF036940) salicylate-5- hydroxylase small oxygenase component [Ralstonia sp. U2] gb AAD12607.1 (AF036940) salicylate-5- hydroxylase large oxygenase component [Ralstonia sp. U2] pir C71664 hypothetical protein RP592 - Rickettsia prowazekii emb CAA15037.1 (AJ235272) unknown [Rickettsia prowazekii] gb AAG02168.1 AF212041_24 (AF212041) 3-oxoacyl- (acylcarrier protein) reductase [Zymomonas mobilis]	SEQ ID n-3291
SEQ ID n° 7861	PL-3542.1	Contig9 from 2316032 to 2316481	m	49%	gb AAD12608.1 (AF036940) salicylate-5- hydroxylase small oxygenase component [Ralstonia sp. U2] gb AAD12607.1 (AF036940) salicylate-5- hydroxylase large oxygenase component [Ralstonia sp. U2] pir C71664 hypothetical protein RP592 - Rickettsia prowazekii emb CAA15037.1 (AJ235272) unknown [Rickettsia prowazekii] gb AAG02168.1 AF212041_24 (AF212041) 3-oxoacyl- (acylcarrier protein) reductase [Zymomonas mobilis]	SEQ ID n-2744
SEQ ID n° 7862	PL-481.1	Contig9 from 2316510 to 2317718	m	63%	gb AAD12608.1 (AF036940) salicylate-5- hydroxylase small oxygenase component [Ralstonia sp. U2] gb AAD12607.1 (AF036940) salicylate-5- hydroxylase large oxygenase component [Ralstonia sp. U2] pir C71664 hypothetical protein RP592 - Rickettsia prowazekii emb CAA15037.1 (AJ235272) unknown [Rickettsia prowazekii] gb AAG02168.1 AF212041_24 (AF212041) 3-oxoacyl- (acylcarrier protein) reductase [Zymomonas mobilis]	SEQ ID n-3292
SEQ ID n° 7863	PL-482.1	Contig9 from 2317729 to 2318823	m	29%	gb AAD12608.1 (AF036940) salicylate-5- hydroxylase small oxygenase component [Ralstonia sp. U2] gb AAD12607.1 (AF036940) salicylate-5- hydroxylase large oxygenase component [Ralstonia sp. U2] pir C71664 hypothetical protein RP592 - Rickettsia prowazekii emb CAA15037.1 (AJ235272) unknown [Rickettsia prowazekii] gb AAG02168.1 AF212041_24 (AF212041) 3-oxoacyl- (acylcarrier protein) reductase [Zymomonas mobilis]	SEQ ID n-3293
SEQ ID n° 7864	PL-5842.1	Contig9 from 2319369 to 2319662	m	25%	gb AAG02168.1 AF212041_24 (AF212041) 3-oxoacyl- (acylcarrier protein) reductase [Zymomonas mobilis]	#N/A
SEQ ID n° 7865	PL-3543.1	Contig9 from 2321108 to 2321617	p	54%	gb AAG58930.1 AE005604_7 (AE005604) putative major fimbrial subunit [Escherichia coli O157:H7]	SEQ ID n-2745

TABLEAU II

SEQ ID n° 7866	PL-483.1	Contig9 from 2321674 to 2322342	p	54%	sp P42914 YRAI_ECOLI HYPOTHETICAL 25.7 KD FIMBRIAL CHAPERONE IN AGAI-MTR INTERGENIC REGION PRECURSOR pir C65104 hypothetical 25.7 kd fimbrial chaperone in agai- mtr intergeni - Escherichia coli (strain K-12) gb AA57946.1 (U18997) ORF_0231 [Escherichia coli] gb AAC76177.1 (AE000395) putative chaperone [Escherichia coli K12] gb AAG58277.1 AE005543_7 (AE005543) putative outer membrane protein [Escherichia coli O157:H7]	SEQ ID n° 9294
SEQ ID n° 7867	PL-484.1	Contig9 from 2322348 to 2324861	p	56%	sp P21648 MRKD_KLEPN FIMBRIA ADHESIN PROTEIN PRECURSOR pir B32801 fimbrial adhesin precursor, type 3 - Klebsiella pneumoniae gb AA25096.1 (M55912) mrkD [Klebsiella pneumoniae] gb AA25098.1 (M24536) fimbrial adhesin [Klebsiella pneumoniae]	SEQ ID n° 9295
SEQ ID n° 7868	PL-485.1	Contig9 from 2324889 to 2325869	p	18%	sp P12903 FNL2_KLEPN FIMBRIAL SUBUNIT TYPE 1 PRECURSOR pir YQKBT1 type 1 fimbrial protein precursor - Klebsiella pneumoniae (strain IA565) gb AA25091.1 (M20917) major fimbrial subunit precursor [Klebsiella pneumoniae] pir B83501 hypothetical protein PA1165 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04554.1 AE004546_9 (AE004546) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n° 9296
SEQ ID n° 7870	PL-487.1	Contig9 from 2327333 to 2328076	p	41%	sp Q07095 HPCR_ECOLI HOMOPROTECHUATE DEGRADATIVE OPERON REPRESSOR pir S30280 hpcR protein - Escherichia coli gb AB25801.1 (S56952) Hpc repressor [Escherichia coli, C, Peptide, 148 aa] emb CAA86039.1 (Z37980) regulator of the meta operon of 3,4dhpA metabolic pathway [Escherichia coli] prf 1912302A homoproteocatechuate degradation operon regulator [Escherichia coli]	SEQ ID n° 9297
SEQ ID n° 7871	PL-3544.1	Contig9 from 2328153 to 2328599	m	77%		SEQ ID n° 2746

TABLEAU II

SEQ ID n° 7872	PL-488.1	Contig9 from 2328986 to 2329618	p	76%	sp Q9RPUS HPAG_SALDU_4-HYDROXYPHENYLACETATE DEGRADATION BIFUNCTIONAL ISOMERASE/DECARBOXYLASE [INCLUDES: HYDROXYHEPTA-2,4-DIENE-1,7-DIOATE ISOMERASE (HHDD) ISOMERASE]; 5-CARBOXYMETHYL-2- OXO-HEX-3-ENE-1,7-DIOATE DECARBOXYLASE (OPET DECARBOXYLASE)] gb AAD53501.1 AF144422_8 (AF144422) HpaG [Salmonella dublin] pir G83131 conserved hypothetical protein PA4122 [imported] - Pseudomonas aeruginosa (strain PA01)	SEQ ID n-3299
SEQ ID n° 7873	PL-489.1	Contig9 from 2329471 to 2330376	p	68%	gb AAG07509.1 AE004828_10 (AE004828) conserved hypothetical protein [Pseudomonas aeruginosa] emb CAA86041.1 (Z37980) 5-carboxy-2- hydroxymuconate semialdehyde dehydrogenase [Escherichia coli]	SEQ ID n-3300
SEQ ID n° 7874	PL-490.1	Contig9 from 2330376 to 2331842	p	95%	gb AAD53499.1 AF144422_6 (AF144422) HpaD [Salmonella dublin]	SEQ ID n-3302
SEQ ID n° 7875	PL-491.1	Contig9 from 2331907 to 2332785	p	80%	gb AAD53499.1 AF144422_5 (AF144422) HpaF [Salmonella dublin]	SEQ ID n-3303
SEQ ID n° 7876	PL-3547.1	Contig9 from 2332799 to 2333185	p	69%	gb AAK03617.1 (AE006190) Bcr [Pasteurella multocida]	SEQ ID n-2747
SEQ ID n° 7877	PL-492.1	Contig9 from 2333188 to 2334417	p	54%	pir D83613 succinate-semialdehyde dehydrogenase PA0265 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03654.1 AE004464_7 (AE004464) succinate- semialdehyde dehydrogenase [Pseudomonas aeruginosa] emb CAA86044.1 (Z37980) 2-oxo-hept-3-ene-1,7- dioate hydratase [Escherichia coli] gb AAE91474.1 (AF036583) 2-oxo-hept-4-ene-1,7- dioate hydratase [Escherichia coli]	SEQ ID n-3304
SEQ ID n° 7878	PL-493.1	Contig9 from 2334407 to 2335879	p	79%		SEQ ID n-3305
SEQ ID n° 7879	PL-494.1	Contig9 from 2335884 to 2336687	p	88%		SEQ ID n-3306

TABLEAU II

SEQ ID n° 7880	PL-495.1	Contig9 from 2336699 to 2337505	p	78%	sp Q9RPV0 HPAI_SALDU 2,4-DIHYDROXYHEPT-2-ENE-1,7- DIOIC ACID ALDOLASE (HHED ALDOLASE) gb AAD53496.1 AF144422_3 (AF144422) HpaI [Salmonella dublin] SEQ ID n-3307
SEQ ID n° 7881	PL-496.1	Contig9 from 2337602 to 2338978	p	88%	gb AAD53495.1 AF144422_2 (AF144422) HpaX [Salmonella dublin] SEQ ID n-3308
SEQ ID n° 7882	PL-497.1	Contig9 from 2339004 to 2339894	p	77%	gb AAD53494.1 AF144422_1 (AF144422) HpaA [Salmonella dublin] SEQ ID n-3309
SEQ ID n° 7883	PL-5849.1	Contig9 from 2340332 to 2340643	p	47%	sp P39284 YJEO_ECOLI HYPOTHETICAL 12.6 KD PROTEIN IN GENX-PSD INTERGENIC REGION (O104B) pir s56386 hypothetical 12.6K protein (genx-psd intergenic region) - Escherichia coli gb AAA97057.1 (U14003) ORF_o104b [Escherichia coli] gb AAC77118.1 (AE000488) orf, hypothetical protein [Escherichia coli K12] #N/A
SEQ ID n° 7884	PL-5850.1	Contig9 from 2341255 to 2341575	p	No Hits found	#N/A
SEQ ID n° 7885	PL-5851.1	Contig9 from 2341617 to 2341940	p	No Hits found	#N/A
SEQ ID n° 7886	PL-498.1	Contig9 from 2342300 to 2343046	p	76%	sp P52037 YGEF_ECOLI HYPOTHETICAL OXIDOREDUCTASE IN BGLA-GCVP INTERGENIC REGION pir F65074 hypothetical oxidoreductase - Escherichia coli (strain K-12) gb AAC75940.1 (AE000373) putative oxidoreductase [Escherichia coli K12] SEQ ID n-3310
SEQ ID n° 7887	PL-7176.1	Contig9 from 2343185 to 2343310	p	No Hits found	#N/A
SEQ ID n° 7888	PL-499.1	Contig9 from 2343314 to 2346193	p	61%	gb AAC38630.1 (AF047028) insecticidal toxin complex protein Tccc [Photorhabdus luminescens] SEQ ID n-3311

TABLEAU II

SEQ ID n° 7889	PL-500.1	Contig9 from 2346515 to 2348077	p	94%	gb AAC08739.1 (AF021839) 4-hydroxyphenylacetic acid hydroxylase [Photorhabdus luminescens]	SEQ ID n-9314
SEQ ID n° 7890	PL-3549.1	Contig9 from 2348097 to 2348615	p	87%	gb AAC08740.1 (AF021839) 4-hydroxyphenylacetic acid hydroxylase putative coupling protein [Photorhabdus luminescens] sp P36837 YHIP_ECOLI_HYPOTHETICAL 53.7 KD PROTEIN IN USPA-PRIC INTERGENIC REGION pir C65147 hypothetical 53.7 kD protein in uspa- prlc intergenic region - Escherichia coli (strain K-12) gb AAC76521.1 (AE000426) putative transport protein [Escherichia coli K12]	SEQ ID n-2749
SEQ ID n° 7891	PL-501.1	Contig9 from 2349085 to 2350554	p	86%	pir T33131 hypothetical protein C23H5.1 - Caenorhabditis elegans gb AAC17532.1 (AF067609) contains similarity to methyltransferases [Caenorhabditis elegans]	SEQ ID n-3315
SEQ ID n° 7892	PL-502.1	Contig9 from 2350690 to 2351409	m	40%	gb AAF05542.1 AF188483_1 (AF188483) toxin A [Photorhabdus luminescens]	SEQ ID n-3316
SEQ ID n° 7893	PL-503.1	Contig9 from 2352217 to 2358864	p	38%	gb AAF05542.1 AF188483_1 (AF188483) toxin A [Photorhabdus luminescens]	SEQ ID n-3317
SEQ ID n° 7894	PL-504.1	Contig9 from 2359337 to 2366671	p	67%	gb AAF05542.1 AF188483_1 (AF188483) toxin A [Photorhabdus luminescens]	SEQ ID n-3318
SEQ ID n° 7895	PL-505.1	Contig9 from 2366728 to 2371155	p	72%	gb AAC38625.1 (AF046867) insecticidal toxin complex protein TcaC [Photorhabdus luminescens]	SEQ ID n-9319
SEQ ID n° 7896	PL-5857.1	Contig9 from 2371171 to 2371302	p	No Hits found		#N/A
SEQ ID n° 7897	PL-5859.1	Contig9 from 2371208 to 2371528	p	53%	gb AAG55972.1 AE005330_4 (AE005330) putative holin protein of prophage CP-933X [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7898	PL-506.1	Contig9 from 2371677 to 2374589	p	61%	gb AAC38630.1 (AF047028) insecticidal toxin complex protein Tccc [Photorhabdus luminescens]	SEQ ID n-9320

TABLEAU II

SEQ ID n° 7899	PL-507.1	Contig9 from 2374699 to 2375610	m	13%	gb AAC6441.1 (AF009224) LysR-type transcriptional activator [Acinetobacter sp. ADPI]	SEQ ID n-3321
SEQ ID n° 7900	PL-508.1	Contig9 from 2375984 to 2383360	p	68%	gb AAF05542.1 AF188483_1 (AF188483) toxin A [Photorhabdus luminescens]	SEQ ID n-3322
SEQ ID n° 7901	PL-509.1	Contig9 from 2383553 to 2386369	p	61%	gb AAC38630.1 (AF047028) insecticidal toxin complex protein Tccc [Photorhabdus luminescens]	SEQ ID n-3323
SEQ ID n° 7902	PL-510.1	Contig9 from 2386532 to 2387446	m	18%	gb AAG58047.1 AE005522_5 (AE005522) partial putative transcriptional regulator LysR-type [Escherichia coli O157:H7]	SEQ ID n-3325
SEQ ID n° 7903	PL-511.1	Contig9 from 2388140 to 2395717	p	91%	gb AAF05542.1 AF188483_1 (AF188483) toxin A [Photorhabdus luminescens]	SEQ ID n-3326
SEQ ID n° 7904	PL-512.1	Contig9 from 2395770 to 2400200	p	73%	gb AAC38625.1 (AF046867) insecticidal toxin complex protein TcaC [Photorhabdus luminescens]	SEQ ID n-3327
SEQ ID n° 7905	PL-513.1	Contig9 from 2400781 to 2403528	p	60%	gb AAC38630.1 (AF047028) insecticidal toxin complex protein Tccc [Photorhabdus luminescens]	SEQ ID n-3328
SEQ ID n° 7906	PL-7174.1	Contig9 from 2403675 to 2403779	p	No Hits found	pir G82452 conserved hypothetical protein VCA0482 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96227.1 (AE004370) conserved hypothetical protein [Vibrio cholerae] gb AAF96386.1 (AE004380) conserved hypothetical protein [Vibrio cholerae]	#N/A
SEQ ID n° 7907	PL-5865.1	Contig9 from 2403991 to 2404287	p	54%		#N/A

TABLEAU II

SEQ ID n° 7908	PL-3550.1	Contig9 from 2404343 to 2404777	p	60%	pir F82452 conserved hypothetical protein VCA0481 VCA0318 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96226.1 (AE004370) conserved hypothetical protein [Vibrio cholerae] gb AAF96385.1 (AE004380) conserved hypothetical protein [Vibrio cholerae] SEQ ID n-2751
SEQ ID n° 7909	PL-514.1	Contig9 from 2404845 to 2405921	m	90%	sp O52402 ALF_EDWIC FRUCTOSE-BISPHOSPHATE ALDOLASE gb AAB92572.1 (AF037440) fructose 1,6- bisphosphate aldolase [Edwardsiella ictaluri] SEQ ID n-9329
SEQ ID n° 7910	PL-515.1	Contig9 from 2405984 to 2407147	m	92%	sp P11665 PGK_ECOLI PHOSPHOGLYCERATE KINASE pir TVFCG phosphoglycerate kinase (EC 2.7.2.3) Escherichia coli emb CAA32604.1 (X14436) phosphoglycerate kinase (AA 1-387) [Escherichia coli] gb AA65093.1 (U28377) phosphoglycerate kinase [Escherichia coli] gb AAC75963.1 (AE000376) phosphoglycerate kinase [Escherichia coli K12] SEQ ID n-9330
SEQ ID n° 7911	PL-516.1	Contig9 from 2407231 to 2408250	m	86%	sp P11603 E4PD_ECOLI D-ERYTHROSE 4-PHOSPHATE DEHYDROGENASE (E4PDH) pir DEECGB glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) B - Escherichia coli emb CAA32603.1 (X14436) glyceraldehyde 3- phosphate dehydrogenase (AA 1-339) [Escherichia coli] gb AA69094.1 (U28377) glyceraldehyde 3-phosphate dehydrogenase [Escherichia coli] gb AAC75964.1 (AE000376) D-erythrose 4-phosphate dehydrogenase [Escherichia coli K12] gb AAG58053.1 AE005523_2 (AE005523) D-erythrose 4-phosphate dehydrogenase [Escherichia coli O157:H7] SEQ ID n-9331

TABLEAU II

SEQ ID n° 7912 PL-5866.1	Contig9 from 2408745 to 2408948	m	68%	pir C83622 probable short-chain dehydrogenase PA0182 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03572.1 AE004456_3 (AE004456) probable short-chain dehydrogenase [Pseudomonas aeruginosa] #N/A
SEQ ID n° 7913 PL-5868.1	Contig9 from 2408971 to 2409138	m	38%	pir B83228 probable MFS transporter PA3336 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06724.1 AE004756_2 (AE004756) probable MFS transporter [Pseudomonas aeruginosa] #N/A
SEQ ID n° 7914 PL-5869.1	Contig9 from 2409126 to 2409455	m	No Hits found	#N/A
SEQ ID n° 7915 PL-3552.1	Contig9 from 2409497 to 2409862	m	No Hits found	SEQ ID n-2752
SEQ ID n° 7916 PL-517.1	Contig9 from 2409900 to 2410496	m	45%	emb CAB64355.1 (AJ243941) eugenol hydroxylase flavoprotein subunit [Pseudomonas sp.] SEQ ID n-3332
SEQ ID n° 7917 PL-5872.1	Contig9 from 2410612 to 2410773	p	No Hits found	#N/A
SEQ ID n° 7918 PL-518.1	Contig9 from 2410869 to 2411462	p	59%	pir D83279 probable transcriptional regulator PA2931 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06319.1 AE004719_5 (AE004719) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-9333
SEQ ID n° 7919 PL-3553.1	Contig9 from 2411760 to 2412233	p	38%	sp Q10846 YK11_MYCTU HYPOTHETICAL 15.7 KDA PROTEIN RV2011C PRECURSOR pir A70760 hypothetical protein RV2011c - Mycobacterium tuberculosis (strain H37RV) emb CAA98404.1 (Z74025) hypothetical protein Rv2011c [Mycobacterium tuberculosis] SEQ ID n-2753

TABLEAU II

SEQ ID n° 7920	PL-5873.1	Contig9 from 2412614 to 2412985	p	No Hits found	#N/A
SEQ ID n° 7921	PL-5874.1	Contig9 from 2412973 to 2413110	p	No Hits found	#N/A
SEQ ID n° 7922	PL-519.1	Contig9 from 2413091 to 2415085	m	90%	gb AAG58065.1 AE005524_1 (AE005524) transketolase 1 isozyme [Escherichia coli O157:H7] pir C83477 probable transcription regulator PA1347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-3334
SEQ ID n° 7923	PL-520.1	Contig9 from 2415700 to 2416482	p	32%	gb AAF22961.1 AF157489_1 (AF157489) Pln [Photorhabdus luminescens] sp P14566 DF3E_SALTY DNA POLYMERASE III, EPSILON CHAIN gb AA86422.1 (U44090) dnaQ [Salmonella typhimurium] gb AAC44792.1 (U77465) DNA polymerase III epsilon chain [Salmonella typhimurium] SEQ ID n-3337
SEQ ID n° 7924	PL-5875.1	Contig9 from 2417055 to 2417321	p	44%	pdb 1RBR Ribonuclease H (E.C.3.1.26.4) Mutant With His 62 Replaced By Pro (H62p) SEQ ID n-2754
SEQ ID n° 7925	PL-521.1	Contig9 from 2417768 to 2418514	m	84%	gb AAG54509.1 AE005196_7 (AE005196) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3338
SEQ ID n° 7926	PL-3554.1	Contig9 from 2418572 to 2419042	p	76%	
SEQ ID n° 7927	PL-522.1	Contig9 from 2419043 to 2419756	m	72%	

TABLEAU II

SEQ ID n° 7928	PL-523.1	Contig9 from 2419801 to 2420553	p	70%	sp Q47677 GLO2_ECOLI PROBABLE HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II) (GLX II) pir F64745 probable hydroxyacylglutathione hydrolase (EC 3.1.2.6) gloB - Escherichia coli gb AAB08634.1 (U70214) hypothetical protein [Escherichia coli] gb AAC73317.1 (AE000130) probable hydroxyacylglutathione hydrolase [Escherichia coli K12]
SEQ ID n° 7929	PL-524.1	Contig9 from 2420625 to 2421986	p	71%	dbj BAA77883.1 (D83536) Hypothetical protein 1 [Escherichia coli] gb AAG54508.1 AE005196_6 (AE005196) probable hydroxyacylglutathione hydrolase [Escherichia coli O157:H7] SEQ ID n-3339 gb AAG54507.1 AE005196_5 (AE005196) transcriptional regulator for nitrite reductase (cytochrome c552) [Escherichia coli O157:H7] SEQ ID n-3340
SEQ ID n° 7930	PL-5877.1	Contig9 from 2422484 to 2422669	m	No Hits found	#N/A
SEQ ID n° 7931	PL-525.1	Contig9 from 2422725 to 2423570	p	17%	dbj BAA97424.1 (AB025638) 1-aminocyclopropane-1- carboxylate oxidase [Arabidopsis thaliana] SEQ ID n-3341
SEQ ID n° 7932	PL-526.1	Contig9 from 2423778 to 2424959	m	38%	dbj BAB05758.1 (AP001514) BH2039-unknown conserved protein in others [Bacillus halodurans] SEQ ID n-3342
SEQ ID n° 7933	PL-3555.2	Contig9 from 2425009 to 2425545	m	31%	sp P58157 KTH2_SULSO PROBABLE THYMIDYLATE KINASE 2 (DTMP KINASE 2) gb AAK41441.1 (AE006735) Thymidylate kinase (tmk-2) [Sulfolobus solfataricus] #N/A
SEQ ID n° 7934	PL-527.2	Contig9 from 2425673 to 2426806	m	27%	pir S77024 hypothetical protein sl10785 - Synecocystis sp. (strain PCC 6803) dbj BAA10716.1 (D64005) hypothetical protein [Synecocystis sp.] #N/A

TABLEAU II

SEQ ID n° 7935	PL-528.1	Contig9 from 2426809 to 2427654	m	40%	sp Q57573 Y109_METJA_HYPOTHETICAL_PROTEIN_MJ0109 pir E64313_hypothetical_protein_MJ0109 - Methanococcus_jannaschii_pdb 1DK4 A_Chain_A, Crystal_Structure_Of_Mj0109_Gene_Product Inositol_Monophosphatase_pdb 1DK4 B Chain_B,Crystal_Structure_Of_Mj0109_Gene Product_Inositol_Monophosphatase gb AAB98091.1 (U67468)extragenic suppressor (suha) [Methanococcus_jannaschii]	SEQ ID n-9344
SEQ ID n° 7936	PL-529.1	Contig9 from 2427651 to 2428685	m	No Hits found		SEQ ID n-9345
SEQ ID n° 7937	PL-530.1	Contig9 from 2428691 to 2429734	m	No Hits found		SEQ ID n-9347
SEQ ID n° 7938	PL-5879.1	Contig9 from 2430286 to 2430468	p	No Hits found	#N/A	
SEQ ID n° 7939	PL-531.1	Contig9 from 2431493 to 2432407	p	22%	pir T49209_leucoanthocyanidin_dioxygenase-like protein - Arabidopsis_thaliana_emb CA887851.1 (AL163832) leucoanthocyanidin_dioxygenase-like protein [Arabidopsis_thaliana] emb CAC19787.1 (AJ298225) putative leucoanthocyanidin_dioxygenase [Arabidopsis thaliana]	SEQ ID n-9348
SEQ ID n° 7940	PL-3556.1	Contig9 from 2432530 to 2432874	m	No Hits found		SEQ ID n-2756
SEQ ID n° 7941	PL-5881.1	Contig9 from 2432852 to 2433214	m	No Hits found	#N/A	
SEQ ID n° 7942	PL-532.1	Contig9 from 2433592 to 2434764	p	71%	pir E82951_probable_MFS_transporter_PA5548 [imported] - Pseudomonas_aeruginosa (strain_PA01) gb AAG08933.1 AE004967_4 (AE004967) probable MFS transporter [Pseudomonas aeruginosa]	SEQ ID n-9349

TABLEAU II

SEQ ID n° 7943	PL-533.2	Contig9 from 2434886 to 2436271	m	71%	gb AAK03251.1 (AE006157) unknown. [Pasteurella multocida]	SEQ ID n-3350
SEQ ID n° 7944	PL-5885.1	Contig9 from 2436246 to 2436398	p	No Hits found	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 7945	PL-534.1	Contig9 from 2437427 to 2438149	p	29%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-3351
SEQ ID n° 7946	PL-535.1	Contig9 from 2438310 to 2439032	p	30%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-3352
SEQ ID n° 7947	PL-536.1	Contig9 from 2439194 to 2439916	p	33%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-3353
SEQ ID n° 7948	PL-537.1	Contig9 from 2440202 to 2440924	p	30%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-3354
SEQ ID n° 7949	PL-538.1	Contig9 from 2441242 to 2441964	p	33%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-3355

TABLEAU II

SEQ ID n° 7950	PL-539.1	Contig9 from 2442265 to 2442987	p	33%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AB004564_5 (AB004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-9356
SEQ ID n° 7951	PL-540.1	Contig9 from 2443309 to 2444031	p	34%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AB004564_5 (AB004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-9358
SEQ ID n° 7952	PL-541.1	Contig9 from 2443973 to 2444914	p	27%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AB004564_5 (AB004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-9359
SEQ ID n° 7953	PL-5887.1	Contig9 from 2445235 to 2445447	m	87%	gb AAF22961.1 AF157489_1 (AF157489) Pln [Photorhabdus luminescens] #N/A
SEQ ID n° 7954	PL-542.1	Contig9 from 2446007 to 2447200	m	39%	gb AAK06333.1 AE006452_6 (AE006452) transporter [Lactococcus lactis subsp. lactis] SEQ ID n-9360
SEQ ID n° 7955	PL-543.1	Contig9 from 2447223 to 2448404	m	65%	pir A71652 iron-sulfur cofactor synthesis protein RP486 - Rickettsia prowazekii emb CAA14939.1 (AJ235272) NIFS PROTEIN HOMOLOG (spl1) [Rickettsia prowazekii] SEQ ID n-9361
SEQ ID n° 7956	PL-544.1	Contig9 from 2448595 to 2449308	m	No Hits found	SEQ ID n-9362
SEQ ID n° 7957	PL-546.1	Contig9 from 2449985 to 2451286	m	94%	gb AAK03955.1 (AE006225) Eno [Pasteurella multocida] SEQ ID n-9364

TABLEAU II

SEQ ID n° 7958	PL-547.1	Contig9 from 2451360 to 2452997	m	94%	sp P08398 PYRG_ECOLI_CTP SYNTHASE [UTP--AMMONIA LIGASE] (CTP SYNTHETASE) pir SYECTP CTP synthase (EC 6.3.4.2) [validated] - Escherichia coli gb AAAG9290.1 (U29580) CTP synthetase [Escherichia coli] gb AAC75822.1 (AE000361) CTP synthetase [Escherichia coli K12] gb AAG57893.1 AE005506_1 (AE005506) CTP synthetase [Escherichia coli O157:H7] SEQ ID n-3365
SEQ ID n° 7959	PL-548.1	Contig9 from 2453219 to 2453998	m	78%	sp P33646 MAZG_ECOLI_MAZG PROTEIN pir A65060 mazG protein - Escherichia coli (strain K-12) gb AAAG9291.1 (U29580) CG Site No. 33299 [Escherichia coli] gb AAC75823.1 (AE000362) orf, hypothetical protein [Escherichia coli K12] gb AAG57894.1 AE005506_2 (AE005506) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3366 sp P11585 RELA_ECOLI_GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) ((P)PPGPP SYNTHETASE) pir K1ECG GTP pyrophosphokinase (EC 2.7.6.5) - Escherichia coli gb AAAG9294.1 (U29580) GTP pyrophosphokinase [Escherichia coli] gb AAC75826.1 (AE000362) (p)ppGpp synthetase I (GTP pyrophosphokinase); regulation of RNA synthesis; stringent factor [Escherichia coli K12] gb AAG57897.1 AE005506_5 (AE005506) (p)ppGpp synthetase I (GTP pyrophosphokinase); regulation of RNA synthesis; stringent factor [Escherichia coli O157:H7] SEQ ID n-3367
SEQ ID n° 7960	PL-549.1	Contig9 from 2454066 to 2456297	m	89%	sp P55135 YGCA_ECOLI_HYPOTHETICAL RNA METHYLTRANSFERASE IN RELA-BARA INTERGENIC REGION pir E65060 ygca protein - Escherichia coli (strain K-12) gb AAAG9295.1 (U29580) alternate gene name ygca; ORF_f433 [Escherichia coli] gb AAC75827.1 (AE000362) putative enzyme [Escherichia coli K12] SEQ ID n-3369
SEQ ID n° 7961	PL-550.1	Contig9 from 2456339 to 2457655	m	74%	

TABLEAU II

SEQ ID n° 7962	PL-551.1	Contig9 from 2457709 to 2460036	p 62%	gb AAG57899.1 AE005506_7 (AE005506) sensor- regulator, activates Ompr by phosphorylation [Escherichia coli O157:H7] sp P15723 DGTG_ECOLI_DEOXYGUANOSINETRIPHOSPHATE TRIPHOSPHOHYDROLASE (DGTGASE) pir A35993 dGTPase (EC 3.1.5.1) - Escherichia coli gb AA23679.1 (M31772) dGTP triphosphohydrolase [Escherichia coli] dbj BAA05607.1 (D26562) 'deoxyguanosine triphosphate triphosphohydrolase' [Escherichia coli] gb AAB08590.1 (U70214) deoxyguanosine triphosphate [Escherichia coli] gb AAC73271.1 (AE000125) deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli K12] SEQ ID n-9370
SEQ ID n° 7963	PL-552.1	Contig9 from 2460051 to 2461577	m 73%	sp P24247 PFS_ECOLI_MTA/SAH_NUCLEOSIDASE (P46) [INCLUDES: 5'-METHYLTHIOADENOSINE NUCLEOSIDASE ; S-ADENOSYLHOMOCYSTEINE NUCLEOSIDASE] pir S45227 pfs protein - Escherichia coli dbj BAA05606.1 (D26562) 'ORF' [Escherichia coli] gb AAB08589.1 (U70214) similar to purine nucleoside phosphorylase (deod) [Escherichia coli] gb AAC73270.1 (AE000125) orf, hypothetical protein [Escherichia coli K12] gb AAC38291.1 (U24438) MTA/SAH nucleosidase [Escherichia coli] gb AAG54463.1 AE005192_5 (AE005192) orf, hypothetical protein [Escherichia coli O157:H7] sp P37028 YADT_ECOLI_HYPOTHETICAL_29.4_KD PROTEIN IN HEML-PFS INTERGENIC REGION PRECURSOR pir F64739 yadt protein - Escherichia coli gb AAB08588.1 (U70214) hypothetical [Escherichia coli] gb AAC73269.1 (AE000125) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-9372
SEQ ID n° 7964	PL-553.1	Contig9 from 2461705 to 2462406	p 81%	
SEQ ID n° 7965	PL-554.1	Contig9 from 2462612 to 2463439	p 60%	

TABLEAU II

SEQ ID n° 7966	PL-5891.1	Contig9 from 2463528 to 2463875	m	81%	sp P37026 YADR_ECOLI HYPOTHETICAL 12.1 KD PROTEIN IN HEML-PFS INTERGENIC REGION pir S45225 yadr protein - Escherichia coli dbj BAA05604.1 (D26562) 'ORF' [Escherichia coli] gb AAB08586.1 (U70214) hypothetical protein [Escherichia coli] gb AAC73267.1 (AE000125) orf, hypothetical protein [Escherichia coli K12] gb AAG54460.1 AE005192_2 (AE005192) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 7967	PL-555.1	Contig9 from 2464181 to 2464966	p	58%	pir B2212 hypothetical protein VC1330 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94488.1 (AE004213) hypothetical protein [Vibrio cholerae]	SEQ ID n-9374
SEQ ID n° 7968	PL-556.1	Contig9 from 2465017 to 2466300	p	90%	gb AAG54458.1 AE005191_9 (AE005191) glutamate-1- semialdehyde aminotransferase (aminomutase) [Escherichia coli O157:H7] gb AAC70896.1 (AF006830) virulence plasmid protein [Actinobacillus actinomycetemcomitans] dbj BAJ35114.1 (AB017807) ORF1 [Actinobacillus actinomycetemcomitans] gb AAG09111.1 (AF102554) unknown [Actinobacillus actinomycetemcomitans] ref NP_046944.1 gp48 [Bacteriophage N15] pir T13135 protein gp48 - phage N15 gb AAC19087.1 (AF064539) gp48 [Bacteriophage N15]	SEQ ID n-9375
SEQ ID n° 7969	PL-5893.1	Contig9 from 2466342 to 2466605	m	37%	emb CAC01604.1 (AJ269505) peptide synthetase [Anabaena sp. 90]	#N/A
SEQ ID n° 7970	PL-5894.1	Contig9 from 2466917 to 2467201	p	63%	emb CAC01604.1 (AJ269505) peptide synthetase [Anabaena sp. 90]	SEQ ID n-9376
SEQ ID n° 7971	PL-557.1	Contig9 from 2467342 to 2473371	m	41%		#N/A
SEQ ID n° 7972	PL-558.1	Contig9 from 2473368 to 2478101	m	53%		SEQ ID n-9377

TABLEAU II

SEQ ID n° 7973	PL-559.1	Contig9 from 2478098 to 2481604	m	56%	gb AAF17281.1 (AF204805) NosD [Nostoc sp. GSV224]	SEQ ID n-9378
SEQ ID n° 7974	PL-7053.1	Contig9 from 2482168 to 2482281	p	No Hits found		#N/A
SEQ ID n° 7975	PL-560.1	Contig9 from 2482397 to 2483713	m	48%	gb AAG31049.1 AF264948_11 (AF264948) hypothetical protein [Erwinia amylovora]	SEQ ID n-9380
SEQ ID n° 7976	PL-5895.1	Contig9 from 2483707 to 2484060	m	No Hits found		#N/A
SEQ ID n° 7977	PL-5896.1	Contig9 from 2484188 to 2484496	m	No Hits found		#N/A
SEQ ID n° 7978	PL-3558.1	Contig9 from 2484602 to 2485030	m	50%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] sp P13479 IM9_ECOLI COLICIN E9 IMMUNITY PROTEIN (IM9E9) (MICROCIN E9 IMMUNITY PROTEIN) pdb 1EMV A Chain A, Crystal Structure Of Colicin E9 Dnase Domain With Its Immunity Protein Im9 (1.7 Angstroms) pdb 1IMQ Colicin E9 Immunity Protein Im9, Nmr, Minimized Average Structure emb CAA33863.1 (X15858) E9 immunity protein (86 AA) [Enterobacteriaceae]	SEQ ID n-2758
SEQ ID n° 7979	PL-5897.1	Contig9 from 2485292 to 2485549	m	67%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa]	SEQ ID n-2759
SEQ ID n° 7981	PL-3560.1	Contig9 from 2486143 to 2486610	m	48%		SEQ ID n-2761

TABLEAU II

SEQ ID n° 7982	PL-5898.1	Contig9 from 2486623 to 2486766	m	48%	pir [A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] sp P04482 IMM2_ECOLI COLICIN E2 IMMUNITY PROTEIN (IMME2) (MICROCIN E2 IMMUNITY PROTEIN) pir IMECE2 colicin E2 immunity protein - Escherichia coli plasmids emb CAA26146.1 (X02227) IMM22 polypeptide [Escherichia coli] gb AAA23069.1 (W29885) colicin immunity protein (ceiB) [Plasmid COLE2] emb CAA25610.1 (X01163) E2 immunity protein (aa 1-86) [Escherichia coli] ref NP_068716.1 klebicin B [Klebsiella pneumoniae] gb AAD39262.2 (AF156893) klebicin B [Klebsiella pneumoniae] SEQ ID n-2762	#N/A
SEQ ID n° 7983	PL-5899.1	Contig9 from 2486896 to 2487147	m	71%	pir [B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] pir [B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] SEQ ID n-2763	#N/A
SEQ ID n° 7984	PL-561.1	Contig9 from 2487155 to 2487604	m	68%	pir [A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] gb AAG54453.1 AE005191_4 (AE005191) peptidoglycan synthetase; penicillin-binding protein 1B [Escherichia coli O157:H7] SEQ ID n-3382	#N/A
SEQ ID n° 7985	PL-562.1	Contig9 from 2487701 to 2488153	m	58%	pir [A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] gb AAG54453.1 AE005191_4 (AE005191) peptidoglycan synthetase; penicillin-binding protein 1B [Escherichia coli O157:H7] SEQ ID n-3383	#N/A
SEQ ID n° 7986	PL-563.2	Contig9 from 2488235 to 2488687	m	52%	pir [A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] gb AAG54453.1 AE005191_4 (AE005191) peptidoglycan synthetase; penicillin-binding protein 1B [Escherichia coli O157:H7] SEQ ID n-3384	#N/A
SEQ ID n° 7987	PL-561.2	Contig9 from 2488687 to 2490360	m	27%	pir [A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] gb AAG54453.1 AE005191_4 (AE005191) peptidoglycan synthetase; penicillin-binding protein 1B [Escherichia coli O157:H7] SEQ ID n-3385	#N/A
SEQ ID n° 7988	PL-562.1	Contig9 from 2490845 to 2493301	m	83%	pir [A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] gb AAG54453.1 AE005191_4 (AE005191) peptidoglycan synthetase; penicillin-binding protein 1B [Escherichia coli O157:H7] SEQ ID n-3386	#N/A
SEQ ID n° 7989	PL-563.1	Contig9 from 2493395 to 2495884	m	74%	pir [A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] gb AAG54453.1 AE005191_4 (AE005191) peptidoglycan synthetase; penicillin-binding protein 1B [Escherichia coli O157:H7] SEQ ID n-3387	#N/A
SEQ ID n° 7990	PL-564.1	Contig9 from 2496425 to 2497258	p	61%	pir [A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] gb AAG54453.1 AE005191_4 (AE005191) peptidoglycan synthetase; penicillin-binding protein 1B [Escherichia coli O157:H7] SEQ ID n-3388	#N/A

TABLEAU II

SEQ ID n° 7991	PL-3564.1	Contig9 from 2497248 to 2497784	p	55%	gb AAD38235.1 (U17224) Carg [Pectobacterium carotovorum]	SEQ ID n-2765
SEQ ID n° 7992	PL-3565.1	Contig9 from 2497781 to 2498326	p	53%	gb AAD38236.1 (U17224) CarH [Pectobacterium carotovorum]	SEQ ID n-2766
SEQ ID n° 7993	PL-5900.1	Contig9 from 2498390 to 2498659	p	37%	gb AAG53986.1 AF327444_2 (AF327444) putative transposase B [Erwinia herbicola]	#N/A
SEQ ID n° 7994	PL-1579.2	Contig9 from 2498792 to 2499538	p	70%	pir F82304 sugar fermentation stimulation protein VC0597 [imported] - Vibrio cholerae (group O1 strain N16961)	#N/A
SEQ ID n° 7995	PL-7169.1	Contig9 from 2499552 to 2499653	m	No Hits found	gb AAF93764.1 (AE004144) sugar fermentation stimulation protein [Vibrio cholerae]	#N/A
SEQ ID n° 7996	PL-3566.1	Contig9 from 2499734 to 2500189	p	93%	sp Q9ZIW3 DKSA_SALTY DNAK SUPPRESSOR PROTEIN gb AAD01437.1 (AF010249) DksA homolog [Salmonella typhimurium]	SEQ ID n-2767
SEQ ID n° 7997	PL-1580.1	Contig9 from 2500252 to 2501202	p	68%	sp P27305 YADB_ECOLI HYPOTHETICAL 34.9 KD PROTEIN IN PCNB-DKSA INTERGENIC REGION pir H64737 glutamate--trna ligase homolog yadb Escherichia coli (strain K-12) gb AAC73255.1 (AE000123) putative tRNA synthetase [Escherichia coli K12]	SEQ ID n-679
SEQ ID n° 7998	PL-1581.1	Contig9 from 2501230 to 2502795	p	72%	sp P13685 PCNB_ECOLI POLY(A) POLYMERASE (PAP) (PLASMID COPY NUMBER PROTEIN)	SEQ ID n-680
SEQ ID n° 7999	PL-3567.1	Contig9 from 2502801 to 2503316	p	69%	gb AAG54446.1 AE005190_8 (AE005190) 7,8-dihydro- 6-hydroxymethylpterin-pyrophosphokinase [Escherichia coli O157:H7]	SEQ ID n-2768

TABLEAU II

Contig9 from SEQ ID n° 8000 PL-1582.1 2503387 to 2504178	P	82%	<p>pir [A47152 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) - Escherichia coli emb CAA46505.1 (X65538) 3- methyl-2-oxobutanoate hydroxymethyltransferase [Escherichia coli] seq P31663 PANC_ECOLI PANTOATE--BETA-ALANINE LIGASE (PANTOTHENATE SYNTHETASE) (PANTOATE ACTIVATING ENZYME) pir [E64736 pantoate--beta- alanine ligase (EC 6.3.2.1) - Escherichia coli gb AAA24272.1 (L17086) pantothenate synthetase [Escherichia coli] gb AAC73244.1 (AE000122) pantothenate synthetase [Escherichia coli K12] sp P31664 PAND_ECOLI ASPARTATE 1-DECARBOXYLASE PRECURSOR (ASPARTATE ALPHA-DECARBOXYLASE) pir [C64736 aspartate 1-decarboxylase (EC 4.1.1.11) [validated] - Escherichia coli gb AAA24274.1 (L17086) aspartate-1- decarboxylase [Escherichia coli] gb AAC73242.1 (AE000122) aspartate 1-decarboxylase [Escherichia coli K12] gb AAG54435.1 AE005189_8 (AE005189) aspartate 1-decarboxylase [Escherichia coli O157:H7] sp P36880 YADH_ECOLI HYPOTHETICAL 28.5 KD PROTEIN IN HPT-PAND INTERGENIC REGION pir [H64735 probable ABC-2-type transport protein yadh - Escherichia coli gb AAC73239.1 (AE000122) orf, hypothetical protein [Escherichia coli K12] gb AAG54432.1 AE005189_5 (AE005189) orf, hypothetical protein [Escherichia coli O157:H7]</p>	SEQ ID n-681
Contig9 from SEQ ID n° 8001 PL-1583.1 2504205 to 2505059	P	83%		SEQ ID n-682
Contig9 from SEQ ID n° 8002 PL-5902.1 2505127 to 2505507	P	80%		
Contig9 from SEQ ID n° 8003 PL-1584.1 2505586 to 2506356	m	68%		#N/A

SEQ ID n-683

TABLEAU II

SEQ ID n° 8004	PL-1585.1	Contig9 from 2506368 to 2507279	m	88%	<p>sp P36879 YADG_ECOLI HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YADG</p> <p>pir S45204 probable ABC-type transport protein yagD - Escherichia coli dbj BAA05583.1 (D26562) 'ORF' [Escherichia coli]</p> <p>gb AAC73238.1 (AE000122) putative ATP-binding component of a transport system [Escherichia coli K12]</p> <p>sp P36857 YADF_ECOLI HYPOTHETICAL 25.1 KD PROTEIN IN HPT-PAND INTERGENIC REGION</p> <p>pir F64735 yadF protein - Escherichia coli gb AAC73237.1 (AE000122) putative carbonic anhydrase (EC 4.2.1.1) [Escherichia coli K12]</p>	SEQ ID n-884
SEQ ID n° 8005	PL-1586.1	Contig9 from 2507467 to 2508120	p	84%	<p>pir H82771 proteic killer suppression protein XF0721 [imported] - Xylella fastidiosa (strain 9a5c)</p> <p>gb AAF83531.1 AE003914_12 (AE003914) proteic killer suppression protein [Xylella fastidiosa]</p> <p>pir G82771 proteic killer active protein XF0720 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF83530.1 AE003914_11 (AE003914) proteic killer active protein [Xylella fastidiosa]</p>	SEQ ID n-885
SEQ ID n° 8006	PL-5903.1	Contig9 from 2509640 to 2509921	p	77%	<p>sp O33799 HPRT_SALTY HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE (HPRT) gb AAC46255.1 (AF008931) hypoxanthine phosphoribosyltransferase [Salmonella typhimurium]</p>	#N/A
SEQ ID n° 8007	PL-5905.1	Contig9 from 2509932 to 2510210	p	66%		#N/A
SEQ ID n° 8008	PL-3568.1	Contig9 from 2510310 to 2510861	m	89%		
SEQ ID n° 8009	PL-3569.1	Contig9 from 2511181 to 2511735	m	No Hits found		SEQ ID n-2769
SEQ ID n° 8010	PL-3570.1	Contig9 from 2511875 to 2512375	m	58%	emb CAC05783.1 (AL391753) ORF47,	SEQ ID n-2770
						SEQ ID n-2772

TABLEAU II

SEQ ID n° 8011	PL-5906.1	Contig9 from 2512380 to 2512658	m	54%	gb AAG58522.1 AE005564_7 (AE005564)orf; hypothetical protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 8012	PL-3571.1	Contig9 from 2512879 to 2513424	m	89%	sp P36766 HPRT_ECOLI HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE (HPRT) pir S45202 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - Escherichia coli dbj BA05581.1 (D26562) 'ORF' [Escherichia coli] gb AAC73236.1 (AE000122) hypoxanthine phosphoribosyltransferase [Escherichia coli K12] gb AAG54429.1 AE005189_2 (AE005189) hypoxanthine phosphoribosyltransferase [Escherichia coli O157:H7] SEQ ID n-2773
SEQ ID n° 8013	PL-5907.1	Contig9 from 2513794 to 2514057	m	43%	gb AAF22961.1 AF157489_1 (AF157489) Pln [Photorhabdus luminescens] #N/A
SEQ ID n° 8014	PL-3572.1	Contig9 from 2515163 to 2515627	p	No Hits found	
SEQ ID n° 8015	PL-5910.1	Contig9 from 2515641 to 2516015	p	41%	sp P05790 FBOH_BOMMO FIBROIN HEAVY CHAIN PRECURSOR (FIB-H) (H-FIBROIN) gb AAF76983.1 AF226688_1 (AF226688) fibroin heavy chain Fib-H [Bombyx mori] pir C81043 hypothetical protein NMB1786 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF42125.1 (AE002528) hypothetical protein [Neisseria meningitidis MC58] #N/A
SEQ ID n° 8016	PL-1587.1	Contig9 from 2516175 to 2517341	p	55%	pir H83126 probable secretion protein PA4142 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07529.1 AE004831_1 (AE004831) probable secretion protein [Pseudomonas aeruginosa] SEQ ID n-686
SEQ ID n° 8017	PL-5911.1	Contig9 from 2517331 to 2517759	p	53%	#N/A

TABLEAU II

SEQ ID n° 8018	PL-1588.1	Contig9 from 2517830 to 2518798	p	60%	pir C81839 probable transposase for IS1655 NMAL481 [imported] - Neisseria meningitidis (group B strain MD58, group A strain Z2491) emb CAB84714.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] emb CAB84719.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] SEQ ID n-687
SEQ ID n° 8019	PL-1589.1	Contig9 from 2518780 to 2519691	p	53%	gb AAF61809.1 (AF129811) unknown [Moraxella catarrhalis] SEQ ID n-688
SEQ ID n° 8020	PL-1590.1	Contig9 from 2519697 to 2521790	p	69%	gb AAF61810.1 (AF129811) unknown [Moraxella catarrhalis] SEQ ID n-690
SEQ ID n° 8021	PL-3573.1	Contig9 from 2521980 to 2522360	p	47%	pir B64781 hypothetical protein b0502 - Escherichia coli gb AAB40255.1 (U82664) similar to A. pleuropneumoniae orf1 [Escherichia coli] gb AAC73604.1 (AE000156) orf, hypothetical protein [Escherichia coli K12] gb AAG54858.1 AE005231_5 (AE005231) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2775
SEQ ID n° 8022	PL-5914.1	Contig9 from 2522380 to 2522613	m	64%	gb AAG55933.1 AE005327_3 (AE005327) putative integrase of prophage CP-933C [Escherichia coli O157:H7] #N/A
SEQ ID n° 8023	PL-5915.1	Contig9 from 2522632 to 2522826	m	No Hits found	#N/A
SEQ ID n° 8024	PL-3574.2	Contig9 from 2523372 to 2523857	m	19%	emb CAB60145.1 (Y15953) ClpX protein [Oenococcus oeni] #N/A
SEQ ID n° 8025	PL-1591.1	Contig9 from 2524048 to 2524821	m	No Hits found	SEQ ID n-691
SEQ ID n° 8026	PL-5917.1	Contig9 from 2524828 to 2525052	m	No Hits found	#N/A

TABLEAU II

SEQ ID n° 8027	PL-1592.1	Contig9 from 2525321 to 2526865	m	77%	sp P36649 YACK_ECOLI PROBABLE BLUE-COPPER PROTEIN YACK PRECURSOR pir C64735 probable copper-binding protein yack - Escherichia coli gb AAC73234.1 (AE000121) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-892
SEQ ID n° 8028	PL-5918.1	Contig9 from 2527192 to 2527539	p	62%	__pir B64735 yacC protein - Escherichia coli gb AAC73233.1 (AE000121) orf, hypothetical protein [Escherichia coli K12] gb AAG54426.1 AE005188_7 (AE005188) yacC gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8029	PL-1593.1	Contig9 from 2527652 to 2528521	p	81%	gb AAG54425.1 AE005188_6 (AE005188) spermidine synthase = putrescine aminopropyltransferase [Escherichia coli O157:H7] sp P09159 DCAM_ECOLI S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) pir DCECDM adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - - Escherichia coli gb AAA24644.1 (J02804) S-adenosylmethionine decarboxylase [Escherichia coli] gb AAC73231.1 (AE000121) S-adenosylmethionine decarboxylase [Escherichia coli K12] dbj BAA05576.1 (D26562) 'adenosylmethionine decarboxylase proenzyme' [Escherichia coli] gb AAG54424.1 AE005188_5 (AE005188) S- adenosylmethionine decarboxylase [Escherichia coli O157:H7]	SEQ ID n-893
SEQ ID n° 8030	PL-1594.1	Contig9 from 2528560 to 2529354	p	91%	dbj BAA88679.1 (AB029373) ORF [Thermus thermophilus]	SEQ ID n-894
SEQ ID n° 8032	PL-1595.1	Contig9 from 2530073 to 2531992	m	No Hits found	gb AAC44684.1 (U65015) putative aldolase [Vibrio furnissii]	SEQ ID n-895
SEQ ID n° 8033	PL-1596.1	Contig9 from 2532017 to 2532877	m	81%		SEQ ID n-896

TABLEAU II

SEQ ID n° 8034	PL-5920.1	Contig9 from 2532887 to 2533321	m	66%	gb AAG58266.1 AE005542_8 (AE005542) putative phosphotransferase system enzyme subunit [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8035	PL-1597.1	Contig9 from 2533344 to 2534237	m	70%	gb AAG58265.1 AE005542_7 (AE005542) putative phosphotransferase system enzyme subunit [Escherichia coli O157:H7]	SEQ ID n-697
SEQ ID n° 8036	PL-1598.1	Contig9 from 2534227 to 2535024	m	75%	gb AAC44680.1 (U65015) PTS permease for mannose subunit IIPMan [Vibrio furnissii]	SEQ ID n-698
SEQ ID n° 8037	PL-3576.1	Contig9 from 2535035 to 2535517	m	73%	pir A65103 pts system, n-acetylgalactosamine- specific IIB component 2 - Escherichia coli (strain K-12) gb AA57936.1 (U18997) ORF_0169 [Escherichia coli] gb AAC76167.1 (AE000394) PTS system, cytoplasmic, N-acetylgalactosamine-specific IIB component 2 (EIIIB-AGA) [Escherichia coli K12] gb AAF81083.1 AF228498_3 (AF228498) Agav [Escherichia coli]	SEQ ID n-2778
SEQ ID n° 8038	PL-1599.1	Contig9 from 2535483 to 2536706	m	51%	gb AAG58268.1 AE005542_10 (AE005542) putative tagatose-6-phosphate aldose/ketose isomerase [Escherichia coli O157:H7] sp P42903 AGAZ_ECOLI PUTATIVE TAGATOSE 6- PHOSPHATE KINASE AGAZ pir H65102 probable tagatose 6-phosphate kinase agaz (EC 2.7.1.-) - Escherichia coli (strain K-12) gb AA57935.1 (U18997) ORF_0426 [Escherichia coli] gb AAC76166.1 (AE000394) putative tagatose 6- phosphate kinase 2 [Escherichia coli K12] gb AAF81082.1 AF228498_2 (AF228498) KbaZ [Escherichia coli]	SEQ ID n-699
SEQ ID n° 8039	PL-1600.1	Contig9 from 2536703 to 2537998	m	65%		SEQ ID n-702

TABLEAU II

SEQ ID n° 8040	PL-1601.1	Contig9 from 2538034 to 2538807	m	61%	sp P42902 AGAR_ECOLI_PUTATIVE_AGA_OPERON TRANSCRIPTIONAL_REPRESSOR_pir G55102 probable transcription repressor of aga operon - Escherichia coli gb AAA57934.1 (U18997) ORF f269 [Escherichia coli] gb AAC76165.1 (AE000394) putative DEOR- type transcriptional regulator of aga operon [Escherichia coli K12] gb AAF81081.1 AF228498_1 (AF228498) Agar [Escherichia coli] gb AAG58261.1 AE005542_3 (AE005542) putative DEOR-type transcriptional regulator of aga operon [Escherichia coli O157:H7]	SEQ ID n-703
SEQ ID n° 8041	PL-1602.1	Contig9 from 2539207 to 2540364	p	69%	emb CAA63264.1 (X92508) ES-beta-lactamase [Klebsiella pneumoniae]	SEQ ID n-704
SEQ ID n° 8042	PL-1603.1	Contig9 from 2540445 to 2541743	m	20%	gb AAD10476.2 (U37262) phospholipase A1 [Serratia sp. MK1]	SEQ ID n-705
SEQ ID n° 8043	PL-3579.1	Contig9 from 2541777 to 2542187	m	No Hits found		SEQ ID n-2779
SEQ ID n° 8044	PL-5925.1	Contig9 from 2542279 to 2542419	m	No Hits found		#N/A
SEQ ID n° 8045	PL-5926.1	Contig9 from 2542479 to 2542724	m	No Hits found		#N/A
SEQ ID n° 8046	PL-1604.1	Contig9 from 2543174 to 2545288	p	41%	gb AAG54536.1 AE005199_6 (AE005199) Z0267 gene product [Escherichia coli O157:H7]	SEQ ID n-706
SEQ ID n° 8047	PL-1605.1	Contig9 from 2545291 to 2546649	p	No Hits found		SEQ ID n-707

TABLEAU II

SEQ ID n° 8048	PL-1606.1	Contig9 from 2546654 to 2547811	p	30%	pir E83542 hypothetical protein PA0821 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04210.1 AE004517_5 (AE004517) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-708
SEQ ID n° 8049	PL-5933.1	Contig9 from 2547849 to 2548082	p	No Hits found		#N/A
SEQ ID n° 8050	PL-1607.1	Contig9 from 2548163 to 2549389	p	43%	sp P55220 VRP2_SALEN 65 KD VIRULENCE PROTEIN dbj BAA03383.1 (D14490) SpvB [Salmonella enteritidis]	SEQ ID n-709
SEQ ID n° 8051	PL-5936.1	Contig9 from 2550025 to 2550258	p	No Hits found		#N/A
SEQ ID n° 8052	PL-1608.1	Contig9 from 2550301 to 2551659	p	No Hits found		
SEQ ID n° 8053	PL-1609.1	Contig9 from 2551676 to 2552821	p	31%	pir E83542 hypothetical protein PA0821 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04210.1 AE004517_5 (AE004517) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-710
SEQ ID n° 8054	PL-1610.1	Contig9 from 2552858 to 2554003	p	31%	pir E83542 hypothetical protein PA0821 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04210.1 AE004517_5 (AE004517) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-711
SEQ ID n° 8055	PL-5939.1	Contig9 from 2554007 to 2554279	p	43%	pir H83457 hypothetical protein PA1508 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04897.1 AE004579_9 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-713
SEQ ID n° 8056	PL-5941.1	Contig9 from 2555349 to 2555642	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 8057	PL-1611.1	Contig9 from 2556250 to 2556882	p	82%	gb AAG54714.1 AE005216_2 (AE005216) putative response regulator; hexosephosphate transport [Escherichia coli O157:H7]	SEQ ID n-714
SEQ ID n° 8058	PL-1612.1	Contig9 from 2556879 to 2558423	p	69%	gb AAG54713.1 AE005216_1 (AE005216) putative sensor kinase; hexosephosphate transport [Escherichia coli O157:H7]	SEQ ID n-715
SEQ ID n° 8059	PL-1613.1	Contig9 from 2558512 to 2559837	p	75%	gb AAG54712.1 AE005215_9 (AE005215) putative permease; hexosephosphate transport [Escherichia coli O157:H7]	SEQ ID n-716
SEQ ID n° 8060	PL-1614.1	Contig9 from 2559851 to 2560885	p	86%	gb AAG54711.1 AE005215_8 (AE005215) periplasmic ferric iron-binding protein [Escherichia coli O157:H7]	SEQ ID n-717
SEQ ID n° 8061	PL-1615.1	Contig9 from 2561007 to 2563073	p	85%	gb AAG54710.1 AE005215_7 (AE005215) putative permease component of transport system for ferric iron [Escherichia coli O157:H7]	SEQ ID n-718
SEQ ID n° 8062	PL-1616.1	Contig9 from 2563089 to 2564144	p	87%	sp P37009 AFUC_ECOLI PUTATIVE FERRIC TRANSPORT ATP-BINDING PROTEIN AFUC	SEQ ID n-719
SEQ ID n° 8063	PL-5948.1	Contig9 from 2564316 to 2564516	p	No Hits found		#N/A
SEQ ID n° 8064	PL-5949.1	Contig9 from 2564513 to 2564824	p	73%	gb AAG57125.1 AE005432_6 (AE005432) Z3231 gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8065	PL-5950.1	Contig9 from 2564875 to 2565111	m	67%	pir [G82653 HicB-related protein XF1668 [imported] - Xylella fastidiosa (strain 9a5c) gb AAP84477.1 AE003992_13 (AE003992) HicB-related protein [Xylella fastidiosa]	#N/A
SEQ ID n° 8066	PL-1617.1	Contig9 from 2565213 to 2569628	m	36%	gb AAC38629.1 (AF047028) insecticidal toxin complex protein Tccb [Photobacterium luminescens]	SEQ ID n-720
SEQ ID n° 8067	PL-1618.2	Contig9 from 2569677 to 2572622	m	48%	gb AAC38628.1 (AF047028) insecticidal toxin complex protein Tcca [Photobacterium luminescens]	SEQ ID n-721

TABLEAU II

SEQ ID n° 8068	PL-1619.2	Contig9 from 2572884 to 2575193	m	No Hits found	pir T41325 probable serine-threonine dehydratase - fission yeast (Schizosaccharomyces pombe) pir T41297 threonine dehydratase (EC 4.2.1.16) SPCC320.14 [similarity] - fission yeast (Schizosaccharomyces pombe) emb CAA18316.1 (AL022245) putative serine/threonine dehydratase [Schizosaccharomyces pombe] emb CAA20920.1 (AL031603) putative serine-threonine dehydratase. [Schizosaccharomyces pombe]	SEQ ID n-922
SEQ ID n° 8069	PL-1620.1	Contig9 from 2575543 to 2576511	m	84%		
SEQ ID n° 8070	PL-1621.1	Contig9 from 2576678 to 2577304	m	No Hits found	sp P55606 Y4OU_RHISN HYPOTHETICAL PROTEIN Y4OU PRECURSOR gb AAB91807.1 (AE000089) Y4OU [Rhizobium sp. NGR234]	SEQ ID n-925
SEQ ID n° 8071	PL-1622.1	Contig9 from 2577659 to 2578870	p	68%	gb AAG58297.1 AE005544_11 (AE005544) tryptophan- specific transport protein [Escherichia coli O157:H7]	SEQ ID n-926
SEQ ID n° 8072	PL-1623.1	Contig9 from 2579218 to 2580462	m	85%	sp Q59342 TNAI_ENTAE TRYPTOPHANASE (L-TRYPTOPHAN INDOLE-LYASE) (TNASE) dbj BA032249.1 (D14297) tryptophanase [Enterobacter aerogenes]	SEQ ID n-927
SEQ ID n° 8073	PL-1624.1	Contig9 from 2580573 to 2581973	m	84%	pir B81410 probable integral membrane protein Cj0619 [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB75255.1 (AL139075) putative integral membrane protein [Campylobacter jejuni]	SEQ ID n-928
SEQ ID n° 8074	PL-1625.1	Contig9 from 2583347 to 2584687	p	62%		SEQ ID n-929

TABLEAU II

SEQ ID n° 8075	PL-1626.1	Contig9 from 2585598 to 2586374	p	64%	sp P16250 HIS4_STRCO PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE pir JQ0641 N-(5'-phospho-D-riboseylformimino)-5-amino-1-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16) - Streptomyces coelicolor 9b AA26760.1 (M31628) isomerase (hisa) [Streptomyces coelicolor] emb CAB51442.1 (AL096884) phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Streptomyces coelicolor A3(2)]	SEQ ID n° 730
SEQ ID n° 8076	PL-1627.1	Contig9 from 2586425 to 2587579	p	No Hits found	emb CAB90911.1 (AL355774) putative phosphatase [Streptomyces coelicolor A3(2)]	SEQ ID n° 731
SEQ ID n° 8077	PL-1628.1	Contig9 from 2587582 to 2588241	p	65%	pir F81950 probable adenylosuccinate synthase (EC 6.3.4.4) NMA1024 [imported] Neisseria meningitidis (group A strain Z2491) emb CAB84293.1 (AL162754) putative adenylosuccinate synthetase [Neisseria meningitidis Z2491]	SEQ ID n° 732
SEQ ID n° 8078	PL-1629.1	Contig9 from 2588420 to 2589679	p	56%	sp P41354 MUTX_STRPN MUTATOR MUTT PROTEIN (7,8-DIHYDRO-8-OXOGUANINE-TRIPHOSPHATASE) (8-OXO-DGTPASE) (DGTP PYROPHOSPHOHYDROLASE) pir S41532 mutX protein - Streptococcus pneumoniae emb CAA79807.1 (Z21702) MutX [Streptococcus pneumoniae]	SEQ ID n° 733
SEQ ID n° 8079	PL-5955.1	Contig9 from 2589696 to 2590124	p	28%		#N/A
SEQ ID n° 8080	PL-1630.1	Contig9 from 2590271 to 2591425	m	No Hits found		SEQ ID n° 735

TABLEAU II

SEQ ID n° 8081	PL-1631.1	Contig9 from 2591518 to 2594160	m	56%	sp P30130 FIMD_ECOLI OUTER MEMBRANE USHER PROTEIN FIMD PRECURSOR pir S56542 outer membrane usher protein fimd precursor - Escherichia coli gb AAA97213.1 (U14003) CG Site No. 18349 [Escherichia coli] gb AAC77273.1 (AE000502) outer membrane protein; export and assembly of type 1 fimbriae, interrupted [Escherichia coli K12]	SEQ ID n° 936
SEQ ID n° 8082	PL-1632.1	Contig9 from 2594243 to 2595100	m	37%	emb CAB01713.1 (Z78535) type 1 fimbrial chaperone [Proteus mirabilis]	SEQ ID n° 937
SEQ ID n° 8083	PL-1633.1	Contig9 from 2595131 to 2595880	m	46%	gb AAD26595.1 (AF012835) chaperone protein AafD [Escherichia coli]	SEQ ID n° 938
SEQ ID n° 8084	PL-3581.2	Contig9 from 2595914 to 2596486	m	No Hits found	#N/A	
SEQ ID n° 8085	PL-1634.2	Contig9 from 2596486 to 2597202	m	42%	sp P46008 FOCC_ECOLI CHAPERONE PROTEIN FOCC PRECURSOR pir I41062 periplasmic chaperone focc protein - Escherichia coli emb CAA86604.1 (Z46635) focc [Escherichia coli]	#N/A
SEQ ID n° 8086	PL-3582.1	Contig9 from 2597304 to 2597864	m	No Hits found		SEQ ID n° 2783
SEQ ID n° 8087	PL-1635.1	Contig9 from 2598188 to 2599342	m	No Hits found		SEQ ID n° 740
SEQ ID n° 8088	PL-1636.1	Contig9 from 2599489 to 2602131	m	57%	sp P30130 FIMD_ECOLI OUTER MEMBRANE USHER PROTEIN FIMD PRECURSOR pir S56542 outer membrane usher protein fimd precursor - Escherichia coli gb AAA97213.1 (U14003) CG Site No. 18349 [Escherichia coli] gb AAC77273.1 (AE000502) outer membrane protein; export and assembly of type 1 fimbriae, interrupted [Escherichia coli K12]	SEQ ID n° 741

TABLEAU II

SEQ ID n° 8089	PL-1637.1	Contig9 from 2602215 to 2602997	m	38%	gb AAG58694.1 AE005581.6 (AE005581) putative fimbrial chaperone [Escherichia coli O157:H7]	SEQ ID n-742
SEQ ID n° 8090	PL-1639.1	Contig9 from 2603028 to 2603762	m	44%	sp P46008 FOCC_ECOLI CHAPERONE PROTEIN FOCC PRECURSOR pir r41062 periplasmic chaperone focC protein - Escherichia coli emb CAA86604.1 (Z46635) focC [Escherichia coli]	SEQ ID n-743
SEQ ID n° 8091	PL-3585.1	Contig9 from 2603796 to 2604368	m	No Hits found		SEQ ID n-2784
SEQ ID n° 8092	PL-1640.1	Contig9 from 2604368 to 2605156	m	41%	gb AAC45720.1 (AF022140) Fl7a-D [Escherichia coli]	SEQ ID n-745
SEQ ID n° 8093	PL-3586.1	Contig9 from 2605205 to 2605783	m	No Hits found		SEQ ID n-2785
SEQ ID n° 8094	PL-5964.1	Contig9 from 2606630 to 2606929	m	56%	emb CAB61440.1 (Z32686) mrpJ [Proteus mirabilis]	#N/A
SEQ ID n° 8095	PL-1641.1	Contig9 from 2606966 to 2607781	m	72%	emb CAB61439.1 (Z32686) mrpH [Proteus mirabilis]	SEQ ID n-746
SEQ ID n° 8096	PL-3587.1	Contig9 from 2607809 to 2608354	m	58%	pir C39415 fimbrial protein smfF - Serratia marcescens gb AAA26578.1 (M68877) smfF [Serratia marcescens]	SEQ ID n-2786
SEQ ID n° 8097	PL-3588.1	Contig9 from 2608366 to 2608848	m	58%	emb CAA83638.1 (Z32686) mrpF [Proteus mirabilis]	SEQ ID n-2787
SEQ ID n° 8098	PL-3589.1	Contig9 from 2608872 to 2609363	m	53%	emb CAA83637.1 (Z32686) mrpE [Proteus mirabilis]	SEQ ID n-2788
SEQ ID n° 8099	PL-1642.1	Contig9 from 2609440 to 2610033	m	40%	sp P42185 PRSH_ECOLI PRS FIMBRIAL MINOR PILIN PROTEIN PRECURSOR pir S25205 fimbrial protein prSH - Escherichia coli (strain 1442) emb CAA44082.1 (X62157) prSH [Escherichia coli]	SEQ ID n-747

TABLEAU II

SEQ ID n° 8100	PL-1643.1	Contig9 from 2610058 to 2610807	m	83%	emb CAA83636.1 (Z32686) mrpD [Proteus mirabilis]	SEQ ID n-748
SEQ ID n° 8101	PL-1644.1	Contig9 from 2610931 to 2613447	m	75%	emb CAA83635.1 (Z32686) mrpC [Proteus mirabilis]	SEQ ID n-749
SEQ ID n° 8102	PL-3591.1	Contig9 from 2613506 to 2613943	m	50%	emb CAA83634.1 (Z32686) mrpB [Proteus mirabilis]	SEQ ID n-2790
SEQ ID n° 8103	PL-1645.1	Contig9 from 2614138 to 2614677	m	67%	sp Q03011 MRPA_PROMI MAJOR MR/P FIMBRIA PROTEIN PRECURSOR pir A40643 MR/P fimbriae, major fimbrial subunit - Proteus mirabilis emb CAA79244.1 (Z18753) MR/P major fimbrial subunit polypeptide [Proteus mirabilis] emb CAA83633.1 (Z32686) mrpA [Proteus mirabilis]	SEQ ID n-750
SEQ ID n° 8104	PL-1646.1	Contig9 from 2615361 to 2615933	p	78%	emb CAB61438.1 (Z32686) MrpI [Proteus mirabilis]	SEQ ID n-751
SEQ ID n° 8105	PL-1647.1	Contig9 from 2617192 to 2617806	p	38%	emb CAB54047.1 (AJ245436) hypothetical protein, 21.8 kD [Pseudomonas putida]	SEQ ID n-752
SEQ ID n° 8106	PL-5969.1	Contig9 from 2618006 to 2618209	p	No Hits found		#N/A
SEQ ID n° 8107	PL-5971.1	Contig9 from 2618915 to 2619178	p	54%	sp P11830 ACP_SACER ACYL CARRIER PROTEIN (ACP) pir A47030 acyl carrier protein - Saccharopolyspora erythraea gb AA26476.1 (M64477) acyl carrier protein [Saccharopolyspora erythraea]	#N/A
SEQ ID n° 8108	PL-1648.1	Contig9 from 2619180 to 2620058	p	No Hits found		SEQ ID n-753
SEQ ID n° 8109	PL-1649.1	Contig9 from 2620069 to 2620743	p	No Hits found		SEQ ID n-754

TABLEAU II

SEQ ID n° 8110	PL-1650.1	Contig9 from 2620736 to 2621815	p 38%	pir T45319 hypothetical protein MLCB1779.31 [imported] - Mycobacterium leprae emb CAB11012.1 (Z98271) hypothetical protein MLCB1779.31 [Mycobacterium leprae] pir H70158 conserved hypothetical integral membrane protein BB0473 - Lyme disease spirochete gb AAC66867.1 (AE001152) conserved hypothetical integral membrane protein [Borrelia burgdorferi] pir A69831 probable acid-CoA ligase (EC 6.2.1.1.) yhfL [similarity] - Bacillus subtilis emb CAA74533.1 (Y14083) hypothetical protein [Bacillus subtilis] emb CAB12867.1 (Z99109) similar to long-chain fatty-acid-CoA ligase [Bacillus subtilis] pir D83099 probable RND efflux membrane fusion protein precursor PA4374 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07762.1 AE004853_5 (AE004853) probable RND efflux membrane fusion protein precursor [Pseudomonas aeruginosa] pir A82357 probable multidrug resistance protein VC0164 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93340.1 (AE004106) multidrug resistance protein, putative [Vibrio cholerae] sp P30790 FABH_RHOCA 3-OXOACYL-[ACYL-CARRIER- PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) pir C41608 hypothetical protein 3 (hima 5' region) - Rhodobacter capsulatus gb AAA26127.1 (M84030) ORF3; putative [Rhodobacter capsulatus]	SEQ ID n-756
SEQ ID n° 8111	PL-1651.1	Contig9 from 2621820 to 2623220	p 34%		SEQ ID n-757
SEQ ID n° 8112	PL-1652.1	Contig9 from 2623246 to 2624823	p 46%		SEQ ID n-758
SEQ ID n° 8113	PL-1653.1	Contig9 from 2624820 to 2625893	p 45%		SEQ ID n-759
SEQ ID n° 8114	PL-1654.1	Contig9 from 2625890 to 2628931	p 56%		SEQ ID n-760
SEQ ID n° 8115	PL-1655.1	Contig9 from 2628928 to 2629875	p 42%		SEQ ID n-761

TABLEAU II

SEQ ID n° 8116	PL-1656.1	Contig9 from 2629872 to 2631437	p	50%	pir [B82182 enterobactin synthetase component F-related protein VC1579 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94733.1 (AE004235) enterobactin synthetase component F-related protein [Vibrio cholerae] SEQ ID n-762
SEQ ID n° 8117	PL-1657.1	Contig9 from 2631777 to 2632736	p	24%	pir [S76481 hypothetical protein - Synecocystis sp. (strain PCC 6803) dbj BAA18610.1 (D90915) hypothetical protein [Synecocystis sp.] SEQ ID n-763
SEQ ID n° 8118	PL-1658.1	Contig9 from 2632729 to 2633643	p	No Hits found	SEQ ID n-764
SEQ ID n° 8119	PL-1659.1	Contig9 from 2633649 to 2634587	p	38%	sp O67185 FABH_AQUAE 3-OXOACYL-[ACYL-CARRIER- PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) pir [F70394 3-oxoacyl- [acyl-carrier-protein] synthase III - Aquifex aeolicus gb AAC07144.1 (AE000723) 3-oxoacyl- [acyl-carrier-protein] synthase III [Aquifex aeolicus] SEQ ID n-765
SEQ ID n° 8120	PL-1660.1	Contig9 from 2634928 to 2636187	p	50%	dbj BAB18473.1 (AB033991) BtrK [Bacillus circulans] SEQ ID n-767
SEQ ID n° 8121	PL-5975.1	Contig9 from 2637063 to 2637269	m	No Hits found	#N/A
SEQ ID n° 8122	PL-1661.1	Contig9 from 2637813 to 2638493	m	51%	gb AAG57863.1 AE005503_4 (AE005503) orf; hypothetical protein [Escherichia coli O157:H7] SEQ ID n-768
SEQ ID n° 8123	PL-1662.1	Contig9 from 2638474 to 2639220	m	47%	gb AAG57864.1 AE005503_5 (AE005503) orf; hypothetical protein [Escherichia coli O157:H7] SEQ ID n-769
SEQ ID n° 8124	PL-1663.1	Contig9 from 2639231 to 2640265	m	67%	gb AAG57865.1 AE005503_6 (AE005503) Z4067 gene product [Escherichia coli O157:H7] SEQ ID n-770

TABLEAU II

SEQ ID n° 8125	PL-3592.1	Contig9 from 2640286 to 2640867	m	39%	gb AAG57866.1 AE005503_7 (AE005503) Z4068 gene product [Escherichia coli O157:H7]	SEQ ID n-2791
SEQ ID n° 8126	PL-1664.1	Contig9 from 2640867 to 2642471	m	50%	gb AAG57867.1 AE005503_8 (AE005503) orf; hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-271
SEQ ID n° 8127	PL-1665.1	Contig9 from 2642486 to 2645203	m	48%	gb AAG57868.1 AE005503_9 (AE005503) orf; hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-272
SEQ ID n° 8128	PL-1666.2	Contig9 from 2645725 to 2647179	m	28%	gb AAF08816.1 AF194079_3 (AF194079) Tou1 [Neisseria meningitidis]	SEQ ID n-273
SEQ ID n° 8129	PL-3593.1	Contig9 from 2647264 to 2647815	m	45%	gb AAK06058.1 AE006426_4 (AE006426) HYPOTHETICAL PROTEIN [Lactococcus lactis subsp. lactis]	SEQ ID n-2792
SEQ ID n° 8130	PL-1667.1	Contig9 from 2648312 to 2649343	m	No Hits found		SEQ ID n-274
SEQ ID n° 8131	PL-3594.1	Contig9 from 2650299 to 2650808	p	65%	pir E83406 probable sigma-70 factor, ECF subfamily PA1912 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05300.1 AE004617_4 (AE004617) probable sigma-70 factor, ECF subfamily [Pseudomonas aeruginosa]	SEQ ID n-2793
SEQ ID n° 8132	PL-1668.1	Contig9 from 2650787 to 2651800	p	47%	pir D83406 probable transmembrane sensor PA1911 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05299.1 AE004617_3 (AE004617) probable transmembrane sensor [Pseudomonas aeruginosa]	SEQ ID n-275
SEQ ID n° 8133	PL-1669.1	Contig9 from 2651887 to 2654490	p	49%	pir C83035 hypothetical protein PA4897 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08282.1 AE004902_10 (AE004902) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-276

TABLEAU II

SEQ ID n° 8134	PL-1670.1	Contig9 from 2654828 to 2655841	m	72%	ref[NP_073225.1] ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAA01531.1 (D10589) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	SEQ ID n~778
SEQ ID n° 8135	PL-1671.1	Contig9 from 2656069 to 2657184	p	27%	pir T37097 probable secreted neuraminidase - Streptomyces coelicolor emb CAB52948.1 (AL109950) putative secreted neuraminidase [Streptomyces coelicolor A3(2)] pir T34699 hypothetical protein SC1C3.07 SC1C3.07 - Streptomyces coelicolor emb CAA19231.1 (AL023702) hypothetical protein SC1C3.07 [Streptomyces coelicolor A3(2)]	SEQ ID n~779
SEQ ID n° 8136	PL-1672.1	Contig9 from 2657728 to 2658837	p	25%	emb CAA19231.1 (AL023702) hypothetical protein SC1C3.07 [Streptomyces coelicolor A3(2)]	SEQ ID n~780
SEQ ID n° 8137	PL-1673.1	Contig9 from 2659334 to 2660449	p	29%	pir T37097 probable secreted neuraminidase - Streptomyces coelicolor emb CAB52948.1 (AL109950) putative secreted neuraminidase [Streptomyces coelicolor A3(2)]	SEQ ID n~781
SEQ ID n° 8138	PL-1674.1	Contig9 from 2660909 to 2662024	p	29%	pir T37097 probable secreted neuraminidase - Streptomyces coelicolor emb CAB52948.1 (AL109950) putative secreted neuraminidase [Streptomyces coelicolor A3(2)]	SEQ ID n~782
SEQ ID n° 8139	PL-5982.1	Contig9 from 2662092 to 2662310	m	No Hits found		#N/A
SEQ ID n° 8140	PL-1675.1	Contig9 from 2662687 to 2663817	p	31%	pir T37097 probable secreted neuraminidase - Streptomyces coelicolor emb CAB52948.1 (AL109950) putative secreted neuraminidase [Streptomyces coelicolor A3(2)]	SEQ ID n~783
SEQ ID n° 8141	PL-5986.1	Contig9 from 2664866 to 2665045	m	No Hits found		#N/A

TABLEAU II

SEQ ID n° 8142	PL-5988.1	Contig9 from 2665260 to 2665514	m	53%	sp P18837 SFSB_ECOLI_SUGAR_FERMENTATION STIMULATION PROTEIN B (NER-LIKE PROTEIN) pir BVEGNP_nlp_protein - Escherichia coli emb CAA48736.1 (X68873) Ner-like protein, homologous to Ner protein of bacteriophages Mu and D108 [Escherichia coli] gb AA57989.1 (U18997) Ner-like protein [Escherichia coli] gb AAC76220.1 (AE000399) regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu [Escherichia coli K12] gb AG58322.1 AE005547_8 (AE005547) regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8143	PL-1676.1	Contig9 from 2665718 to 2667004	m	64%	sp O34864 YOAB_BACSU_PUTATIVE_TRANSPORTER_YOAB pir D69895 conserved hypothetical protein yoaB Bacillus subtilis gb AA84444.1 (AF027868) putative transporter [Bacillus subtilis] emb CAB13747.1 (Z99114) similar to hypothetical proteins from B. subtilis [Bacillus subtilis]	SEQ ID n-784
SEQ ID n° 8144	PL-5990.1	Contig9 from 2667445 to 2667828	m	55%	sp Q9WYP7 Y416_THEME_HYPOTHETICAL_PROTEIN_TM0416 pir F72381 D-tagatose 3-epimerase-related protein - Thermotoga maritima (strain MSB8) gb AAD35501.1 AE001720_15 (AE001720) D- tagatose 3-epimerase-related protein [Thermotoga maritima]	#N/A
SEQ ID n° 8145	PL-3596.1	Contig9 from 2667885 to 2668190	m	No Hits found.		SEQ ID n-2794
SEQ ID n° 8146	PL-5993.1	Contig9 from 2669097 to 2669249	m	44%	ref NP_059785.1 ync [Agrobacterium tumefaciens] gb AAD50321.1 (AF242881) ync [Agrobacterium tumefaciens]	#N/A

TABLEAU II

SEQ ID n° 8147	PL-5994.1	Contig9 from 2669275 to 2669517	m	46%	ref NP_059786.1 ynd [Agrobacterium tumefaciens] gb AAF77152.1 (AF242881) ynd [Agrobacterium tumefaciens]	#N/A
SEQ ID n° 8148	PL-1677.1	Contig9 from 2669753 to 2672308	p	89%	gb AA057842.1 AE005501_11 (AE005501) methyl- directed mismatch repair [Escherichia coli O157:H7]	SEQ ID n-785
SEQ ID n° 8149	PL-1678.1	Contig9 from 2672313 to 2673074	p	83%	pir H82142 tRNA-(MS[2]IO[6]A)-hydroxylase VC1910 [Imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95058.1 (AE004266) tRNA-(MS[2]IO[6]A)-hydroxylase [Vibrio cholerae]	SEQ ID n-786
SEQ ID n° 8150	PL-1679.1	Contig9 from 2673556 to 2674581	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-787
SEQ ID n° 8151	PL-1680.1	Contig9 from 2675594 to 2676592	m	95%	gb AAF20816.1 AF198628_2 (AF198628) Rpos [Xenorhabdus nematophilus]	SEQ ID n-789
SEQ ID n° 8152	PL-1681.1	Contig9 from 2676644 to 2677639	m	70%	emb CAA06881.1 (AJ006131) nlpD [Salmonella dublin]	SEQ ID n-790

TABLEAU II

SEQ ID n° 8153	PL-1682.1	Contig9 from 2677791 to 2678417	m	83%	sp P24206 PIMT_ECOLI PROTEIN-L-ISOASPARTATE O- METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) pir JH0242 protein-L-isoaspartate (D-aspartate) O-methyltransferase (EC 2.1.1.77) type II - Escherichia coli gb AA24302.1 (M63493) L-isoaspartyl protein carboxyl methyltransferase [Escherichia coli] gb AA69253.1 (U29579) L-isoaspartyl protein carboxyl methyltransferase type II [Escherichia coli] gb AAC75785.1 (AE000358) L- isoaspartate protein carboxylmethyltransferase type II [Escherichia coli K12] gb AAG57850.1 AE005502_4 (AE005502) L- isoaspartate protein carboxylmethyltransferase type II [Escherichia coli O157:H7] SEQ ID n-791 gb AA69254.1 (U29579) alternate name ygbC; ORF1 of L07942, has different start due to frameshift in L07942; ORF_f255 [Escherichia coli] SEQ ID n-792
SEQ ID n° 8154	PL-1683.1	Contig9 from 2678411 to 2679175	m	72%	sp Q57261 YGB0_ECOLI 39.1 KDA PROTEIN IN SURE- CYSC INTERGENIC REGION pir I69731 hypothetical protein b2745 - Escherichia coli gb AA69255.1 (U29579) was ORF_f292 and ORF_f255 before splice; ORF_f349 [Escherichia coli] gb AA79838.1 (L07942) ORF1 [Escherichia coli] gb AAC75787.1 (AE000358) putative hydrogenase subunit [Escherichia coli K12] SEQ ID n-793
SEQ ID n° 8155	PL-1684.1	Contig9 from 2679153 to 2680205	m	71%	

TABLEAU II

SEQ ID n° 8156 PL-3597.1	Contig9 from 2680206 to 2680679	m	80%	sp P36663 ISEP_ECOLI 2C-METHYL-D-ERYTHRITOL 2,4-CYCLODIPHOSPHATE SYNTHASE (MECPs) pir [I55083 hypothetical 16.9K protein (sure-cysc intergenic region) - Escherichia coli
				gb AAA79837.1 (L07942) ORF0 [Escherichia coli] gb AAA69256.1 (U29579) alternate gene name ygbB; ORF0 of L07942; ORF_f159 [Escherichia coli] gb AAC75788.1 (AE000358) orf, hypothetical protein [Escherichia coli K12] gb AAF44656.1 AF230738_1 (AF230738) 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Escherichia coli] dbj BAA95145.1 (AB038256) 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Escherichia coli] gb AAG57853.1 AE005502_7 (AE005502) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2795
SEQ ID n° 8157 PL-1685.1	Contig9 from 2680693 to 2681424	m	69%	sp Q46893 ISPD_ECOLI 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL SYNTHASE (MEP CYTIDYLTRANSFERASE) (MCT) pir [G65055 hypothetical protein b2747 - Escherichia coli (strain K-12) gb AAA69257.1 (U29579) ORF_f236 [Escherichia coli] gb AAC75789.1 (AE000358) orf, hypothetical protein [Escherichia coli K12] dbj BAA90761.1 (AB037143) 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase [Escherichia coli] gb AAF43207.1 AF230736_1 (AF230736) 4-diphosphocytidyl-2C-methyl-D-erythritol synthase [Escherichia coli] SEQ ID n-794
				gb AAG42461.1 AF308468_2 (AF308468) YgbQ [Klebsiella aerogenes] #N/A
SEQ ID n° 8158 PL-5998.1	Contig9 from 2681430 to 2681750	m	71%	gb AAG42463.1 AF308468_4 (AF308468) APS kinase [Klebsiella aerogenes] SEQ ID n-795
				Contig9 from 2681897 to 2682529

TABLEAU II

SEQ ID n° 8160	PL-1687.1	Contig9 from 2682531 to 2683916	m	79%	gb AAG42464.1 AF308468_5 (AF308468) ATP sulfurylase N subunit [Klebsiella aerogenes]	SEQ ID n-796
SEQ ID n° 8161	PL-1688.1	Contig9 from 2683985 to 2684893	m	93%	gb AAG42465.1 AF308468_6 (AF308468) ATP sulfurylase D subunit [Klebsiella aerogenes]	SEQ ID n-797
SEQ ID n° 8162	PL-1689.1	Contig9 from 2684903 to 2686315	m	73%	gb AAG42466.1 AF308468_7 (AF308468) siroheme synthetase [Klebsiella aerogenes]	SEQ ID n-798
SEQ ID n° 8163	PL-6000.1	Contig9 from 2686583 to 2686858	p	77%	gb AAG58617.1 AE005572_15 (AE005572) Z48B3 gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8164	PL-6001.1	Contig9 from 2686855 to 2687211	p	83%	gb AAG58616.1 AE005572_14 (AE005572) Z48B2 gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8165	PL-1690.1	Contig9 from 2687317 to 2688051	m	78%	sp P17853 CYSH_SALTY PHOSPHOADENOSINE PHOSPHOSULFATE REDUCTASE (PAPS REDUCTASE, THIOREDOXIN DEPENDENT) (PADOPS REDUCTASE) (3'-PHOSPHOADENYLSULFATE REDUCTASE) (PAPS SULFOTRANSFERASE) pir C34354 3'- phosphoadenosine 5'-phosphosulfate reductase (EC 1.8.99.4) - salmonella typhimurium gb AAA27048.1 (M23007) 3'-phosphoadenosine-5'- phosphosulfate sulfotransferase [Salmonella typhimurium]	SEQ ID n-800
SEQ ID n° 8166	PL-1692.1	Contig9 from 2688048 to 2689778	m	87%	gb AAG57871.1 AE005504_3 (AE005504) sulfite reductase, alpha subunit [Escherichia coli O157:H7]	SEQ ID n-801
SEQ ID n° 8167	PL-1693.1	Contig9 from 2689778 to 2691580	m	81%	sp P38038 CYSJ_ECOLI SULFITE REDUCTASE [NADPH] FLAVOPROTEIN ALPHA-COMPONENT (SIR-FP) pir B34231 sulfite reductase (NADPH) (EC 1.8.1.2) - Escherichia coli gb AAA23650.1 (M23008) NADPH-sulfite reductase flavoprotein component [Escherichia coli]	SEQ ID n-802

TABLEAU II

SEQ ID n° 8168	PL-6002.1	Contig9 from 2691847 to 2692209	p	82%	sp Q46903 PTPS_ECOLI PUTATIVE 6-PYRUVOYL TETRAHYDROBIOPTERIN SYNTHASE (PTPS) (PTP SYNTHASE) pir A65058 hypothetical protein b2765 - Escherichia coli (strain K-12) gb AAAG9275.1 (U29579) ORF_0121 [Escherichia coli] gb AAC75807.1 (AE000360) putative 6- pyruvoyl tetrahydrobiopterin synthase [Escherichia coli K12] gb AAG57873.1 AE005504_5 (AE005504) putative 6-pyruvoyl tetrahydrobiopterin synthase [Escherichia coli O157:H7]	#N/A	SEQ ID n-803
SEQ ID n° 8169	PL-1694.1	Contig9 from 2692254 to 2692925	m	80%	gb AAG57887.1 AE005505_5 (AE005505) orf, hypothetical protein [Escherichia coli O157:H7]		
SEQ ID n° 8170	PL-1695.1	Contig9 from 2693096 to 2694481	p	82%	gb AAB86967.1 (AF032970) inducible histidine transporter [Pseudomonas putida]		SEQ ID n-804
SEQ ID n° 8171	PL-1696.1	Contig9 from 2694757 to 2695539	m	76%	pir C64745 yafD protein - Escherichia coli gb AAC73314.1 (AE000130) orf, hypothetical protein [Escherichia coli K12] gb AAG54505.1 AE005196_3 (AE005196) orf, hypothetical protein [Escherichia coli O157:H7] sp P31546 YAE_DCOLI HYPOTHETICAL 21.3 KD PROTEIN IN ABC-RRSH INTERGENIC REGION		SEQ ID n-805
SEQ ID n° 8172	PL-1578.1	Contig9 from 2701657 to 2702223	m	72%	pir H64744 yaeD protein - Escherichia coli gb AAB08628.1 (U70214) hypothetical [Escherichia coli] gb AAC73311.1 (AE000129) putative phosphatase [Escherichia coli K12] dbj BAA77877.1 (D83536) Hypothetical 21.3 kd protein in abc-rrnH intergenic region. [Escherichia coli] dbj BAA93568.1 (AB035926) phosphatase [Escherichia coli O157:H7] gb AAG54502.1 AE005195_11 (AE005195) putative phosphatase [Escherichia coli O157:H7]		SEQ ID n-876

TABLEAU II

SEQ ID n° 8173	PL-1577.1	Contig9 from 2702419 to 2703450	P 88%	gb AAG54501.1 AE005195_10 (AE005195) ATP-binding component of a transporter [Escherichia coli O157:H7]	SEQ ID n-875
SEQ ID n° 8174	PL-1576.1	Contig9 from 2703443 to 2704096	P 92%	sp P31547 YAEI_ECOLI_HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN YAEI pir F64744 probable transport protein yaeI - Escherichia coli gb AA08626.1 (U70214) hypothetical [Escherichia coli] gb AAC73309.1 (AE000129) putative transport system permease protein [Escherichia coli K12] dbj BAA77875.1 (D83536) Hypothetical 23.3 kd protein in rcsF-abc intergenic region. [Escherichia coli]	SEQ ID n-874
SEQ ID n° 8175	PL-1575.1	Contig9 from 2704162 to 2704977	P 94%	sp P28635 YAEI_ECOLI_PUTATIVE LIPOPROTEIN YAEI PRECURSOR pir F64744 probable lipoprotein yaeI - Escherichia coli dbj BAA03657.1 (D15061) ORF271 [Escherichia coli] gb AA08625.1 (U70214) hypothetical [Escherichia coli] gb AAC73308.1 (AE000129) putative lipoprotein [Escherichia coli K12] dbj BAA77874.1 (D83536) Hypothetical 29.4 kd lipoprotein in rcsF-abc intergenic region precursor. [Escherichia coli]	SEQ ID n-873
SEQ ID n° 8176	PL-6032.1	Contig9 from 2705120 to 2705518	P 55%	sp P28633 RCSF_ECOLI_RCSF PROTEIN pir B47040 exopolysaccharide synthesis regulator RcsF -- Escherichia coli gb AAA24508.1 (L04474) RCSF [Escherichia coli] dbj BAA77873.1 (D83536) Exopolysaccharide synthesis regulator RcsF. [Escherichia coli]	#N/A

TABLEAU II

SEQ ID n° 8177 PL-1574.1	Contig9 from 2705515 to 2706222	p	75%	sp P28634 YAEB_ECOLI HYPOTHETICAL 26.4 KDA PROTEIN IN PROS-RCSF INTERGENIC REGION (ORF3) pir C64744 yaeB protein - Escherichia coli dbj BAA03655.1 (D15061) ORF235 [Escherichia coli] gb AAB08623.1 (U70214) hypothetical [Escherichia coli] gb AAC73306.1 (AE000128) orf, hypothetical protein [Escherichia coli K12] dbj BAA77871.1 (D83536) Hypothetical 26.4 kd protein in pros-rsf intergenic region (orf3). [Escherichia coli]	SEQ ID n-672
				gb AAG54496.1 AE005195_5 (AE005195) proline trna synthetase [Escherichia coli O157:H7]	
				gb AAG54494.1 AE005195_3 (AE005195) copper homeostasis protein (lipoprotein) [Escherichia coli O157:H7]	
				pir E64743 yaeO protein - Escherichia coli emb CAA90752.1 (Z50870) orf4 [Escherichia coli] gb AAC73300.1 (AE000128) orf, hypothetical protein [Escherichia coli K12]	
SEQ ID n° 8179 PL-1572.1	Contig9 from 2708168 to 2708839	m	54%	gb AAG54491.1 AE005194_12 (AE005194) orf, hypothetical protein [Escherichia coli O157:H7] sp P52097 MESJ_ECOLI PUTATIVE CELL CYCLE PROTEIN MESJ pir D64743 cell cycle protein mesJ - Escherichia coli emb CAA90751.1 (Z50870) similar to Acc.No. D26185 [Escherichia coli] dbj BAA08428.1 (D49445) YaeN [Escherichia coli] gb AAB08617.1 (U70214) hypothetical [Escherichia coli] gb AAC73299.1 (AE000128) cell cycle protein [Escherichia coli K12] dbj BAA77863.1 (D83536) Cell cycle protein MesJ. [Escherichia coli]	#N/A
SEQ ID n° 8180 PL-6035.1	Contig9 from 2709174 to 2709440	p	71%		
SEQ ID n° 8181 PL-1571.1	Contig9 from 2709473 to 2710801	m	64%		

TABLEAU II

SEQ ID n° 8182 PL-1570.1	Contig9 from 2711140 to 2712099	m 92%	sp P30867 ACCA_ECOLI ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT ALPHA pir A43452 acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain [validated] - Escherichia coli gb AA070370.1 (M96394) acetyl-CoA carboxylase [Escherichia coli] gb AB08614.1 (U70214) acetyl-CoA carboxylase alpha subunit [Escherichia coli] dbj BA08425.1 (D49445) AccA, alpha subunit of acetyl-CoA carboxylase [Escherichia coli] gb AAC73296.1 (AE000127) acetylCoA carboxylase, carboxytransferase component, alpha subunit [Escherichia coli K12] gb AAG54487.1 AE005194_8 (AE005194) acetylCoA carboxylase, carboxytransferase component, alpha subunit [Escherichia coli O157:H7] gb AAG54486.1 AE005194_7 (AE005194) DNA polymerase III, alpha subunit [Escherichia coli O157:H7]
			SEQ ID n-868
SEQ ID n° 8183 PL-1569.1	Contig9 from 2712113 to 2715595	m 92%	sp P10442 RNH2_ECOLI RIBONUCLEASE HII (RNASE HII) pir Q9ECBB ribonuclease H (EC 3.1.26.4) II - Escherichia coli gb AAB08612.1 (U70214) ribonuclease HII [Escherichia coli] gb AAC73294.1 (AE000127) RNase HII, degrades RNA of DNA-RNA hybrids [Escherichia coli K12] pir SYECTA lipid-A-disaccharide synthase (EC 2.4.1.182) - Escherichia coli gb AAB08611.1 (U70214) lipid A disaccharide synthase [Escherichia coli] gb AAC73293.1 (AE000127) tetraacyldisaccharide-1-P; lipid A biosynthesis, penultimate step [Escherichia coli K12]
			SEQ ID n-866
SEQ ID n° 8184 PL-3600.1	Contig9 from 2715649 to 2716239	m 81%	sp P10442 RNH2_ECOLI RIBONUCLEASE HII (RNASE HII) pir Q9ECBB ribonuclease H (EC 3.1.26.4) II - Escherichia coli gb AAB08612.1 (U70214) ribonuclease HII [Escherichia coli] gb AAC73294.1 (AE000127) RNase HII, degrades RNA of DNA-RNA hybrids [Escherichia coli K12] pir SYECTA lipid-A-disaccharide synthase (EC 2.4.1.182) - Escherichia coli gb AAB08611.1 (U70214) lipid A disaccharide synthase [Escherichia coli] gb AAC73293.1 (AE000127) tetraacyldisaccharide-1-P; lipid A biosynthesis, penultimate step [Escherichia coli K12]
			SEQ ID n-2799
SEQ ID n° 8185 PL-1568.1	Contig9 from 2716239 to 2717408	m 85%	sp P10442 RNH2_ECOLI RIBONUCLEASE HII (RNASE HII) pir Q9ECBB ribonuclease H (EC 3.1.26.4) II - Escherichia coli gb AAB08612.1 (U70214) ribonuclease HII [Escherichia coli] gb AAC73294.1 (AE000127) RNase HII, degrades RNA of DNA-RNA hybrids [Escherichia coli K12] pir SYECTA lipid-A-disaccharide synthase (EC 2.4.1.182) - Escherichia coli gb AAB08611.1 (U70214) lipid A disaccharide synthase [Escherichia coli] gb AAC73293.1 (AE000127) tetraacyldisaccharide-1-P; lipid A biosynthesis, penultimate step [Escherichia coli K12]
			SEQ ID n-865

TABLEAU II

SEQ ID n° 8186	PL-1567.1	Contig9 from 2717428 to 2718216	m	91%	sp P72215 LPXA_PROMI ACYL- [ACYL-CARRIER-PROTEIN] -UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE) emb CAA70456.1 (Y09263) lpxa [Proteus mirabilis]	SEQ ID n-864
SEQ ID n° 8187	PL-6038.1	Contig9 from 2718220 to 2718672	m	89%	sp P32205 FABZ_YEREN (3R)-HYDROXYMYRISTOYL- [ACYL CARRIER PROTEIN] DEHYDRATASE pir [S35968] (3R)- hydroxymyristoyl- [acyl carrier protein] dehydratase (EC 4.2.1.-) - Yersinia enterocolitica emb CAA80952.1 (Z25463) unknown [Yersinia enterocolitica]	#N/A
SEQ ID n° 8188	PL-1565.1	Contig9 from 2718835 to 2719863	m	88%	sp P32203 LPXD_YEREN UDP-3-O- [3- HYDROXYMYRISTOYL] GLUCOSAMINE N-ACYLTRANSFERASE (FIRA PROTEIN) (RIFAMPICIN RESISTANCE PROTEIN) pir [S41752 UDP-3-O- [3- hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-) - Yersinia enterocolitica emb CAA80951.1 (Z25463) Fira [Yersinia enterocolitica]	SEQ ID n-862
SEQ ID n° 8189	PL-1564.1	Contig9 from 2719867 to 2720364	m	77%	emb CAB51930.1 (AJ236920) periplasmic protein [Photorhabdus luminescens]	SEQ ID n-861
SEQ ID n° 8190	PL-1563.1	Contig9 from 2720475 to 2722868	m	96%	emb CAB51929.1 (AJ236920) outer membrane antigen [Photorhabdus luminescens]	SEQ ID n-860
SEQ ID n° 8191	PL-1562.1	Contig9 from 2722903 to 2724258	m	81%	sp P37764 YAEI_ECOLI HYPOTHETICAL 49.1 KDA PROTEIN IN CDSA-HLPA INTERGENIC REGION pir [H64741 yael protein - Escherichia coli gb AA08605.1 (U70214) hypothetical [Escherichia coli] gb AAC73287.1 (AE000127) orf, hypothetical protein [Escherichia coli K12] dbj BA077851.1 (D83536) Hypothetical 49.1 kd protein in cdsA-hlpa intergenic region. [Escherichia coli] gb AAG54478.1 AE005193_8 (AE005193) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-859

TABLEAU II

SEQ ID n° 8192	PL-1561.1	Contig9 from 2724287 to 2725135	63%	m	<p>sp P06466 CDSA_ECOLI PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGlycerol SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) (CDP-DG SYNTHETASE) pif SYECDG phosphatidate cytidylyltransferase (EC 2.7.7.41) - Escherichia coli gb AA23545.1 (M11330) CDP- diglyceride synthetase [Escherichia coli] gb AA08604.1 (U70214) phosphatidate cytidylyltransferase [Escherichia coli] gb AAC73286.1 (AE000127) CDP-diglyceride synthetase [Escherichia coli K12] dbj BAA77850.1 (D93536) Phosphatidate cytidylyltransferase (EC 2.7.7.41) [Escherichia coli] gb AAG54477.1 AE005193_7 (AE005193) CDP-diglyceride synthetase [Escherichia coli O157:H7] sp Q47675 UPPS_ECOLI UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (UPP SYNTHETASE) (DI-TRANS- POLY-CIS-DECAPRENYLCISTRANSFERASE) (UNDECAPRENYL DIPHOSPHATE SYNTHASE) (UDS) pir F64741 conserved hypothetical protein b0174 - Escherichia coli gb AAC73285.1 (AE000127) orf, hypothetical protein [Escherichia coli K12] gb AAG54476.1 AE005193_6 (AE005193) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG54475.1 AE005193_5 (AE005193) putative ATP- binding component of a transport system [Escherichia coli O157:H7] gb AAK04071.1 (AE006235) Errf [Pasteurella multocida]</p>	SEQ ID n-858
SEQ ID n° 8193	PL-1560.1	Contig9 from 2725145 to 2725909	79%	m		
SEQ ID n° 8194	PL-1559.1	Contig9 from 2726124 to 2727320	77%	m		
SEQ ID n° 8195	PL-3602.1	Contig9 from 2727587 to 2728144	87%	m		

TABLEAU II

SEQ ID n° 8196	PL-1558.1	Contig9 from 2728263 to 2728991	m 85%	<p>sp P29464 PYRH_ECOLI URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) (SMBA PROTEIN) pir B45269 uridine 5'- monophosphate kinase [EC 2.7.4.-] [validated] - Escherichia coli dbj BAA02598.1 (D13334) SmbA [Escherichia coli] dbj BAA05615.1 (D26562) 'mukB suppressor protein'smbA' [Escherichia coli] gb AAB08600.1 (U70214) uridine 5'- monophosphate (UMP) kinase [Escherichia coli] gb AAC73282.1 (AE000126) uridylylate kinase [Escherichia coli] KI2j dbj BAA77846.1 (D83536) MukB suppressor protein. [Escherichia coli] gb AAG54473.1 AE005193_3 (AE005193) uridylylate kinase [Escherichia coli O157:H7]</p> <p>sp P02997 EFTS_ECOLI ELONGATION FACTOR TS (EF- TS) pir EFPCS translation elongation factor EF- Ts - Escherichia coli_emb CAA23632.1 (V00343) elongation factor Ts [Escherichia coli] dbj BAA05614.1 (D26562) 'elongation factor EF- Ts' [Escherichia coli] gb AAB08599.1 (U70214) elongation factor EF-Ts [Escherichia coli] gb AAC73281.1 (AE000126) protein chain elongation factor EF-Ts [Escherichia coli KI2j] dbj BAA77845.1 (D83536) Translation elongation factor TS. [Escherichia coli] gb AAG54472.1 AE005193_2 (AE005193) protein chain elongation factor EF-Ts [Escherichia coli O157:H7]</p>	SEQ ID n-654
SEQ ID n° 8197	PL-1557.1	Contig9 from 2729146 to 2729997	m 82%		SEQ ID n-653

TABLEAU II

SEQ ID n° 8199 PL-6039.1	Contig9 from 2731065 to 2731232	m	No Hits found	#N/A	SEQ ID n-652
SEQ ID n° 8200 PL-1555.1	Contig9 from 2731305 to 2732102	p	83%		SEQ ID n-651
SEQ ID n° 8201 PL-1554.1	Contig9 from 2732240 to 2734888	p	77%		SEQ ID n-650

sp P02351 RS2_ECOLI 30S RIBOSOMAL PROTEIN S2	
pir R3EC2 ribosomal protein S2 [validated] -	
Escherichia coli emb CAA23631.1 (V00343)	
ribosomal protein S2 [Escherichia coli]	
dbj BAA05613.1 (D26562) 'ribosomal protein S2'	
[Escherichia coli] gb AAB08598.1 (U70214)	
ribosomal protein S2 [Escherichia coli]	
gb AAC73280.1 (AF000126) 30S ribosomal subunit	
protein S2 [Escherichia coli K12]	
gb AAG54471.1 AE005193_1 (AE005193) 30S	
ribosomal subunit protein S2 [Escherichia coli	
O157:H7]	

sp P10882 AMPM_SALTY METHIONINE AMINOPEPTIDASE	
(MAP) (PEPTIDASE M) pir S12027 methionyl	
aminopeptidase (EC 3.4.11.18) - Salmonella	
typhimurium emb CAA39298.1 (X55778) peptidase	
M [Salmonella typhimurium]	
sp P27249 GLND_ECOLI [PROTEIN-PII]	
URIDYLTRANSFERASE (PII URIDYL-TRANSFERASE)	
(URIDYL REMOVING ENZYME) (UTASE) pir G64740	
uridylyltransferase (EC 2.7.7.59) - Escherichia	
coli gb AAB08596.1 (U70214) PII uridylyl-	
transferase [Escherichia coli] gb AAC73278.1	
(AE000126) protein PII; uridylyltransferase acts	
on regulator of glnA [Escherichia	
coli K12]	

TABLEAU II

SEQ ID n° 8202	PL-1553.1	Contig9 from 2735060 to 2735884	P	89%	sp P03948 DAPD_ECOLI_2,3,4,5-TETRAHYDROPYRIDINE- 2-CARBOXYLATE N-SUCCINYLTRANSFERASE (TETRAHYDRODIPICOLINATE N-SUCCINYLTRANSFERASE) (THP SUCCINYLTRANSFERASE) (TETRAHYDRODIPICOLINATE SUCCINYLASE) pir XNECSD 2,3,4,5-tetrahydropyridine-2-carboxylate N- succinyltransferase [EC 2.3.1.117] Escherichia coli dbj BAA05610.1 (D26562) 'tetrahydrodipicolinate N-succinyltransferase' [Escherichia coli] gb AAB08595.1 (U70214) tetrahydrodipicolinate N-succinyltransferase [Escherichia coli] gb AAC73277.1 (AE000126) 2,3,4,5-tetrahydropyridine-2- carboxylate N-succinyltransferase [Escherichia coli K12] sp P37048 YAEH_ECOLI_HYPOTHETICAL_15.1_KD PROTEIN IN HTRA-DAPD INTERGENIC REGION pir S45230 yaeH protein - Escherichia coli dbj BAA05609.1 (D26562) 'ORF' [Escherichia coli] gb AAB08593.1 (U70214) hypothetical [Escherichia coli] gb AAC73274.1 (AE000126) putative structural protein [Escherichia coli K12] gb AAG54467.1 AE005192_9 (AE005192) putative structural protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 8203	PL-6043.1	Contig9 from 2736099 to 2736485	P	88%	pir S45108 hypothetical protein 2 - Erwinia carotovora emb CAA55983.1 (X79474) ORF2 [Pectobacterium carotovorum] #N/A
SEQ ID n° 8204	PL-3603.2	Contig9 from 2736543 to 2736992	M	76%	gb AAG43452.1 AF188518_1 (AF188518) EmrB-like protein Smb [Staphylococcus aureus] #N/A
SEQ ID n° 8205	PL-1552.2	Contig9 from 2737363 to 2737965	P	37%	sp Q47417 YQCB_ERWCA_EXOENZYME_REGULATION REGULON ORF1 pir S45107 hypothetical protein 1 - Erwinia carotovora emb CAA55982.1 (X79474) ORF1 [Erwinia carotovora] #N/A
SEQ ID n° 8206	PL-1551.1	Contig9 from 2738457 to 2739227	M	68%	SEQ ID n-647

TABLEAU II

SEQ ID n° 8207	PL-6045.1	Contig9 from 2739229 to 2739561	m	56%	sp Q57152 YQCC_HABIN HYPOTHETICAL PROTEIN HI1436 pir I64171 hypothetical protein HI1436 - Haemophilus influenzae (strain Rd KW20) gb AAC23085.1 (U32822) conserved hypothetical protein [Haemophilus influenzae Rd] sp P43526 SYDP_ECOLI SYD PROTEIN pir A59944 syd protein - Escherichia coli dbj BA07525.1 (D38520) Syd protein [Escherichia coli] gb AAB40443.1 (U29581) GTG start [Escherichia coli] gb AAC75835.1 (AE000363) interacts with secY [Escherichia coli K12] -	#N/A
SEQ ID n° 8208	PL-3605.1	Contig9 from 2740085 to 2740639	m	65%	sp Q46920 YQCD_ECOLI HYPOTHETICAL 32.6 KD PROTEIN IN SYD-SDAC INTERGENIC REGION pir F65061 hypothetical protein b2794 - Escherichia coli (strain K-12) gb AAB40444.1 (U29581) ORF_0282 [Escherichia coli] gb AAC75836.1 (AE000363) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-2803
SEQ ID n° 8209	PL-1550.1	Contig9 from 2740785 to 2741633	p	76%	sp P37350 YGDH_ECOLI HYPOTHETICAL 51.0 KD PROTEIN IN BARA-SDAC INTERGENIC REGION pir G65061 hypothetical protein b2795 - Escherichia coli (strain K-12) gb AAB40445.1 (U29581) TTG start; alternate gene name ygdH; ORF_0455 [Escherichia coli] gb AAC75837.1 (AE000363) orf, hypothetical protein [Escherichia coli K12] gb AAG57909.1 (AE005507_10 (AE005507) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-646
SEQ ID n° 8210	PL-1549.1	Contig9 from 2741756 to 2743123	p	83%	gb AAG57912.1 (AE005508_3 (AE005508) 5'-3' exonuclease [Escherichia coli O157:H7]	SEQ ID n-644
SEQ ID n° 8211	PL-1548.1	Contig9 from 2743187 to 2743945	p	81%	dbj BAA25796.1 (D49826) Lipid [serratia marcescens]	SEQ ID n-643
SEQ ID n° 8212	PL-1547.1	Contig9 from 2743942 to 2745318	m	71%		SEQ ID n-642

TABLEAU II

SEQ ID n° 8213	PL-1546.1	Contig9 from 2745318 to 2746652	m	75%	dbj BAA08632.1 (D49826) LipC [Serratia marcescens]	SEQ ID n-841
SEQ ID n° 8214	PL-1545.1	Contig9 from 2746713 to 2748443	m	83%	dbj BAA08631.1 (D49826) LipB [Serratia marcescens]	SEQ ID n-840
SEQ ID n° 8215	PL-3607.1	Contig9 from 2748503 to 2748835	m	42%	gb AAD49576.1 AF141295_2 (AF141295) protease inhibitor [Pectobacterium carotovorum subsp. carotovorum]	SEQ ID n-2804
SEQ ID n° 8216	PL-1544.1	Contig9 from 2748962 to 2750404	m	63%	pdb 1AXL Alkaline Protease From Pseudomonas Aeruginosa Ifc3080	SEQ ID n-839
SEQ ID n° 8217	PL-1543.1	Contig9 from 2751589 to 2752689	m	84%	sp P32066 YGDE_ECOLI HYPOTHETICAL 41.9 KD PROTEIN IN FUCR-GCVA INTERGENIC REGION (ORF3) pir I41067 hypothetical 41.9K protein (fucR- gcvA intergenic region) - Escherichia coli emb CAA51815.1 (X73413) ORF3 [Escherichia coli gb AAB40456.1 (U29581) alternate name Orf2 of X73413 and U01030; ORF_f366 [Escherichia coli] gb AAC75848.1 (AE000364) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-838 sp P32065 YGDD_ECOLI HYPOTHETICAL 14.3 KD PROTEIN IN FUCR-GCVA INTERGENIC REGION (ORF2) pir I41066 hypothetical 14.3K protein (fucR- gcvA intergenic region) - Escherichia coli emb CAA51814.1 (X73413) ORF2 [Escherichia coli gb AAB40457.1 (U29581) alternate name Orf3 of X73413; ORF_f131 [Escherichia coli] gb AAC75849.1 (AE000364) orf, hypothetical protein [Escherichia coli K12] gb AAG57921.1 AE005508_12 (AE005508) orf, hypothetical protein [Escherichia coli O157:H7]	
SEQ ID n° 8218	PL-6047.1	Contig9 from 2752682 to 2753077	m	68%		#N/A

TABLEAU II

SEQ ID n° 8219	PL-1542.1	Contig9 from 2753138 to 2754058	87%	<p>sp P32064 GCVA_ECOLI GLYCINE CLEAVAGE SYSTEM TRANSCRIPTIONAL ACTIVATOR (GCV OPERON ACTIVATOR) pir I41065 glycine cleavage system transcription activator - Escherichia coli emb CAA51813.1 (X73413) glycine cleavage activator protein [Escherichia coli] gb AAC13742.1 (U01030) GCVA [Escherichia coli] gb AB40458.1 (U29581) CG Site No. 28676 [Escherichia coli] gb AAC75850.1 (AE000364) positive regulator of gcv operon [Escherichia coli K12] gb AAG57922.1 (AE005508_13 (AE005508) positive regulator of gcv operon [Escherichia coli O157:H7] pir P65063 hypothetical protein b2810 - Escherichia coli (strain K-12) gb AB40460.1 (U29581) ORF_o401 [Escherichia coli] gb AAC75852.1 (AE000364) orf, hypothetical protein [Escherichia coli K12] dbj BAB21541.1 (AB055109) Nifs-like cysteine sulfinatase desulfinate [Escherichia coli] sp Q46926 YGD_X_ECOLI HYPOTHETICAL 15.9 KD PROTEIN IN GCVA-METZ INTERGENIC REGION (O147) pir G65063 hypothetical protein b2811 - Escherichia coli (strain K-12) gb AB40461.1 (U29581) ORF_o147 [Escherichia coli] gb AAC75853.1 (AE000364) orf, hypothetical protein [Escherichia coli K12] gb AAG57925.1 (AE005509_3 (AE005509) orf, hypothetical protein [Escherichia coli O157:H7] sp Q46927 YGD_X_ECOLI HYPOTHETICAL 28.6 KD PROTEIN IN GCVA-METZ INTERGENIC REGION pir H65063 hypothetical protein b2812 - Escherichia coli (strain K-12) gb AB40462.1 (U29581) ORF_f368 [Escherichia coli] gb AAC75854.1 (AE000364) putative enzyme [Escherichia coli K12]</p>	SEQ ID n-637
SEQ ID n° 8220	PL-1541.1	Contig9 from 2754611 to 2755864	69%		
SEQ ID n° 8221	PL-3608.1	Contig9 from 2755885 to 2756340	63%		
SEQ ID n° 8222	PL-1540.1	Contig9 from 2756343 to 2757155	88%		

TABLEAU II

SEQ ID n° 8223 PL-1539.1	Contig9 from 2757204 to 2758301	m	77%	gb AAB40463.1 (U29581) ORF_f432 [Escherichia coli]	SEQ ID n-833
SEQ ID n° 8224 PL-6051.1	Contig9 from 2758558 to 2758782	m	No Hits found		#N/A
SEQ ID n° 8225 PL-6052.1	Contig9 from 2759074 to 2759199	p	No Hits found		#N/A
SEQ ID n° 8226 PL-6053.1	Contig9 from 2759163 to 2759360	p	44%	ref NP_061700.1 conserved hypothetical protein [Xylella fastidiosa] pir D82866-conserved hypothetical protein xfa0045 [imported] - xylella fastidiosa (strain 9a5c) gb AAF85613.1 AE003851_44 (AE003851) conserved hypothetical protein [Xylella fastidiosa] ref NP_061701.1 hypothetical protein [Xylella fastidiosa] pir E82866 hypothetical protein xfa0046 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85614.1 AE003851_45 (AE003851) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 8227 PL-6055.1	Contig9 from 2759357 to 2759497	p	71%		#N/A
SEQ ID n° 8228 PL-1538.1	Contig9 from 2759575 to 2760819	m	84%	sp Q46929 AMIC_ECOLI N-ACETYL-MURAMOYL-L-ALANINE AMIDASE AMIC PRECURSOR	SEQ ID n-832

TABLEAU II

SEQ ID n° 8229	PL-1537.1	2761064 to 2762410	p	87%	Contig9 from	sp P08205 ARGA_ECOLI_AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS) pir XYCAA amino-acid N-acetyltransferase (EC 2.3.1.1) - Escherichia coli emb CAA68547.1 (Y00492) N-acetylglutamate synthase (AA 1 - 443) [Escherichia coli] gb AAB40465.1 (U29581) N-acetylglutamate synthase [Escherichia coli] gb AAC75857.1 (AE000365) N-acetylglutamate synthase; amino acid acetyltransferase [Escherichia coli K12] gb XAG57929.1 (AE005510) N-acetylglutamate synthase; amino acid acetyltransferase [Escherichia coli]	SEQ ID n-631
SEQ ID n° 8230	PL-1535.1	2762642 to 2769034	m	11%	Contig9 from	gb AAB63525.1 (U12682) celfur protein [Caenorhabditis elegans]	SEQ ID n-630
SEQ ID n° 8231	PL-3611.1	2769064 to 2769585	m	No Hits found	Contig9 from		SEQ ID n-2808
SEQ ID n° 8232	PL-3612.1	2769634 to 2770155	m	No Hits found	Contig9 from		SEQ ID n-2809
SEQ ID n° 8233	PL-3613.1	2770204 to 2770725	m	No Hits found	Contig9 from		SEQ ID n-2810
SEQ ID n° 8234	PL-3614.1	2770784 to 2771314	m	No Hits found	Contig9 from		SEQ ID n-2811
SEQ ID n° 8235	PL-3615.1	2771373 to 2771894	m	No Hits found	Contig9 from		SEQ ID n-2812
SEQ ID n° 8236	PL-3616.1	2771953 to 2772474	m	No Hits found	Contig9 from		SEQ ID n-2813

TABLEAU II

SEQ ID n°	Contig9 from	m	No Hits found	SEQ ID n°
8237 PL-3617.1	2772523 to 2773044	m		2814
8238 PL-1530.1	2773154 to 2774569	m	63%	826
8239 PL-1529.1	2774711 to 2776846	m	77%	824
8240 PL-1528.1	2777712 to 2779568	m	68%	823
8241 PL-1527.1	2779565 to 2783173	m	73%	822

<p>pir P82561 hemolysin secretion protein D XF2398 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85197.1 AE004049.2 (AE004049) hemolysin secretion protein D [Xylella fastidiosa]</p> <p>pir E82561 toxin secretion ABC transporter ATP-binding protein XF2397 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85196.1 AE004049.1 (AE004049) toxin secretion ABC transporter ATP-binding protein [Xylella fastidiosa]</p> <p>sp P04993 EXSA_ECOLI EXODEOXYRIBONUCLEASE V ALPHA CHAIN (EXODEOXYRIBONUCLEASE V 67 KDA POLYPEPTIDE) pir NCEKXF exodeoxyribonuclease V (EC 3.1.11.5) 67K chain - Escherichia coli gb AAB40466.1 (U29581) exonuclease V alpha-subunit [Escherichia coli] gb AAC75858.1 (AE000365) DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease [Escherichia coli K12] sp P08394 EXSB_ECOLI EXODEOXYRIBONUCLEASE V BETA CHAIN (EXODEOXYRIBONUCLEASE V 135 KDA POLYPEPTIDE) pir NCEKX5 exodeoxyribonuclease V (EC 3.1.11.5) 135K chain - Escherichia coli emb CAA28250.1 (X04581) exonuclease V (AA 1-1180) [Escherichia coli] gb AAB40467.1 (U29581) exonuclease V subunit [Escherichia coli] gb AAC75859.1 (AE000365) DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease [Escherichia coli K12] gb AAD56369.1 AF179304.1 (AF179304) RecB2109 [Escherichia coli]</p>	<p>SEQ ID n-2814</p> <p>SEQ ID n-826</p> <p>SEQ ID n-824</p> <p>SEQ ID n-823</p> <p>SEQ ID n-822</p>
---	--

TABLEAU II

SEQ ID n° 8242	PL-1526.1	Contig9 from 2783170 to 2786061	m	71%	gb AAB40468.1 (U29581) protease III precursor (pitrilysin) [Escherichia coli]	SEQ ID n-821
SEQ ID n° 8243	PL-1525.1	Contig9 from 2786077 to 2789466	m	74%	sp P07648 EX5C_ECOLI EXODEOXYRIBONUCLEASE V GAMMA CHAIN (EXODEOXYRIBONUCLEASE V 125 KDA POLYPEPTIDE) pir NCECXV exodeoxyribonuclease V (EC 3.1.11.5) 125K chain - Escherichia coli emb CAA27604.1 (X03966) recC protein (aa 1- 1122) [Escherichia coli] gb AAB40469.1 (U29581) exonuclease V subunit [Escherichia coli] gb AAC75861.1 (AE000366) DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit, ssDNA endonuclease [Escherichia coli K12]	SEQ ID n-820
SEQ ID n° 8244	PL-6060.1	Contig9 from 2789459 to 2789836	m	No Hits found		#N/A
SEQ ID n° 8245	PL-3619.2	Contig9 from 2789827 to 2790312	m	No Hits found		#N/A
SEQ ID n° 8246	PL-6062.2	Contig9 from 2790318 to 2790905	m	42%	gb AAG57936.1 AE005511_4 (AE005511) prepilin peptidase dependent protein B [Escherichia coli O157:H7 EDL933] dbj BAB37105.1 (AP002563) prepilin peptidase dependent protein B [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8247	PL-3620.1	Contig9 from 2791073 to 2791576	m	40%	gb AAG57937.1 AE005511_5 (AE005511) prepilin peptidase dependent protein A [Escherichia coli O157:H7]	SEQ ID n-2817
SEQ ID n° 8248	PL-6064.1	Contig9 from 2792068 to 2792400	m	33%	gb AAG31734.1 AF264949_2 (AF264949) unknown [Erwinia amylovora] gb AAG31738.1 AF264951_2 (AF264951) unknown [Erwinia amylovora]	#N/A
SEQ ID n° 8249	PL-6065.1	Contig9 from 2792397 to 2792663	m	46%	gb AAG31733.1 AF264949_1 (AF264949) unknown [Erwinia amylovora] gb AAG31737.1 AF264951_1 (AF264951) unknown [Erwinia amylovora]	#N/A

TABLEAU II

SEQ ID n° 8250 PL-1524.1	Contig9 from 2792791 to 2793585	m	91%	<p> pdb 1AXW A Chain A, E. Coli Thymidylate Synthase In Complex With Methotrexate (Mtx) And 2'-Deoxyuridine 5'-Monophosphate (Dump) pdb 1AXW B Chain B, E. Coli Thymidylate Synthase In Complex With Methotrexate (Mtx) And 2'-Deoxyuridine 5'-Monophosphate (Dump) pdb 1TRG E. Coli Thymidylate Synthase In Symmetric Complex With Cb3717 And 2'- Deoxyuridine 5'-Monophosphate (Dump) pdb 1TSD A Chain A, Thymidylate Synthase Complex With 2'- Deoxyuridine 5'-Monophosphate (Dump) And Folate Analog 1843u89 pdb 1TSD B Chain B, Thymidylate Synthase Complex With 2'- Deoxyuridine 5'-Monophosphate (Dump) And Folate Analog 1843u89 pdb 1DDU A Chain A, E. Coli Thymidylate Synthase In Complex With Cb3717 And 2',5'-Dideoxyuridine (Ddurd) pdb 1DDU B Chain B, E. Coli Thymidylate Synthase In Complex With Cb3717 And 2',5'-Dideoxyuridine (Ddurd) pdb 1TDU A Chain A, E. Coli Thymidylate Synthase In Complex With Cb3717 And 2'-Deoxyuridine (Durd) pdb 1TDU B Chain B, E. Coli Thymidylate Synthase SEQ ID n° 819 sp Q07293 LGT_SALTY PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE pir A47354 probable prolipoprotein glyceryl transferase - Salmonella typhimurium gb AAA20896.1 (L13259) prolipoprotein diacylglycerol transferase [Salmonella typhimurium] gb AAG57940.1 AE005511_8 (AE005511) PTS system, enzyme I, transcriptional regulator (with NPR and NTR proteins) [Escherichia coli O157:H7 EDL933] dbj BAB37109.1 (AP002563) PTS system transcriptional regulator enzyme I [Escherichia coli O157:H7] </p>	#N/A
SEQ ID n° 8251 PL-1523.3	Contig9 from 2793582 to 2794457	m	78%		#N/A
SEQ ID n° 8252 PL-1522.3	Contig9 from 2794533 to 2796779	m	82%		#N/A

TABLEAU II

SEQ ID n° 8253	PL-3622.1	Contig9 from 2796789 to 2797319	m	84%	sp Q46930 NUDH_ECOLI PROBABLE (DI)NUCLEOSIDE POLYPHOSPHATE HYDROLASE (AP4A PYROPHOSPHATASE) pir G65065 hypothetical protein b2830 - Escherichia coli (strain K-12) gb AA040477.1 (U29581) ORF_f176 [Escherichia coli] gb AAC75869.1 (AE000366) putative invasion protein [Escherichia coli K12]	SEQ ID n-2818
SEQ ID n° 8254	PL-1521.1	Contig9 from 2797610 to 2798623	p	77%	gb AAG57941.1 AE005511_9 (AE005511) putative invasion protein [Escherichia coli O157:H7] pir S40584 hypothetical protein - Escherichia coli pir T45293 thiamin-binding protein precursor [imported] - Escherichia coli dbj BAA01339.1 (D10483) sfua protein homolog (PIR:A35108) [Escherichia coli] gb AA18833.1 (U09984) thiamin binding protein [Escherichia coli]	SEQ ID n-616
SEQ ID n° 8255	PL-1520.1	Contig9 from 2798599 to 2800209	p	83%	sp P31549 THIP_ECOLI THIAMINE TRANSPORT SYSTEM PERMEASE PROTEIN THIP pir C64728 probable membrane protein yabK - Escherichia coli gb AAC73178.1 (AE000117) putative transport system permease protein [Escherichia coli K12]	SEQ ID n-615
SEQ ID n° 8256	PL-1519.1	Contig9 from 2800196 to 2800903	p	60%	gb AAG54370.1 AE005183_7 (AE005183) putative ATP binding component of a transport system [Escherichia coli O157:H7]	SEQ ID n-613
SEQ ID n° 8257	PL-6069.1	Contig9 from 2801169 to 2801363	p	52%	gb AAG43149.1 AF063187_1 (AF063187) DNA polymerase II [Pseudomonas fluorescens]	#N/A
SEQ ID n° 8258	PL-1518.1	Contig9 from 2801561 to 2804473	p	88%	sp P23852 HEPA_ECOLI RNA POLYMERASE ASSOCIATED PROTEIN (ATP-DEPENDENT HELICASE HEPA) pir C64727 probable ATP-dependent helicase hepa - Escherichia coli gb AAC73170.1 (AE000116) probable ATP-dependent RNA helicase [Escherichia coli K12] gb AAG54363.1 AE005182_12 (AE005182) Z0067 gene product [Escherichia coli O157:H7]	SEQ ID n-612

TABLEAU II

SEQ ID n° 8259	PL-1517-1	Contig9 from 2804570-to- 2805220	p	80%	sp P39219 RLUA_ECOLI_RIBOSOMAL_LARGE_SUBUNIT_PSEUDOURIDINE_SYNTHASE_A (PSEUDOURIDYLATE SYNTHASE) (URACIL_HYDROLYASE) pir B64727 yabo protein - Escherichia coli gb AAC73169.1 (AE000116) pseudouridylylate synthase [Escherichia coli K12]	SEQ ID n-611
SEQ ID n° 8260	PL-1516.1	Contig9 from 2805456 to 2806277	m	79%	gb AA54360.1 AE005182_9 (AE005182) putative DNA binding protein [Escherichia coli O157:H7]	SEQ ID n-610
SEQ ID n° 8261	PL-1515.1	Contig9 from 2806587 to 2808911	p	79%	sp P31554 OSTA_ECOLI_ORGANIC_SOLVENT_TOLERANCE_PROTEIN-PRECURSOR pir F64726 organic solvent tolerance protein precursor - Escherichia coli gb AAC73165.1 (AE000115) organic solvent tolerance [Escherichia coli K12]	
SEQ ID n° 8262	PL-1514.1	Contig9 from 2808981 to 2810282	p	79%	dbj BAA34130.1 (AB013134) osta/imp [Escherichia coli] sp F21202 SURA_ECOLI_SURVIVAL_PROTEIN_SURA_PRECURSOR (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SURA) (PPIASE) (ROTAMASE C) pir E64726 probable peptidylprolyl isomerase (EC 5.2.1.8) surA precursor - Escherichia coli gb AAC73164.1 (AE000115) survival protein [Escherichia coli K12]	SEQ ID n-609
SEQ ID n° 8263	PL-1513.1	Contig9 from 2810260 to 2811279	p	79%	gb AAG54358.1 AE005182_7 (AE005182) survival protein [Escherichia coli O157:H7] sp P19624 PDXA_ECOLI_PYRIDOXAL_PHOSPHATE BIOSYNTHETIC PROTEIN PDXA pir BVECX pyridoxal phosphate biosynthetic protein pdxA - Escherichia coli gb AA24305.1 (M68521) pdxA [Escherichia coli] gb AAC73163.1 (AE000115) pyridoxine biosynthesis [Escherichia coli K12]	SEQ ID n-608

TABLEAU II

SEQ ID n° 8264	PL-1512.1	Contig9 from 2811272 to 2812090	P 89%	sp P06992 KSGA_ECOLI_DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (16S RNA DIMETHYLASE) (HIGH LEVEL KASUGAMYCIN RESISTANCE PROTEIN KSGA) (KASUGAMYCIN DIMETHYLTRANSFERASE) pir XYECKO rRNA (adenine- N6,N6-)-dimethyltransferase (EC 2.1.1.-) - Escherichia coli emb CAA28417.1 (X04711) put. 16S rRNA methyltransferase (ksgA) (AA 1-273) [Escherichia coli] gb AAA24049.1 (M11054) methyltransferase-(ksgA)-[Escherichia coli] dbj BAA01327.1 (D10483) rRNA (adenosine-N6,N6-)- dimethyltransferase [Escherichia coli] gb AAC73162.1 (AE000115) S- adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase [Escherichia coli K12] prf 1112172A methyltransferase [Escherichia coli]	SEQ ID n-606
SEQ ID n° 8265	PL-6070.1	Contig9 from 2812103 to 2812480	P 83%	sp P05636 APAG_ECOLI_APAG_PROTEIN pir BVECAG apaG protein - Escherichia coli emb CAA28418.1 (X04711) URF (apaG) (AA 1-375) [Escherichia coli] dbj BAA01326.1 (D10483) apaG protein [Escherichia coli] gb AAC73161.1 (AE000115) orf, hypothetical protein [Escherichia coli K12] gb AGS4355.1 AE005182_4 (AE005182) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8266	PL-1511.1	Contig9 from 2812483 to 2813310	P 79%	gb AGS4354.1 AE005182_3 (AE005182) diadenosine tetraphosphatase [Escherichia coli O157:H7]	SEQ ID n-605

sp|P00907|CARA_ECOLI CARBAMOYL-PHOSPHATE
 SYNTHASE SMALL CHAIN (CARBAMOYL-PHOSPHATE
 SYNTHETASE GLUTAMINE CHAIN) .pir||SYECCS
 carbamoyl-phosphate synthase (glutamine-
 hydrolyzing) (EC 6.3.5.5) small chain
 [validated] - Escherichia coli dbj|BAA01310.1|
 (D10483) carbamoyl-phosphate synthase small
 chain [Escherichia coli]
 gb|AA23538.1| (J01597) carbamoyl-phosphate
 synthetase subunit A (ttg start codon)
 [Escherichia coli] gb|AAC73143.1| (AE000113)
 carbamoyl-phosphate synthetase, glutamine
 (small) subunit [Escherichia coli
 K12] gb|AG54334.1|AE005180_1 (AE005180)
 carbamoyl-phosphate synthetase, glutamine
 (small) subunit [Escherichia coli
 O157:H7 EDL933] dbj|BAB33458.1| (AP002550)
 carbamoyl-phosphate synthetase small subunit
 [Escherichia coli O157:H7]

#N/A

Contig9 from
 SEQ ID n° 8270 PL-1508.2 2817970 to m 86%
 -----2819133

SEQ ID n° 8271	PL-1507.2	Contig9 from 2819569 to 2820390	m	88%	<p>sp P04036 DAPB_ECOLI DIHYDRODIPICOLINATE REDUCTASE (DHPR) pir RDECD... dihydrodipicolinate reductase (EC 1.3.1.26) - Escherichia coli pdb 1ARZ D Chain D, Escherichia Coli Dihydrodipicolinate Reductase In Complex With Nadh And 2,6 Pyridine Dicarboxylate pdb 1ARZ B Chain B, Escherichia Coli Dihydrodipicolinate Reductase In Complex With Nadh And 2,6 Pyridine Dicarboxylate pdb 1ARZ C Chain C, Escherichia Coli Dihydrodipicolinate Reductase In Complex With Nadh And 2,6 Pyridine Dicarboxylate pdb 1DIR Mol_id: 1; Molecule: Dihydrodipicolinate Reductase; Chain: Null; EC: 1.3.1.26; Engineered: Yes pdb 1DRW Escherichia Coli DhpRNHDH COMPLEX pdb 1DRU Escherichia Coli DhpRNADH COMPLEX pdb 1DRV Escherichia Coli DhpACNADH COMPLEX pdb 1ARZ A Chain A, Escherichia Coli Dihydrodipicolinate Reductase In Complex With Nadh And 2,6 Pyridine Dicarboxylate gb AA23666.1 (M10611) dihydrodipicolinate reductase [Escherichia coli] dbj BAA01309.1 (D10483) dihydrodipicolinate reductase [Escherichia coli]</p>	#N/A
SEQ ID n° 8272	PL-6073.1	Contig9 from 2820660 to 2820821	m	No Hits found	<p>sp P43420 MTB6_BACSP MODIFICATION METHYLASE BSP61 (CYTOSINE-SPECIFIC METHYLTRANSFERASE BSP61) (M.BSP61) pir T40138 site-specific DNA- methyltransferase (cytosine-specific) (EC 2.1.1.73) - Bacillus sp emb CAA57293.1 (X81638) site-specific DNA-methyltransferase (cytosine-specific) [Bacillus sp.] prf 2115268B methyltransferase Bsp61M [Bacillus sp.]</p>	#N/A
SEQ ID n° 8273	PL-1506.1	Contig9 from 2821161 to 2822300	p	22%		

SEQ ID n-599

SEQ ID n° 8274	PL-1505.1	Contig9 from 2822293 to 2823288	p	No Hits found		SEQ ID n-998
SEQ ID n° 8275	PL-1504.1	Contig9 from 2823343 to 2824911	p	24%	gb AAK01531.1 (AF241171) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-997
SEQ ID n° 8276	PL-1503.1	Contig9 from 2824896 to 2825927	p	11%	gb AAK01530.1 (AF241171) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-996
SEQ ID n° 8277	PL-6078.1	Contig9 from 2826089 to 2826202	m	67%	sp P33997 ALPA_ECOLI_PROPHAGE_CP4-57 REGULATORY PROTEIN ALPA pir B65041 prophage cp4-57 regulatory protein Alpa - Escherichia coli (strain K-12) gb AAA18418.1 (U03737) Alpa [Escherichia coli] gb AAA79793.1 (U36840) Alpa [Escherichia coli] gb AAC75672.1 (AE000348) prophage CP4-57 regulatory protein alpa [Escherichia coli K12]	#N/A
SEQ ID n° 8278	PL-6079.1	Contig9 from 2826265 to 2826528	p	33%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]	#N/A
SEQ ID n° 8279	PL-1502.1	Contig9 from 2826541 to 2827494	m	83%	sp P22565 LYTB_ECOLI_LYTB_PROTEIN pir [JHE0403 lytB protein - Escherichia coli emb CAA38707.1 (X54945) ORF 2 [Escherichia coli] dbj BAA01307.1 (D10483) hypothetical 34.8K protein(PIR:JHE0403) [Escherichia coli] gb AAC73140.1 (AE000113) control of stringent response; involved in penicillin tolerance [Escherichia coli K12]	SEQ ID n-995
SEQ ID n° 8280	PL-3624.1	Contig9 from 2827475 to 2827945	m	71%	gb AAG54331.1 AE005179_8 (AE005179) control of stringent response; involved in penicillin tolerance [Escherichia coli O157:H7] gb AAF19641.1 AF201388_3 (AF201388) FkbB-type peptidyl-propyl cis-trans isomerase [Klebsiella pneumoniae]	SEQ ID n-2820

SEQ ID n° 8281	PL-3625.1	Contig9 from 2827951 to 2828454	m	80%	gb AAG54329.1 AE005179_6 (AE005179) prolipoprotein signal peptidase (spase II) [Escherichia coli O157:H7]	SEQ ID n-2821
SEQ ID n° 8282	PL-1501.1	Contig9 from 2828454 to 2831267	m	88%	sp P00956 SYI_ECOLI ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS) pir SYECIT isoleucine--trna ligase (EC 6.1.1.5) - Escherichia coli gb AAC73137.1 (AE000113) isoleucine trna synthetase [Escherichia coli K12]	SEQ ID n-994
SEQ ID n° 8283	PL-1500.1	Contig9 from 2831292 to 2832236	m	78%	sp P08391 RIBF_ECOLI RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBF [INCLUDES: RIBOFLAVIN KINASE (FLAVOKINASE); FMN ADENYLYLTRANSFERASE (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE)] pir QOECIL conserved hypothetical protein, 34.6K (tpst-iles intergenic region) Escherichia coli gb AAC73136.1 (AE000113) putative regulator [Escherichia coli K12] gb AAG54327.1 AE005179_4 (AE005179) putative regulator [Escherichia coli O157:H7] sp P02378 RS20_ECOLI 30S RIBOSOMAL PROTEIN S20 pir R3EC20 ribosomal protein S20/L26 [validated] - Escherichia coli dbj BAA01302.1 (D10483) ribosomal protein S20 [Escherichia coli] emb CAA27968.1 (X04382) ribosomal protein S20 [Escherichia coli] gb AAC73134.1 (AE000113) 30S ribosomal subunit protein S20 [Escherichia coli K12]	SEQ ID n-593
SEQ ID n° 8284	PL-6082.1	Contig9 from 2832587 to 2832850	p	83%	gb AAG54325.1 AE005179_2 (AE005179) 30S ribosomal subunit protein S20 [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8285	PL-1499.1	Contig9 from 2832921 to 2833835	m	81%	pir QOEC3R transcription activator nhaR - Escherichia coli gb AAC73131.1 (AE000112) transcriptional activator of nhaA [Escherichia coli K12]	SEQ ID n-590

Contig9 from SEQ ID n° 8286 PL-1498.1	2834059 to 2835225	m	71%	pir B82177 Na+/H+ antiporter protein VC1637 [imported] - Vibrio cholerae (group -- O1 strain N16961) gb AAC33562.1 (AF051158) sodium-proton antiporter affecting protein [Vibrio cholerae] gb AAF94778.1 (AE004240) Na+/H+ antiporter protein [Vibrio cholerae]	SEQ ID n-589
Contig9 from SEQ ID n° 8287 PL-6083.1	2835474 to 2835899	m	No Hits found	sp P40739 PTEA_BACSU PTS SYSTEM, BETA-GLUCOSIDES SPECIFIC IIABC COMPONENT (EIIABC-BGL) (BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EII-BGL) pir I40406 beta-glucoside permease - Bacillus subtilis emb CAA84286.1 (Z34526) beta- glucoside permease [Bacillus subtilis] sp P39805 LICT_BACSU TRANSCRIPTION ANTITERMINATOR LICT pir S47216 transcription antiterminator lict - Bacillus subtilis emb CAA82194.1 (Z28340) antiterminator [Bacillus subtilis]	#N/A
Contig9 from SEQ ID n° 8288 PL-1496.2	2836340 to 2838187	m	59%	sp P26207 PTEA_ERWCH PTS SYSTEM, BETA-GLUCOSIDES SPECIFIC IIABC COMPONENT (EIIABC-BGL) (BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EII-BGL) pir B42603 beta-glucoside-specific phosphotransferase system-dependent permease - Erwinia chrysanthemi gb AAA24814.1 (M81772) beta-glucoside permease [Pectobacterium chrysanthemi]	SEQ ID n-586
Contig9 from SEQ ID n° 8290 PL-1494.1	2839844 to 2841286	p	69%	gb AAG46031.1 AF309637_1 (AF309637) 6-phospho- beta-glucosidase-like protein [Leishmania infantum]	SEQ ID n-585
Contig9 from SEQ ID n° 8291 PL-1493.1	2841362 to 2842783	p	82%		SEQ ID n-584

SEQ ID n° 8292	PL-1492.1	Contig9 from 2842812 to 2844071	p	43%	gb AAG60975.1 AF322013_94 (AF322013) ID668 [Bradyrhizobium japonicum]	SEQ ID n-593
SEQ ID n° 8293	PL-1491.1	Contig9 from 2844168 to 2845286	m	91%	gb AAG54315.1 AE005178_5 (AE005178) chaperone with DnaK; heat shock protein [Escherichia coli O157:H7]	SEQ ID n-592
SEQ ID n° 8294	PL-1489.1	Contig9 from 2845400 to 2847310	m	94%	sp Q56073 DNAK_SALTY DNAK PROTEIN [HEAT SHOCK PROTEIN 70] (HSP70) gb AB02910.1 (U58360) DnaK [Salmonella typhimurium] sp P28695 YAAH_ECOLI HYPOTHETICAL 20.1 KD PROTEIN-IN-MOG-HTGA INTERGENIC REGION (ORF5) pir E56688 protein yaaH - Escherichia coli emb CAA47931.1 (X67700) ORF5 [Escherichia coli] gb AAC73121.1 (AF000111) orf, hypothetical protein [Escherichia coli K12] gb AAG54310.1 AE005177_10 (AE005177) orf, hypothetical protein [Escherichia coli O157:H7] pir E82181 aldose 1-epimerase VC1594 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94748.1 (AE004236) aldose 1- epimerase [Vibrio cholerae] pir F82181 galactokinase VC1595 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94749.1 (AE004236) galactokinase [Vibrio cholerae] pir G82181 galactose-1-phosphate uridylyltransferase VC1596 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94750.1 (AE004236) galactose-1-phosphate uridylyltransferase [Vibrio cholerae] ref NP_066722.1 hypothetical protein [Agrobacterium rhizogenes] dbj BAB16260.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]	SEQ ID n-579
SEQ ID n° 8295	PL-3628.1	Contig9 from 2847740 to 2848309	p	78%	gb AAG54310.1 AE005177_10 (AE005177) orf, hypothetical protein [Escherichia coli O157:H7] pir E82181 aldose 1-epimerase VC1594 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94748.1 (AE004236) aldose 1- epimerase [Vibrio cholerae] pir F82181 galactokinase VC1595 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94749.1 (AE004236) galactokinase [Vibrio cholerae] pir G82181 galactose-1-phosphate uridylyltransferase VC1596 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94750.1 (AE004236) galactose-1-phosphate uridylyltransferase [Vibrio cholerae] ref NP_066722.1 hypothetical protein [Agrobacterium rhizogenes] dbj BAB16260.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]	SEQ ID n-2822
SEQ ID n° 8296	PL-1487.1	Contig9 from 2848387 to 2849448	m	64%	gb AAG54310.1 AE005177_10 (AE005177) orf, hypothetical protein [Escherichia coli O157:H7] pir E82181 aldose 1-epimerase VC1594 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94748.1 (AE004236) aldose 1- epimerase [Vibrio cholerae] pir F82181 galactokinase VC1595 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94749.1 (AE004236) galactokinase [Vibrio cholerae] pir G82181 galactose-1-phosphate uridylyltransferase VC1596 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94750.1 (AE004236) galactose-1-phosphate uridylyltransferase [Vibrio cholerae] ref NP_066722.1 hypothetical protein [Agrobacterium rhizogenes] dbj BAB16260.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]	SEQ ID n-577
SEQ ID n° 8297	PL-1486.1	Contig9 from 2849481 to 2850671	m	74%	gb AAG54310.1 AE005177_10 (AE005177) orf, hypothetical protein [Escherichia coli O157:H7] pir E82181 aldose 1-epimerase VC1594 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94748.1 (AE004236) aldose 1- epimerase [Vibrio cholerae] pir F82181 galactokinase VC1595 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94749.1 (AE004236) galactokinase [Vibrio cholerae] pir G82181 galactose-1-phosphate uridylyltransferase VC1596 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94750.1 (AE004236) galactose-1-phosphate uridylyltransferase [Vibrio cholerae] ref NP_066722.1 hypothetical protein [Agrobacterium rhizogenes] dbj BAB16260.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]	SEQ ID n-576
SEQ ID n° 8298	PL-1485.1	Contig9 from 2850664 to 2851737	m	84%	gb AAG54310.1 AE005177_10 (AE005177) orf, hypothetical protein [Escherichia coli O157:H7] pir E82181 aldose 1-epimerase VC1594 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94748.1 (AE004236) aldose 1- epimerase [Vibrio cholerae] pir F82181 galactokinase VC1595 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94749.1 (AE004236) galactokinase [Vibrio cholerae] pir G82181 galactose-1-phosphate uridylyltransferase VC1596 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94750.1 (AE004236) galactose-1-phosphate uridylyltransferase [Vibrio cholerae] ref NP_066722.1 hypothetical protein [Agrobacterium rhizogenes] dbj BAB16260.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]	SEQ ID n-575
SEQ ID n° 8299	PL-1484.2	Contig9 from 2852146 to 2853624	m	61%	gb AAG54310.1 AE005177_10 (AE005177) orf, hypothetical protein [Escherichia coli O157:H7] pir E82181 aldose 1-epimerase VC1594 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94748.1 (AE004236) aldose 1- epimerase [Vibrio cholerae] pir F82181 galactokinase VC1595 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94749.1 (AE004236) galactokinase [Vibrio cholerae] pir G82181 galactose-1-phosphate uridylyltransferase VC1596 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94750.1 (AE004236) galactose-1-phosphate uridylyltransferase [Vibrio cholerae] ref NP_066722.1 hypothetical protein [Agrobacterium rhizogenes] dbj BAB16260.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]	#N/A

SEQ ID n° 8300	PL-1483.2	Contig9 from 2853564 to 2854448	m 59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]	#N/A
SEQ ID n° 8301	PL-1482.1	Contig9 from 2854436 to 2855377	m 45%	ref NP_066722.1 hypothetical protein [Agrobacterium rhizogenes] dbj BAB16260.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]	SEQ ID n~572
SEQ ID n° 8302	PL-1481.1	Contig9 from 2855383 to 2856489	m 68%	ref NP_066721.1 similar to orf300 gene (putative AAA-family ATPase gene) in Escherichia coli [Agrobacterium rhizogenes] dbj BAB16259.1 (AP002086) similar to orf300 gene (putative AAA-family ATPase gene) in Escherichia coli [Agrobacterium rhizogenes] sp P42517 CHMU_ERWHE MONOFUNCTIONAL CHORISMATE MUTASE PRECURSOR (CM-F) pir A40607 monofunctional chorismate mutase AroQ - Erwinia herbicola gb AAV73360.1 (M95628) chorismate mutase [Erwinia herbicola]	SEQ ID n~571
SEQ ID n° 8303	PL-3629.1	Contig9 from 2856925 to 2857485	m 55%	sp P28694 MOG_ECOLI MOLYBDOPTERIN BIOSYNTHESIS MOG PROTEIN pir B56688 molybdopterin biosynthesis protein mog - Escherichia coli emb CAA47930.1 (X67700) ORF1 [Escherichia coli] gb AAC73120.1 (AE000111) required for the efficient incorporation of molybdate into molybdoproteins [Escherichia coli K12]	SEQ ID n~2823
SEQ ID n° 8304	PL-3630.1	Contig9 from 2857623 to 2858198	m 90%	gb AAG54309.1 AE005177_9 (AE005177) required for the efficient incorporation of molybdate into molybdoproteins [Escherichia coli O157:H7]	SEQ ID n~2825

SEQ ID n° 8305 PL-1480.1	Contig9 from 2858280 to 2859233	m	85%	sp P30148 TALB_ECOLI TRANSALDOLASE B
				pir S40535.transaldolase (EC 2.2.1.2) B - Escherichia coli dbj BAA01290.1 (D10483) transaldolase homolog (SWISS:PI5019) [Escherichia coli] gb AAC73119.1 (AE000111) transaldolase B [Escherichia coli K12] gb AAB47022.1 (S80045) transaldolase B, D-sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate dihydroxyacetone transferase {EC 2.2.1.2} [Escherichia coli, K-12, Peptide, 317 aa] dbj BAA21822.1 (D13161) transaldolase [Escherichia coli] gb AAG54308.1 AE005177_8 (AE005177) transaldolase B [Escherichia coli O157:H7]
SEQ ID n° 8306 PL-1479.1	Contig9 from 2859957 to 2861168	m	41%	pir H81390 probable integral membrane protein Cj0461c [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB75099.1 (AL139075) putative integral membrane protein [Campylobacter jejuni]
				sp P11288 YAAA_ECOLI PROTEIN YAAA pir Q3ECTC yaaA protein - Escherichia coli dbj BAA01289.1 (D10483) Hypothetical protein 126: PIR:Q3ECTC [Escherichia coli] gb AAC73117.1 (AE000111) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-567
SEQ ID n° 8307 PL-1478.1	Contig9 from 2861669 to 2862445	p	70%	sp P27735 THRC_SERMA THREONINE SYNTHASE pir S16043 threonine synthase (EC 4.2.99.2) - Serratia marcescens emb CAA43214.1 (X60821) threonine synthase [Serratia marcescens] dbj BAA01222.1 (D10387) threonine synthase [Serratia marcescens]
				sp P27722 KHSE_SERMA HOMOSERINE KINASE (HK) pir C47057 homoserine kinase (EC 2.7.1.39) - Serratia marcescens emb CAA43213.1 (X60821) homoserine kinase [Serratia marcescens] dbj BAA38482.1 (D10387) homoserine kinase [Serratia marcescens]
SEQ ID n° 8308 PL-1477.1	Contig9 from 2862496 to 2863794	m	87%	
SEQ ID n° 8309 PL-1476.1	Contig9 from 2863798 to 2864727	m	82%	

SEQ ID n° 8310	PL-1475.1	Contig9 from 2864730 to 2867189	m	86%	dbj BAA38477.1 (D10386) aspartokinase I- homoserine dehydrogenase I [Serratia marcescens] sp P03026 ARCA_ECOLI AEROBIC RESPIRATION CONTROL PROTEIN ARCA (DYE RESISTANCE PROTEIN) pir JVECR dye resistance protein - Escherichia coli gb AAA23718.1 (M10044) dye [Escherichia coli] gb AAA97297.1 (U14003) alternate gene names arcA, fexA, msp, seg, sfrA; CG Site No. 831 [Escherichia coli] gb AAC77354.1 (AE000510) negative response regulator of genes in aerobic pathways, (sensors, ArcB and CpxA) [Escherichia coli K12] gb AAG59581.1 AE005671_5 (AE005671) negative response regulator of genes in aerobic pathways, (sensors, ArcB and CpxA) [Escherichia coli... Ol57:H7] sp P08367 CREA_ECOLI CREA PROTEIN pir QOECF1 creA protein - Escherichia coli gb AA24373.1 (M13608) 17 kd protein [Escherichia coli] gb AAA97293.1 (U14003) creA [Escherichia coli] gb AAC77350.1 (AE000510) orf, hypothetical protein [Escherichia coli K12] gb AAG59577.1 AE005671_1 (AE005671) orf, hypothetical protein [Escherichia coli Ol57:H7] sp P27292 ROB_ECOLI RIGHT ORIGIN-BINDING PROTEIN pir JU0158 right oriC-binding protein - Escherichia coli gb AAA24569.1 (M97495) right origin-binding protein [Escherichia coli] gb AAA97292.1 (U14003) rob [Escherichia coli] gb AAC77349.1 (AE000509) right origin-binding protein [Escherichia coli K12] gb AAG59576.1 AE005670_9 (AE005670) right origin- binding protein [Escherichia coli Ol57:H7]	SEQ ID n-964
SEQ ID n° 8311	PL-1474.1	Contig9 from 2868000 to 2868716	p	93%		
SEQ ID n° 8312	PL-3633.1	Contig9 from 2868780 to 2869265	m	82%		
SEQ ID n° 8313	PL-1473.1	Contig9 from 2869649 to 2870524	p	72%		

Contig9 from 2870521 to 2871168	m	85%	pir S56619 gpmb protein - Escherichia coli gb AAAG7291.1 (U14003) Kenn Rudd identifies as gpmb [Escherichia coli] gb AAC77348.1 (AE000509) phosphoglyceromutase 2 [Escherichia coli K12]	SEQ ID n-561
Contig9 from 2871223 to 2871753	p	64%	gb AAG59574.1 AE005670_7 (AE005670)-exf- hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-3827
Contig9 from 2871789 to 2872109	m	76%	sp P39439 TRPR_ENTAE TRP OPERON REPRESSOR pir S45254 trp operon repressor - Enterobacter aerogenes gb AAC36892.1 (L26582) tryptophan repressor [Enterobacter aerogenes] pir S56616 soluble lytic transglycosylase - Escherichia coli pir QQECW1 soluble lytic transglycosylase (EC 3.2.1.-) precursor - Escherichia coli gb AAAG7288.1 (U14003) soluble lytic transglycosylase [Escherichia coli] gb AAC77345.1 (AE000509) soluble lytic murein transglycosylase [Escherichia coli K12]	#N/A
Contig9 from 2872169 to 2874109	m	69%	gb AAG59572.1 AE005670_5 (AE005670) soluble lytic murein transglycosylase [Escherichia coli O157:H7]	SEQ ID n-360
Contig9 from 2874582 to 2876249	p	90%	gb AAK02509.1 (AE006078) unknown [Pasteurella multocida]	SEQ ID n-359
Contig9 from 2876288 to 2877028	m	46%	pir H72342 ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8) gb AAD35787.1 AE001742_2 (AE001742) ABC transporter, ATP-binding protein [Thermotoga maritima]	SEQ ID n-957
Contig9 from 2877709 to 2878965	m	85%	pir S56614 transcription regulator nadR - Escherichia coli gb AAAG7286.1 (U14003) nadR [Escherichia coli] gb AAC77343.1 (AE000509) probable nadAB transcriptional regulator [Escherichia coli K12]	SEQ ID n-556

812

SEQ ID n° 8321	PL-1467.1	Contig9 from 2878958 to 2880340	m	96%	sp P24554 RADA_ECOLI DNA REPAIR PROTEIN RADA (DNA REPAIR PROTEIN SMS) pir JCI1417 DNA repair protein sms - Escherichia coli gb AAA97285.1 (U14003) sms [Escherichia coli] emb CAA44856.1 (X63155) sms [Escherichia coli] gb AAC44380.1 (U59449) Rada [Escherichia coli] gb AAC77342.1 (AE000509) probable ATP-dependent protease [Escherichia coli K12] SEQ ID n-955
SEQ ID n° 8322	PL-1466.1	Contig9 from 2880487 to 2881464	m	82%	sp P06862 SERB_ECOLI PHOSPHOSERINE PHOSPHATASE (PSP) (O-PHOSPHOSERINE PHOSPHOHYDROLASE) (PSPASE) pir PAECS phosphoserine phosphatase (EC 3.1.3.3) - Escherichia coli emb CAA26852.1 (X03046) phosphoserine phosphatase (EC 3.1.3.3) [Escherichia coli] gb AAA97284.1 (U14003) phosphoserine phosphatase [Escherichia coli] gb AAC77341.1 (AE000509) 3-phosphoserine phosphatase [Escherichia coli K12] gb AAG59567.1 AE005669_11 (AE005669) putative lipoate-protein ligase A [Escherichia coli O157:H7] SEQ ID n-954
SEQ ID n° 8323	PL-1465.1	Contig9 from 2881580 to 2882224	p	64%	pir P82543 outer membrane hemolysin activator protein XF2550 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85347.1 AE004062_2 (AE004062) outer membrane hemolysin activator protein [Xylella fastidiosa] SEQ ID n-953
SEQ ID n° 8324	PL-1464.1	Contig9 from 2882961 to 2884652	p	57%	pir C83339 hypothetical protein PA2462 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05850.1 AE004673_10 (AE004673) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-952
SEQ ID n° 8325	PL-1463.3	Contig9 from 2884711 to 2898459	p	29%	pir A82955 hypothetical protein PA5527 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08912.1 AE004965_4 (AE004965) hypothetical protein [Pseudomonas aeruginosa] #N/A
SEQ ID n° 8326	PL-6677.1	Contig9 from 2898468 to 2898887	p	56%	pir A82955 hypothetical protein PA5527 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG08912.1 AE004965_4 (AE004965) hypothetical protein [Pseudomonas aeruginosa] #N/A

SEQ ID n° 8336	PL-3211.2	Contig9 from 2905116 to 2906141	p	21%	dbj BAB07424.1 (AP001519) transposase (12) [Bacillus halodurans]	#N/A
SEQ ID n° 8337	PL-6469.1	Contig9 from 2906177 to 2906473	p	No Hits found		#N/A
SEQ ID n° 8338	PL-773.1	Contig9 from 2906637 to 2908436	p	22%	pir F81045 hemagglutinin/hemolysin-related protein NMB1768 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF42109.1 (AE002526) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	SEQ ID n-3608
SEQ ID n° 8339	PL-6467.1	Contig9 from 2908433 to 2908663	p	No Hits found		#N/A
SEQ ID n° 8340	PL-774.1	Contig9 from 2908998 to 2911820	p	40%	pir F81045 hemagglutinin/hemolysin-related protein NMB1768 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF42109.1 (AE002526) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	SEQ ID n-3609
SEQ ID n° 8341	PL-6464.1	Contig9 from 2911985 to 2912137	p	No Hits found		#N/A
SEQ ID n° 8342	PL-3746.1	Contig9 from 2912134 to 2912649	p	No Hits found		SEQ ID n-2927
SEQ ID n° 8343	PL-3745.1	Contig9 from 2913015 to 2913374	p	No Hits found		SEQ ID n-2926
SEQ ID n° 8344	PL-6463.1	Contig9 from 2915075 to 2915326	m	75%	gb AAG57523.1 AE005470_10 (AE005470) putative virulence protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8345	PL-775.1	Contig9 from 2915459 to 2916082	m	No Hits found		SEQ ID n-3610

SEQ ID n° 8345	PL-6462.1	Contig9 from 2916100 to 2916252	m	No Hits found	ref NP_052816.1 pX01-120 [Bacillus anthracis] pir H59105 hypothetical protein pX01-120 - Bacillus anthracis virulence plasmid pX01 gb AAD32424.1 AAD32424 (AF065404) pX01-120 [Bacillus anthracis]	#N/A
SEQ ID n° 8347	PL-6460.1	Contig9 from 2916407 to 2916565	m	48%		#N/A
SEQ ID n° 8348	PL-6459.1	Contig9 from 2916643 to 2916801	m	No Hits found		#N/A
SEQ ID n° 8349	PL-776.1	Contig9 from 2917157 to 2918233	p	No Hits found		SEQ ID n-9611
SEQ ID n° 8350	PL-777.1	Contig9 from 2918237 to 2919016	p	No Hits found		SEQ ID n-9612
SEQ ID n° 8351	PL-778.1	Contig9 from 2919511 to 2920695	p	No Hits found		SEQ ID n-9613
SEQ ID n° 8352	PL-3741.1	Contig9 from 2920656 to 2921198	p	51%	pir E82459 probable acetyltransferase VCA0436 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAP96342.1 (AE004377) acetyltransferase, putative [Vibrio cholerae] pir E83595 cystathionine beta-synthase PA0399 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03788.1 AE004477_5 (AE004477) cystathionine beta-synthase [Pseudomonas aeruginosa]	SEQ ID n-2924
SEQ ID n° 8353	PL-779.1	Contig9 from 2921528 to 2922895	p	70%	pir S52983 probable cystathionine gamma-lyase (EC 4.4.1.1) - Erwinia herbicola (fragment) gb AA064984.1 (M87280) transcription must start in the vector; putative ORF12 [Erwinia herbicola]	SEQ ID n-3614
SEQ ID n° 8354	PL-780.1	Contig9 from 2922913 to 2924067	p	83%		SEQ ID n-3616

Contig9 from 2924158 to 2924874	<p>sp P09743 DEOD_ECOLI PURINE NUCLEOSIDE PHOSPHORYLASE (INOSINE PHOSPHORYLASE) (PNP) pir A27854 purine-nucleoside phosphorylase (EC 2.4.2.1) - Escherichia coli gb AAA24401.1 (M60917) purine nucleoside phosphorylase [Escherichia coli] gb AAA97280.1 (U14003) purine-nucleoside phosphorylase [Escherichia coli] gb AAC77337.1 (AE000508) purine- nucleoside phosphorylase [Escherichia coli K12] gb AAG59565.1 AE005669_9 (AE005669) purine- nucleoside phosphorylase [Escherichia coli O157:H7]</p>	SEQ ID n-3617
Contig9 from 2924957 to 2926180	<p>sp P07651 DEOB_ECOLI PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE) pir S56607 phosphopentomutase (EC 5.4.2.7) deoB - Escherichia coli gb AAA97279.1 (U14003) phosphopentomutase [Escherichia coli] gb AAC77336.1 (AE000508) phosphopentomutase [Escherichia coli K12] gb AAG59564.1 AE005669_8 (AE005669) phosphopentomutase [Escherichia coli O157:H7]</p>	SEQ ID n-3618
Contig9 from 2926380 to 2927159	<p>sp P00882 DEOC_ECOLI DEOXYRIBOSE-PHOSPHATE ALDOLASE (PHOSPHODEOXYRIBOALDOLASE) (DEOXYRIBOALDOLASE) pir ADEC deoxyribose- phosphate aldolase (EC 4.1.2.4) - Escherichia coli gb AAA97277.1 (U14003) deoxyribose- phosphate aldolase [Escherichia coli] gb AAC77334.1 (AE000508) 2-deoxyribose-5- phosphate aldolase [Escherichia coli K12]</p>	SEQ ID n-3619
Contig9 from 2927486 to 2928763	<p>pir H82087 NupC family protein VC2352 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95495.1 (AE004305) NupC family protein [Vibrio cholerae]</p>	SEQ ID n-3620

SEQ ID n° 8359	PL-785.1	Contig9 from 2929076 to 2929771	p	56%	sp P46144 YEDJ_ECOLI_HYPOTHETICAL_25.9_KDA PROTEIN IN DCM-SERU INTERGENIC REGION pir F64960 membrane protein yedJ - Escherichia coli dbj BAAI5796.1 (D90835) ORF_ID:0344#10; similar to [SwissProt Accession Number P46144] [Escherichia coli] gb AAC75028.1 (AE000288)orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-3621
SEQ ID n° 8360	PL-786.1	Contig9 from 2930005 to 2930778	m	76%	sp P39408 YJJV_ECOLI_PUTATIVE_DEOXYRIBONUCLEASE YJJV	SEQ ID n-3622
SEQ ID n° 8361	PL-6456.1	Contig9 from 2930790 to 2930927	m	No Hits found	#N/A	
SEQ ID n° 8362	PL-6455.1	Contig9 from 2931241 to 2931624	p	57%	gb AAC38623.1 (AF046867) insecticidal toxin complex protein Tcaa [Photorhabdus luminescens]	#N/A
SEQ ID n° 8363	PL-787.1	Contig9 from 2931689 to 2936146	p	95%	gb AAC38625.1 (AF046867) insecticidal toxin complex protein Tcac [Photorhabdus luminescens]	SEQ ID n-3623
SEQ ID n° 8364	PL-788.1	Contig9 from 2936440 to 2938032	m	95%	gb AAC38626.1 (AF046867) insecticidal toxin complex protein Tcaz [Photorhabdus luminescens]	SEQ ID n-3624
SEQ ID n° 8365	PL-6450.1	Contig9 from 2938661 to 2938852	m	No Hits found	#N/A	
SEQ ID n° 8366	PL-789.1	Contig9 from 2939099 to 2939767	m	82%	pir G82578 conserved hypothetical protein XF2273 [imported] - Xylella fastidiosia (strain 9a5c) gb AAF85072.1 AE004039_7 (AE004039) conserved hypothetical protein [Xylella fastidiosia] pir D64895 probable membrane protein b1433 - Escherichia coli gb AAC74515.1 (AE000240) putative membrane transport protein [Escherichia coli K12]	SEQ ID n-3625
SEQ ID n° 8367	PL-790.1	Contig9 from 2940039 to 2941244	p	73%		SEQ ID n-3627

SEQ ID n° 8368	PL-791.1	Contig9 from 2941277 to 2942398	P	38%	pir H82161 hypothetical protein VC1748 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94898.1 (AE004252) hypothetical protein [Vibrio cholerae] SEQ ID n-3628
SEQ ID n° 8369	PL-792.1	Contig9 from 2942398 to 2943543	P	52%	pir A82162 hypothetical protein VC1749 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94899.1 (AE004252) hypothetical protein [Vibrio cholerae] SEQ ID n-3629
SEQ ID n° 8370	PL-793.1	Contig9 from 2943540 to 2944661	P	51%	pir B82162 hypothetical protein VC1750 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94900.1 (AE004252) hypothetical protein [Vibrio cholerae] SEQ ID n-3630
SEQ ID n° 8371	PL-794.1	Contig9 from 2945494 to 2946075	P	43%	gb AAG55653.1 AE005303_9 (AE005303) putative pilin subunit [Escherichia coli O157:H7] sp P33342 YEH_C_ECOLI HYPOTHETICAL 26.6 KD FIMBRIAL CHAPERONE IN GATY-MRP INTERGENIC REGION PRECURSOR pir E64978 hypothetical 26.6 kd fimbrial chaperone in mrp 5' region - Escherichia coli (strain K-12) gb AA60474.1 (U00007) yehC [Escherichia coli] gb AAC75171.1 (AE000300) putative chaperone [Escherichia coli K12] prf 2014253C yehC gene [Escherichia coli] sp P33341 YEH_C_ECOLI HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GATY-MRP INTERGENIC REGION PRECURSOR pir D64978 probable outer membrane usher protein precursor (mrp 5' region) Escherichia coli (strain K-12) gb AA60473.1 (U00007) yehB [Escherichia coli] gb AAC75170.1 (AE000300) putative outer membrane protein [Escherichia coli K12] prf 2014253B yehB gene [Escherichia coli] SEQ ID n-3633
SEQ ID n° 8372	PL-795.1	Contig9 from 2946143 to 2946841	P	61%	
SEQ ID n° 8373	PL-796.1	Contig9 from 2946867 to 2949341	P	62%	

Contig9 from	Contig9 from	Contig9 from	Contig9 from	Contig9 from	Contig9 from
2949353 to 2950444	2951712 to 2952503	2952709 to 2954130	2954117 to 2955253	2955240 to 2956460	2956671 to 2957591
SEQ ID n° 8374 PL-797.1	SEQ ID n° 8375 PL-798.1	SEQ ID n° 8376 PL-799.1	SEQ ID n° 8377 PL-800.1	SEQ ID n° 8378 PL-801.1	SEQ ID n° 8379 PL-802.1
34%	55%	60%	47%	43%	51%
<p>sp P33340 YEHA_ECOLI HYPOTHETICAL 36.9 KDA</p> <p>PROTEIN IN GATY-MRP INTERGENIC REGION</p> <p>PRECURSOR pir C64978 hypothetical 36.9 KD</p> <p>protein in mrp 5' region precursor -</p> <p>Escherichia coli (strain K-12) gb AA60472.1 </p> <p>(U00007) yehA [Escherichia coli]</p> <p>dbj BAAL5974.1 (D90848) ORF_ID:0359#20-similar</p> <p>to [SwissProt Accession Number</p> <p>P33340] [Escherichia coli] gb AAC75169.1 </p> <p>(AE000300) putative type-1 fimbrial protein</p> <p>[Escherichia coli K12] prf 2014253A.yehA gene</p> <p>[Escherichia coli]</p> <p>SEQ ID n-3634</p>	<p>gb AAG58719.1 AE005584_1 (AE005584) putative ATP</p> <p>binding protein [Escherichia coli O157:H7]</p> <p>pir C81103 alginate O-acetylation protein AlgI,</p> <p>probable NME1273 [imported] -</p> <p>Neisseria meningitidis (group B strain MD58)</p> <p>gb AAP41650.1 (AE002475) alginate O-acetylation</p> <p>protein AlgI, putative [Neisseria</p> <p>meningitidis MCS8]</p> <p>pir AB1839 probable periplasmic protein NMA1479</p> <p>[imported] - Neisseria meningitidis</p> <p>(group A strain Z2491) emb CAB84712.1 </p> <p>(AL162756) putative periplasmic protein</p> <p>[Neisseria meningitidis Z2491]</p> <p>pir B81839 probable periplasmic protein NMA1480</p> <p>[imported] - Neisseria meningitidis</p> <p>(group A strain Z2491) emb CAB84713.1 </p> <p>(AL162756) putative periplasmic protein</p> <p>[Neisseria meningitidis Z2491]</p> <p>SEQ ID n-3635</p>	<p>gb AAG31201.1 AF020810_2 (AF020810) Mig-14</p> <p>[Salmonella enterica]</p> <p>SEQ ID n-3641</p>			

820

SEQ ID n° 8380	PL-803.1	Contig9 from 2957681 to 2959018	m	89%	sp P46858 GNTU_ECOLI LOW-AFFINITY GLUCONATE TRANSPORTER (GLUCONATE PERMEASE) (GNT-I SYSTEM) pir JJC4989 gluconate permease component U - Escherichia coli dbj BAAL2326.1 (D84362) low affinity gluconate permease [Escherichia coli] gb AAG58545.1 AE005567_6 (AE005567) low affinity gluconate permease [Escherichia coli O157:H7] sp P46859 GNTK_ECOLI THERMORESISTANT GLUCONOKINASE (GLUCONATE KINASE 2) dbj BAAL2325.1 (D84362) thermoresistant gluconokinase [Escherichia coli] sp P46860 GNTU_ECOLI GLUCONATE UTILIZATION SYSTEM GNT-I TRANSCRIPTIONAL REPRESSOR dbj BAAL2324.1 (D84362) repressor [Escherichia coli] SEQ ID n-3642
SEQ ID n° 8381	PL-3739.1	Contig9 from 2959018 to 2959557	m	79%	sp P46860 GNTU_ECOLI GLUCONATE UTILIZATION SYSTEM GNT-I TRANSCRIPTIONAL REPRESSOR dbj BAAL2324.1 (D84362) repressor [Escherichia coli] SEQ ID n-2922
SEQ ID n° 8382	PL-804.1	Contig9 from 2959726 to 2960721	m	82%	sp P46860 GNTU_ECOLI GLUCONATE UTILIZATION SYSTEM GNT-I TRANSCRIPTIONAL REPRESSOR dbj BAAL2324.1 (D84362) repressor [Escherichia coli] SEQ ID n-3643
SEQ ID n° 8383	PL-3737.1	Contig9 from 2967190 to 2967633	p	No Hits found	sp P46860 GNTU_ECOLI GLUCONATE UTILIZATION SYSTEM GNT-I TRANSCRIPTIONAL REPRESSOR dbj BAAL2324.1 (D84362) repressor [Escherichia coli] SEQ ID n-2920
SEQ ID n° 8384	PL-771.2	Contig9 from 2967709 to 2969298	p	87%	gb AAG59203.1 AE005632_4 (AE005632) phosphoribosylaminoimidazolecarboxamide formyltransferase = AICAR formyltransferase; IMP cyclohydrolase [Escherichia coli O157:H7] gb AAG59202.1 AE005632_3 (AE005632) phosphoribosylglycinamide synthetase = GAR synthetase [Escherichia coli O157:H7] SEQ ID n-3606
SEQ ID n° 8385	PL-770.1	Contig9 from 2969320 to 2970603	p	83%	gb AAG59202.1 AE005632_3 (AE005632) phosphoribosylglycinamide synthetase = GAR synthetase [Escherichia coli O157:H7] SEQ ID n-3605
SEQ ID n° 8386	PL-769.1	Contig9 from 2970622 to 2971326	m	58%	gb AAG59198.1 AE005631_13 (AE005631) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3603

SEQ ID n° 8387	PL-6426.1	Contig9 from 2971332 to 2971604	m	89%	sp P02342 DBHA_ECOLI DNA-BINDING PROTEIN HU- ALPHA (NS2) (HU-2) pir DNECS2 DNA-binding protein HU-2 - Escherichia coli emb CAA29412.1 (X05994) HU 2-protein (AA 1-90) [Escherichia coli] gb AAC43098.1 (U00006) histonelike DNA- binding protein HU-alpha (NS2) (HU-2) [Escherichia coli] gb AAC76974.1 (AE000473) DNA-binding protein HU-alpha (HU-2) [Escherichia coli K12] gb AAG59197.1 (AE005631_12 (AE005631) DNA-binding protein HU-alpha (HU-2) [Escherichia coli] O157:H7	#N/A
SEQ ID n° 8388	PL-3736.1	Contig9 from 2971791 to 2972381	m	87%	gb AAF33519.1 (AF170176) 95% identity over 196 amino acids with E. coli hypothetical 22.6 kD protein in heme-hupa intergenic region (yJag) (SW:P32680) [Salmonella typhimurium LT2]	SEQ ID n-2919
SEQ ID n° 8389	PL-768.1	Contig9 from 2972458 to 2973126	m	53%	pir A65207 hypothetical 24.9 kD protein in heme- hupa intergenic region - Escherichia coli (strain K-12) gb AAC43096.1 (U00006) similar to O.berteriana mitochon. protein involved in cytochrome c biogenesis [Escherichia coli] gb AAC76972.1 (AE000473) endonuclease V (deoxyinosine 3'endonuclease) [Escherichia coli K12]	SEQ ID n-3602
SEQ ID n° 8390	PL-767.1	Contig9 from 2973131 to 2974195	m	91%	sp P29680 DCUP_ECOLI UROPORPHYRINOGEN DECARBOXYLASE (URO-D) (UPD) pir H65206 uroporphyrinogen decarboxylase (EC 4.1.1.37) - Escherichia coli gb AAC76971.1 (AE000473) uroporphyrinogen decarboxylase [Escherichia coli K12]	SEQ ID n-3601
SEQ ID n° 8391	PL-766.1	Contig9 from 2974308 to 2975081	m	79%	gb AAG59193.1 (AE005631_8 (AE005631) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-3600

Contig9 from SEQ ID n° 8392 PL-765.1 2975366 to 2976028	p 67%	pir D82139 conserved hypothetical protein VC1940 [imported] - Vibrio cholerae (group O1 strain N1961) gb AAF95088.1 (AE004269) conserved hypothetical protein [Vibrio cholerae] SEQ ID n-3599
Contig9 from SEQ ID n° 8393 PL-764.1 2976328 to 2978265	p 87%	sp P30136 THIC_ECOLI THIAMINE BIOSYNTHESIS PROTEIN THIC pir E65206 thiamin biosynthesis protein thic - Escherichia coli gb AAC43092.1 (U00006) CG Site No. 115 [Escherichia coli] gb AAC76968.1 (AE000473) thiamin biosynthesis, pyrimidine moiety [Escherichia coli K12] SEQ ID n-3598
Contig9 from SEQ ID n° 8394 PL-762.1 2978249 to 2978899	p 71%	sp P30137 THIE_ECOLI THIAMINE-PHOSPHATE PYROPHOSPHORYLASE (TMP PYROPHOSPHORYLASE) (TMP-PPASE) (THIAMINE-PHOSPHATE SYNTHASE) pir S35118 thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) thie - Escherichia coli gb AAC43091.1 (U00006) thie [Escherichia coli] gb AAB95617.1 (M88701) thie [Escherichia coli] gb AAC76967.1 (AE000473) thiamin biosynthesis, thiazole moiety [Escherichia coli K12] SEQ ID n-3597
Contig9 from SEQ ID n° 8395 PL-761.1 2978910 to 2979659	p 74%	sp P30138 THIF_ECOLI THIF PROTEIN gb AAG59188.1 AE005631.3 (AE005631) thiamin biosynthesis, probable sulfur donor [Escherichia coli O157:H7] SEQ ID n-3596
Contig9 from SEQ ID n° 8396 PL-6424.1 2979656 to 2979856	p 56%	pir D49695 4-methyl-5- (beta- hydroxyethyl)thiazole monophosphate synthesis protein Thig - Escherichia coli gb AAD48429.1 AF154064_1 (AF154064) Thih [Salmonella typhimurium] gb AAF33524.1 (AF170176) 89% identity over 377 amino acids with E. coli THIH (SW:P30140) #N/A
Contig9 from SEQ ID n° 8397 PL-760.1 2979858 to 2980625	p 76%	
Contig9 from SEQ ID n° 8398 PL-759.1 2980673 to 2981764	p 77%	gb AAD48429.1 AF154064_1 (AF154064) Thih [Salmonella typhimurium] gb AAF33524.1 (AF170176) 89% identity over 377 amino acids with E. coli THIH (SW:P30140) [Salmonella typhimurium LT2] SEQ ID n-3595

SEQ ID n° 8399	PL-3735.1	Contig9 from 2982169 to 2982645	p	No Hits found	SEQ ID n-2918
SEQ ID n° 8400	PL-3734.1	Contig9 from 2982957 to 2983442	p	No Hits found	SEQ ID n-2917
SEQ ID n° 8401	PL-758.1	Contig9 from 2983476 to 2984501	m	21%	SEQ ID n-3592
dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]					
ref NP_012318.1 YJ1217wp [Saccharomyces cerevisiae] sp P40893 YJV7_YEAST HYPOTHETICAL 22.0 KD PROTEIN IN HXT11-HXT8 INTERGENIC REGION					
SEQ ID n° 8402	PL-757.1	Contig9 from 2984729 to 2985310	m	64%	SEQ ID n-3591
pir S50710 hypothetical protein YJL217w - Yeast (Saccharomyces cerevisiae) emb CAA83993.1 (Z34098) ORF [Saccharomyces cerevisiae] emb CAA89514.1 (Z49492) ORF YJL217w [Saccharomyces cerevisiae]					
pir B83205 hypothetical protein PA3532 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06920.1 AE004773_9 (AE004773) hypothetical protein [Pseudomonas aeruginosa]					
SEQ ID n° 8403	PL-756.1	Contig9 from 2985325 to 2986476	m	48%	SEQ ID n-3590
emb CAC18787.1 (AL499607) putative hydrolase [Streptomyces coelicolor]					
SEQ ID n° 8404	PL-755.1	Contig9 from 2986548 to 2987189	m	43%	SEQ ID n-3589
pir T36915 probable zinc-binding dehydrogenase Streptomyces coelicolor emb CAB46402.1 (AL096743) putative zinc-binding dehydrogenase [Streptomyces coelicolor A3(2)]					
pir G75036 4-aminobutyrate transaminase (EC 2.6.1.19) PAB2386 - Pyrococcus abyssi (strain Orsay) emb CAB50188.1 (AJ248287) 4-AMINOBUTYRATE qui se dilate AMINOTRANSFERASE (EC 2.6.1.19) [Pyrococcus abyssi]					
SEQ ID n° 8405	PL-754.1	Contig9 from 2987194 to 2988255	m	44%	SEQ ID n-3588
Contig9 from 2988255 to 2989508					
SEQ ID n° 8406	PL-753.1	Contig9 from 2988255 to 2989508	m	51%	SEQ ID n-3587

SEQ ID n° 8407	PL-752.1	Contig9 from 2990187 to 2991380	p	53%	pir E82367 probable multidrug resistance protein VC0069 [imported] - <i>Vibrio</i> cholerae (group O1 strain N16961) gb AAF93247.1 (AE004098) multidrug resistance protein, putative [<i>Vibrio cholerae</i>] pir RGE0MT regulatory protein malt - Escherichia coli gb AAC76443.1 (AE000413) positive regulator of mal regulon [Escherichia coli K12]	SEQ ID n-3586
SEQ ID n° 8408	PL-751.1	Contig9 from 2991389 to 2994103	m	79%		SEQ ID n-3585
SEQ ID n° 8409	PL-750.1	Contig9 from 2994645 to 2997047	p	82%	gb AAC58518.1 AB005564_3 (AE005564) maltodextrin phosphorylase [Escherichia coli O157:H7]	SEQ ID n-3584
SEQ ID n° 8410	PL-749.1	Contig9 from 2997057 to 2999144	p	75%	sp P15977 MALQ_EC0LI 4-ALPHA-GLUCANOTRANSFERASE (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME) pir C65137 4-alpha- glucanotransferase (EC 2.4.1.25) - Escherichia coli gb AA58214.1 (U18997) amylomaltase [Escherichia coli] gb AAC76441.1 (AE000417) 4- alpha-glucanotransferase (amylomaltase) [Escherichia coli K12]	SEQ ID n-3582
SEQ ID n° 8411	PL-748.1	Contig9 from 3000459 to 3001472	p	72%	ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-3581
SEQ ID n° 8412	PL-6412.1	Contig9 from 3002417 to 3002689	m	44%	pir H83457 hypothetical protein PA1508 [imported] - Pseudomonas aeruginosa (strain PA01) gb AA04897.1 AE004579_9 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 8413	PL-747.1	Contig9 from 3002693 to 3003838	m	28%	pir E83542 hypothetical protein PA0821 [imported] - Pseudomonas aeruginosa (strain PA01) gb AA04210.1 AE004517_5 (AE004517) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-3580

SEQ ID n° 8414	PL-746.1	Contig9 from 3003876 to 3005024	m	27%	pir E83542 hypothetical protein PA0821 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04210.1 AE004517_5 (AE004517) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-9579
SEQ ID n° 8415	PL-745.1	Contig9 from 3005059 to 3006054	m	32%	pir E83542 hypothetical protein PA0821 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04210.1 AE004517_5 (AE004517) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-9578
SEQ ID n° 8416	PL-744.1	Contig9 from 3006221 to 3007579	m	No Hits found	SEQ ID n-9577
SEQ ID n° 8417	PL-743.1	Contig9 from 3007582 to 3009723	m	41%	gb AAG54536.1 AE005199_6 (AE005199) Z0267 gene product [Escherichia coli O157:H7] SEQ ID n-9576
SEQ ID n° 8418	PL-742.1	Contig9 from 3010416 to 3012431	p	46%	pir D81308 probable integral membrane protein Cj1055c [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB73311.1 (AL139077) putative integral membrane protein [Campylobacter jejuni] sp P07622 MALG_ECOLI MALTOSE TRANSPORT SYSTEM PERMEASE PROTEIN MALG pir MMECMG maltose transport inner membrane protein malg - Escherichia coli emb CAA26628.1 (X02871) put. mal G protein (aa 1-296) [Escherichia coli] gb AAC43126.1 (U00006) maltose transport inner membrane protein [Escherichia coli] gb AAC77002.1 (AE000476) part of maltose permease, inner membrane [Escherichia coli K12] gb AAG59231.1 AE005636_3 (AE005636) part of maltose permease, inner membrane [Escherichia coli O157:H7] SEQ ID n-9574
SEQ ID n° 8419	PL-741.1	Contig9 from 3012497 to 3013387	m	92%	sp P18812 MALF_ENTAE MALTOSE TRANSPORT SYSTEM PERMEASE PROTEIN MALF pir S05332 inner membrane protein malf - Enterobacter aerogenes SEQ ID n-9573
SEQ ID n° 8420	PL-740.1	Contig9 from 3013400 to 3014956	m	80%	

SEQ ID n° 8425	PL-736.1	Contig9 from 3019337 to 3020269	p 70%	sp P03841 MALM_ECOLI_MALTOSE_OPERON_PERIPLASMIC PROTEIN_PRECURSOR_pir BVECM maltose operon periplasmic protein malm - Escherichia coli emb CAA28166.1 (X04477) periplasmic protein (AA 1-306) [Escherichia coli] gb AAC77007.1 (AE000477) periplasmic protein of mal regulon [Escherichia coli] K12] SEQ ID n-3568
SEQ ID n° 8436	PL-734.1	Contig9 from 3020945 to 3021865	p No Hits found	sp P27127 RFAB_ECOLI_LIPOPOLYSACCHARIDE_176- GALACTOSYLTRANSFERASE (UDP-D- GALACTOSE--(GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1, 3-D-GALACTOSYLTRANSFERASE) pir B42982 UDP-D- galactose--(glucosyl)lipopolysaccharide-alpha-1, 3-D-galactosyltransferase [EC 2.4.1.-) - Escherichia coli gb AAA24085.1 (M80599) lipopolysaccharide core biosynthesis protein [Escherichia coli] gb AAB18605.1 (U00039) UDP-D- galactose:(glucosyl)lipopolysaccharide -alpha-1,3-D-galactosyltransferase [Escherichia coli] gb AAC76652.1 (AE000440) UDP-D- galactose:(glucosyl)lipopolysaccharide-1,6- D-galactosyltransferase [Escherichia coli K12] SEQ ID n-3566 pir T30588 hypothetical protein PCZA361.23 - Amycolatopsis orientalis emb CAA11778.1 (AJ223998) PCZA361.23 [Amycolatopsis orientalis] SEQ ID n-3565
SEQ ID n° 8429	PL-731.1	Contig9 from 3024043 to 3024791	m No Hits found	dbj BAB02685.1 (AB018114) gb AAD14522.1-gene_id:MGF10.2-similar to unknown protein [Arabidopsis thaliana] SEQ ID n-3563
SEQ ID n° 8430	PL-730.1	Contig9 from 3024802 to 3025428	m 49%	

SEQ ID n° 8431	PL-729.1	Contig9 from 3025910 to 3027070	m	49%	dbj BAB07775.1 (AP001520) aminotransferase required for NAD biosynthesis (Nifs protein) [Bacillus halodurans]	SEQ ID n-3561
SEQ ID n° 8432	PL-728.1	Contig9 from 3027070 to 3027726	m	45%	dbj BAB14754.1 (AK023984) unnamed protein product [Homo sapiens]	SEQ ID n-3560
SEQ ID n° 8433	PL-727.1	Contig9 from 3027739 to 3028617	m	No Hits found		SEQ ID n-3559
SEQ ID n° 8434	PL-6401.1	Contig9 from 3029024 to 3029227	m	57%	emb CAB53171.1 (AL109969) putative transcriptional regulator [Yersinia pestis]	#N/A
SEQ ID n° 8435	PL-6400.1	Contig9 from 3029351 to 3029602	m	54%	ref NP_046944.1 gp48 [Bacteriophage N15] pir T13135 protein gp48 - phage N15 gb AAC19087.1 (AF064539) gp48 [Bacteriophage N15]	#N/A
SEQ ID n° 8436	PL-6399.1	Contig9 from 3029619 to 3029942	m	55%	ref NP_046945.1 gp49 [Bacteriophage N15] pir T13136 protein gp49 - phage N15 gb AAC19088.1 (AF064539) gp49 [Bacteriophage N15]	#N/A
SEQ ID n° 8437	PL-6398.1	Contig9 from 3030097 to 3030396	p	51%	emb CAB53172.1 (AL109969) hypothetical protein [Yersinia pestis]	#N/A
SEQ ID n° 8438	PL-725.1	Contig9 from 3030410 to 3034630	m	94%	sp P00577 RPOC_ECOLI DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT) pir [RNECC DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Escherichia coli emb CAA23626.1 (V00339) rpoC [Escherichia coli] gb AAC76962.1 (AE000472) RNA polymerase, beta prime subunit [Escherichia coli K12] gb AAG59184.1 AE005630.4 (AE005630) RNA polymerase, beta prime subunit [Escherichia coli O157:H7]	SEQ ID n-3558

SEQ ID n° 8439	PL-724.1	Contig9 from 3034761 to 3038789	m	97%	sp P00575 RPOB_ECOLI DNA-DIRECTED RNA POLYMERASE BETA CHAIN (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT) pir RNECB DNA- directed RNA polymerase (EC 2.7.7.6) beta chain Escherichia coli gb AA18647.1 (U76222) RNA polymerase beta subunit [Escherichia coli] gb AAC76961.1 (AE000472) RNA polymerase, beta subunit [Escherichia coli K12]	SEQ ID n-9557
SEQ ID n° 8440	PL-6391.1	Contig9 from 3039129 to 3039500	m	86%	sp P18081 RL7_SALTY 50S RIBOSOMAL PROTEIN L7/L12 (L8) pir R5EB12 ribosomal protein L7/L12 - Salmonella typhimurium emb CAA37246.1 (X53072) ribosomal protein L7 /L12 (AA 1-121) [Salmonella typhimurium] gb AAF33498.1 (AF170176) Salmonella typhimurium 50S ribosomal protein L7 (RPLL) (SW:P18981); contains similarity to Pfam domain PF00542 (Ribosomal_L12), Score=133.2, E=4.6e-36, N=1 [Salmonella typhimurium LT2]	#N/A
SEQ ID n° 8441	PL-3732.1	Contig9 from 3039564 to 3040070	m	88%	sp P02408 RL10_ECOLI 50S RIBOSOMAL PROTEIN L10 (L8) pir R5EC10 ribosomal protein L10 [validated] - Escherichia coli emb CAA23623.1 (V00339) rplJ (L10) [Escherichia coli] gb AAC43083.1 (U00006) 50S ribosomal subunit protein L10 [Escherichia coli] gb AAC76959.1 (AE000472) 50S ribosomal subunit protein L10 [Escherichia coli K12] gb AAG59181.1 (AE005630_1 (AE005630) 50S ribosomal subunit protein L10 [Escherichia coli O157:H7]	SEQ ID n-2916

SEQ ID n° 8442	PL-723.1	Contig9 from 3040387 to 3041088	m	96%	<p>sp P02384 RL1_ECOLI 50S RIBOSOMAL PROTEIN L1 pir R5EC1 ribosomal protein L1 [validated] - Escherichia coli emb CAA23622.1 (V00339) rplA (L1) [Escherichia coli] gb AAC43082.1 (U00006) 50S ribosomal subunit protein L1 [Escherichia coli] gb AAC76958.1 (AE000472) 50S ribosomal subunit protein L1, regulates synthesis of L1 and L11 [Escherichia coli K12] gb AAG59180.1 AE005629_9 (AE005629) 50S ribosomal subunit protein L1, regulates synthesis of L1 and L11 [Escherichia coli O157:H7] SEQ ID n-9556</p>
SEQ ID n° 8443	PL-3731.1	Contig9 from 3041092 to 3041520	m	80%	<p>sp P09763 RL11_SERMA 50S RIBOSOMAL PROTEIN L11 pir R5SE11 ribosomal protein L11 - Serratia marcescens emb CAA31095.1 (X12584) L11 protein (AA 1-142) [Serratia marcescens] sp P16921 NUSG_ECOLI TRANSCRIPTION ANTITERMINATION PROTEIN NUSG pir TWEONG transcription antitermination factor nusG - Escherichia coli gb AA24622.1 (M30610) nusG protein [Escherichia coli] gb AAC43080.1 (U00006) nusG [Escherichia coli] gb AAC76956.1 (AE000472) component in transcription antitermination [Escherichia coli K12] gb AAG59178.1 AE005629_7 (AE005629) component in transcription antitermination [Escherichia coli O157:H7] SEQ ID n-2914</p>
SEQ ID n° 8445	PL-6389.1	Contig9 from 3042229 to 3042612	m	80%	<p>gb AAF33494.1 (AF170176) 96% identity over 127 amino acids with E. coli protein- export protein (SECE) (SW:P16920); contains similarity to Pfam domain PF00584 (SecE), Score=96.3, E=6,2e-25, N=1 [Salmonella typhimurium LT2] #N/A</p>
SEQ ID n° 8446	PL-722.1	Contig9 from 3042887 to 3044071	m	92%	<p>pir S13560 translation elongation factor EF- Tu.A - Salmonella typhimurium SEQ ID n-9555</p>

SEQ ID n° 8447	PL-721.1	Contig9 from 3044144 to 3046252	m 90%	sp P26229 EFG_SALTY ELONGATION FACTOR G (EF-G) pir J01424 translation elongation_factor EF-G - Salmonella typhimurium emb CAA45880.1 (X64591) elongation factor G [Salmonella typhimurium] gb AAG58448.1 AE005558_1 (AE005558) 30S ribosomal subunit protein S7, initiates assembly [Escherichia coli O157:H7] SEQ ID n-9554
SEQ ID n° 8448	PL-3729.1	Contig9 from 3046333 to 3046803	m 87%	sp P02367 RS12_ECOLI 30S RIBOSOMAL PROTEIN S12 pir R3EC12 ribosomal protein S12 [validated] - Escherichia coli pir JH0443 ribosomal protein S12 - Salmonella typhimurium emb CAA23648.1 (V00355) reading frame (S12 protein) [Escherichia coli] gb AA50988.1 (J01691) ribosomal protein S12 [Escherichia coli] gb AAA27216.1 (M68548) ribosomal protein S12 [Salmonella typhimurium] gb AAA72526.1 (M12787) ribosomal protein S12 [unidentified cloning vector] gb AA58139.1 (U18997) 30S ribosomal subunit protein S12 [Escherichia coli] gb AAC76367.1 (AE000410) 30S ribosomal subunit protein S12 [Escherichia coli K12] gb AAC53716.1 (U87107) small ribosomal protein [Cloning vector pAL-F] gb AAG30937.1 (AF312717) ribosomal protein S12 [Escherichia coli K12] gb AAG58449.1 AE005558_2 (AE005558) 30S ribosomal subunit protein S12 [Escherichia coli O157:H7] SEQ ID n-2911
SEQ ID n° 8449	PL-3728.1	Contig9 from 3046901 to 3047275	m 72%	sp P45530 YHEL_ECOLI HYPOTHETICAL 10.7 KDA PROTEIN IN RPSL-FKPA INTERGENIC REGION pir B65128 hypothetical 10.7 kD protein in rpsl fkpa intergenic region - Escherichia coli (strain K-12) gb AAA58140.1 (U18997) ORF_f95 [Escherichia coli] gb AAC76368.1 (AE000410) orf, hypothetical protein [Escherichia coli K12] #N/A
SEQ ID n° 8450	PL-6383.1	Contig9 from 3047412 to 3047699	m 62%	

Contig9 from SEQ ID n° 8451 PL-6382.1 3047720 to 3048079	m	74%	gb AAG58451.1 AE005558_4 (AE005558) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
Contig9 from SEQ ID n° 8452 PL-6381.1 3048089 to 3048484	m	78%	sp P45532 YHEN_ECOLI_HYPOTHETICAL_13.6_KD PROTEIN_IN_RPSL-FKPA_INTERGENIC_REGION pir D65128 hypothetical 13.6 kD protein in rpsl. fkpa intergenic region - Escherichia coli (strain K-12) gb AAAS8142.1 (U18997) ORF_fl28 [Escherichia coli] gb AAC76370.1 (AE000410) orf, hypothetical protein [Escherichia coli K12] #N/A
Contig9 from SEQ ID n° 8453 PL-720.1 3048484 to 3049218	m	87%	gb AAG58453.1 AE005558_6 (AE005558) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-9553
Contig9 from SEQ ID n° 8454 PL-6380.1 3049280 to 3049483	p	No Hits found	#N/A
Contig9 from SEQ ID n° 8455 PL-719.1 3049500 to 3050264	m	81%	gb AAG58454.1 AE005558_7 (AE005558) FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli O157:H7] sp P30857 SLYX_ECOLI_SLYX_PROTEIN_pir A49988 slyx protein - Escherichia coli gb AA18573.1 (L13261) orf72 [Escherichia coli]
Contig9 from SEQ ID n° 8456 PL-6379.1 3050515 to 3050733	p	56%	gb AA58145.1 (U18997) slyD [Escherichia coli] gb AAC76373.1 (AF000411) host factor for lysis of phix174 infection [Escherichia coli K12] gb AAG58455.1 AE005558_8 (AE005558) host factor for lysis of phix174 infection [Escherichia coli O157:H7] #N/A

833

sp|P30856|SLYD_ECOLI FKBP-TYPE PEPTIDYL-PROLYL
CIS-TRANS ISOMERASE SLYD (PPIASE)
(ROTAMASE) (HISTIDINE RICH PROTEIN) (WHP)
pir||A49987 probable fkbp-type peptidyl-prolyl
cis-trans isomerase slyd -

Escherichia coli emb|CNA79705.1| (Z21496)
histidine rich protein [Escherichia coli]
gb|AA18574.1| (U13261) sensitivity to lysis
gene [Escherichia coli] gb|AA58146.1| (U18997)
histidine rich protein [Escherichia coli]
gb|AAC41458.1| (L28082) slyd gene product
[Escherichia coli] gb|AAC76374.1| (AE000411)
FKBP-type peptidyl-prolyl cis-trans isomerase
(rotamase) [Escherichia coli K12]
gb|AAG58456.1|AE005558_9 (AE005558) FKBP-type
peptidyl-prolyl cis-trans isomerase (rotamase)
[Escherichia coli O157:H7]

SEQ ID n-9550

sp|P56622|YHEV_ECOLI HYPOTHETICAL 7.6 KD PROTEIN
IN SLYD-KEFB INTERGENIC REGION
gb|AAG58457.1|AE005558_10 (AE005558) Z4708 gene
product [Escherichia coli O157:H7]
sp|P45535|YHEV_ECOLI HYPOTHETICAL ABC
TRANSPORTER ATP-BINDING PROTEIN YHES

#N/A

pir||C65129 hypothetical ABC transporter in kifb-
prkb intergenic region - Escherichia
coli (strain K-12) gb|AA58149.1| (U18997)
ORF_0637 [Escherichia coli] gb|AAC76377.1|
(AE000411) putative ATP-binding component of a
transport system [Escherichia coli
K12]

SEQ ID n-9549

emb|CAB61438.1| (Z32686) MrpI [Proteus
mirabilis]

SEQ ID n-9548

Contig9 from
SEQ ID n° 8457 PL-718.1 3050839 to m 84%
3051411

Contig9 from
SEQ ID n° 8458 PL-6377.1 3051500 to m 67%
3051703

Contig9 from
SEQ ID n° 8459 PL-717.1 3051996 to p 82%
3053921

Contig9 from
SEQ ID n° 8460 PL-716.1 3054256 to m 77%
3054828

SEQ ID n° 8461	PL-3727.1	Contig9 from 305522 to 305608	p 67%	sp PI3421 FWA_SERWA_FIMBRIA_A_PROTEIN_PRECURSOR pir A31096 fimbrial protein precursor, mannose- resistant - Serratia marcescens (strain US46) gb AA26576.1 (M21161) SmfA protein [Serratia marcescens]	SEQ ID n-2910
SEQ ID n° 8462	PL-715.1	Contig9 from 3056218 to 3056814	p 39%	emb CAA83634.1 (Z32686) mrpB [Proteus mirabilis]	SEQ ID n-9547
SEQ ID n° 8463	PL-714.1	Contig9 from 3056829 to 3059417	p 65%	emb CAA83635.1 (Z32686) mrpC [Proteus mirabilis]	SEQ ID n-9546
SEQ ID n° 8464	PL-713.1	Contig9 from 3059747 to 3060505	p 71%	emb CAA83636.1 (Z32686) mrpD [Proteus mirabilis]	SEQ ID n-9545
SEQ ID n° 8465	PL-712.1	Contig9 from 3060548 to 3061141	p 43%	emb CAA83639.2 (Z32686) mrpG [Proteus mirabilis]	SEQ ID n-9544
SEQ ID n° 8466	PL-711.1	Contig9 from 3061184 to 3061981	p 46%	emb CAB61439.1 (Z32686) mrpH [Proteus mirabilis]	SEQ ID n-9543
SEQ ID n° 8467	PL-3724.1	Contig9 from 3062014 to 3062553	p No Hits found		SEQ ID n-2908

pir||T20770 hypothetical protein Fl1C3.3 -
 Caenorhabditis elegans pir||MWKW myosin heavy
 chain B [similarity] - Caenorhabditis elegans
 emb|CAB04089.1| (Z81499) contains similarity to
 Pfam domain: PF00063 (Myosin head
 (motor domain)), Score=1558.5, E-value=0, N=1;
 PF01576 (Myosin tail), Score=1727.6,
 E-value=0, N=3-CDNA EST EMBL:T02297
 comes from this gene; cDNA EST EMBL:T00788
 comes from this gene; c> emb|CAB05505.1|
 (Z83107) contains similarity to Pfam domain:
 PF00063 (Myosin head (motor
 domain)), Score=1558.5, E-value=0, N=1; PF01576
 (Myosin tail), Score=1727.6, E-value=0, N=3-CDNA
 EST EMBL:T02297 comes from this
 gene; cDNA EST EMBL:T00788 comes
 from this gene; c>
 emb|CAB61937.1| (AL133278) putative lysr-family
 transriptional regulator
 [Streptomyces coelicolor A3(2)]
 sp|P77354|YAFU_ECOLI HYPOTHETICAL 12.1 KD
 PROTEIN IN DNAQ-GMHA INTERGENIC REGION
 pir||C64746 yafu protein - Escherichia coli
 gb|AAB08640.1| (U70214) hypothetical protein
 [Escherichia coli] gb|AAC73322.1| (AE000130)
 orf, hypothetical protein [Escherichia coli K12] SEQ ID n-3539
 #N/A
 gb|AAG54517.1|AE005197_6 (AE005197) Z0248 gene
 product [Escherichia coli O157:H7]
 SEQ ID n-2906

Contig9 from					
SEQ ID n° 8468	PL-710.1	p	29%		
3062550 to					
3063812					
Contig9 from					
SEQ ID n° 8469	PL-709.1	m	30%		
3064015 to					
3064905					
Contig9 from					
SEQ ID n° 8470	PL-3723.1	m	No Hits found		
3065324 to					
3065776					
Contig9 from					
SEQ ID n° 8471	PL-708.1	m	14%		
3065594 to					
3067424					
Contig9 from					
SEQ ID n° 8472	PL-6371.1	m	No Hits found		
3067507 to					
3067713					
Contig9 from					
SEQ ID n° 8473	PL-3722.1	p	65%		
3068059 to					
3068538					

SEQ ID n° 8474	PL-707.1	Contig9 from 3068817 to 3069722	p 81%	pir G82352 Gckr family protein VC0206 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93382.1 (AE004110) Gckr family protein [Vibrio cholerae] pir H82352 probable PTS system, sucrose- specific IIBC component VC0207 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93383.1 (AE004110) PTS system, sucrose-specific IIBC component, putative [Vibrio cholerae] pir B83356 conserved hypothetical protein PA2306 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05694.1 AE004657.1 (AE004657) conserved hypothetical protein [Pseudomonas aeruginosa] gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] sp P45524 YHET_ECOLI HYPOTHETICAL 38.5 KD PROTEIN IN KIFB-PRKB INTERGENIC REGION pir D65129 hypothetical 38.5 kD protein in kifb- prkb intergenic region - Escherichia coli (strain K-12) gb AA58150.1 (U18997) ORF_o340 [Escherichia coli] gb AAC76378.1 (AE000411) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-9538
SEQ ID n° 8475	PL-706.1	Contig9 from 3069753 to 3071231	p 81%		
SEQ ID n° 8476	PL-705.1	Contig9 from 3071272 to 3071880	m 58%		
SEQ ID n° 8477	PL-704.1	Contig9 from 3071976 to 3072860	m 59%	SEQ ID n-9536	
SEQ ID n° 8478	PL-703.1	Contig9 from 3072981 to 3073958	p 78%	SEQ ID n-9535	

SEQ ID n° 8479 PL-6369.1	Contig9 from 3073958 to 3074176	p	53%	sp P45536 YHEU_ECOLI_HYPOTHETICAL_8.5_KD_PROTEIN IN_KIFB-PRKB_INTERGENIC_REGION_pir E65129 hypothetical 8.5 kd protein in kifb-prkb intergenic region - Escherichia coli (strain K-12) gb AA58151.1 (U18997) ORF_o72; alternate ORF with good statistics, no frameshift found [Escherichia coli] gb AAC76379.1 (AE000411) orf, hypothetical protein [Escherichia coli K12] gb AG58462.1 AE005558_15 (AE005558) orf, hypothetical protein [Escherichia coli-O157:H7] sp P37307 KPPR_ECOLI_PROBABLE PHOSPHORIBULOKINASE (PHOSPHOPENTOKINASE) (PRK) pir F65129 phosphoribulokinase (EC 2.7.1.19) - Escherichia coli (strain K-12) gb AAC76380.1 (AE000411) probable phosphoribulokinase [Escherichia coli K12] emb CAA61607.1 (X89443) ORF2 [Erwinia chrysanthemi]	SEQ ID n-9533	#N/A
SEQ ID n° 8480 PL-702.1	Contig9 from 3074195 to 3075064	p	93%			
SEQ ID n° 8481 PL-6368.1	Contig9 from 3075190 to 3075597	m	86%			

SEQ ID n° 8482	PL-701.1	Contig9 from 3075918 to 3076550	95%	<p>sp P03020 CRP_ECOLI CATABOLITE GENE ACTIVATOR (CAMP RECEPTOR PROTEIN) (CAMP-REGULATORY PROTEIN) pir QRECC CAMP receptor protein - Escherichia coli pdb 1G6N A Chain A, 2.1 Angstrom Structure Of Cap-Camp pdb 1G6N B Chain B, 2.1 Angstrom Structure Of Cap-Camp pdb 2CGP A Chain A, Catabolite Gene Activator ProteinDNA COMPLEX, ADENOSINE-3', 5'- Cyclic-Monophosphate gb AAA23601.1 (J01598) cAMP receptor protein (crp) [Escherichia coli] gb AAA25515.1 (M13772) catabolite gene activator protein [Shigella flexneri] gb AAA58154.1 (U18997) cyclic AMP receptor protein [Escherichia coli] gb AAC76382.1 (AE000411) cyclic AMP receptor protein [Escherichia coli K12] gb AAG58465.1 AE005559_1 (AE005559) cyclic AMP receptor protein [Escherichia coli O157:H7] sp P18335 ARGD_ECOLI ACETYLORNITHINE AMINOTRANSFERASE (ACoAT) pir B65130 acetylornithine transaminase (EC 2.6.1.11) - Escherichia coli gb AAA58156.1 (U18997) acetylornithine delta-aminotransferase [Escherichia coli] gb AAC76384.1 (AE000412) acetylornithine delta-aminotransferase [Escherichia coli K12] sp P06195 PABA_SERMA PARA-AMINOBENZOATE SYNTHASE GLUTAMINE AMIDOTRANSFERASE COMPONENT II (ADC SYNTHASE) pir S09635 paba protein - Serratia marcescens emb CAA26452.1 (X02605) paba gene product (aa 1-191) [Serratia marcescens]</p>	SEQ ID n-3532
SEQ ID n° 8483	PL-700.1	Contig9 from 3076600 to 3077811	81%		
SEQ ID n° 8484	PL-3721.1	Contig9 from 3077935 to 3078510	85%		SEQ ID n-2905

SEQ ID n° 8485	PL-5367.1	Contig9 from 3078759 to 3079109	p 36%	sp P76001 YCGJ_ECOLI_HYPOTHETICAL_13.4_KDA PROTEIN IN MINC-SHEA INTERGENIC REGION PRECURSOR pir F64863 YCGJ protein precursor - Escherichia coli gb AAC74261.1 (AE000216) orf, hypothetical protein [Escherichia coli K12] dbj BAA36011.1 (D90751) ORF ID:0243#9 [Escherichia coli] dbj BAA36024.1 (D90752) ORF ID:0243#9 [Escherichia coli] sp 053021 PPIA_ERWCH PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A PRECURSOR (PPIASE A) (ROTAMASE A) (CYCLOPHILIN A) emb CAA70935.1 (Y09804) peptidylprolyl cis-trans isomerase [Erwinia chrysanthemi] SEQ ID n-2904	#N/A
SEQ ID n° 8486	PL-3720.1	Contig9 from 3079209 to 3079778	m 83%	sp P24253 YIHA_ECOLI_HYPOTHETICAL_GTP-BINDING PROTEIN IN POLA-HEMN INTERGENIC REGION gb AAC35427.1 (U97057) beta-lactamase inhibitory protein II precursor [Streptomyces exfoliatus] SEQ ID n-3529	#N/A
SEQ ID n° 8487	PL-699.1	Contig9 from 3080086 to 3080718	p 64%	sp P00582 DPO1_ECOLI_DNA_POLYMERASE_I (POL I) pir DJECI DNA-directed DNA polymerase (EC 2.7.7.7) I - Escherichia coli emb CAA23607.1 (V00317) DNA polymerase I [Escherichia coli] gb AAA24402.1 (J01663) DNA polymerase I [Escherichia coli] gb AAB02998.1 (L19201) DNA polymerase I [Escherichia coli] gb AAC76861.1 (AE000461) DNA polymerase I, 3' --> 5' polymerase, 5' --> 3' and 3' --> 5' exonuclease [Escherichia coli K12] SEQ ID n-3528	#N/A
SEQ ID n° 8488	PL-698.1	Contig9 from 3081191 to 3082483	p 23%		
SEQ ID n° 8489	PL-6366.1	Contig9 from 3082862 to 3083080	p No Hits found		
SEQ ID n° 8490	PL-5365.1	Contig9 from 3083109 to 3083330	p No Hits found		
SEQ ID n° 8491	PL-697.1	Contig9 from 3083422 to 3086211	m 84%		

Contig9 from SEQ ID n° 8492 PL-696.1 3086686 to 3087699	m	72%	ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-3526
Contig9 from SEQ ID n° 8493 PL-6363.1 3087825 to 3088064	p	71%	gb AAG57162.1 AE005436_9 (AE005436) Z3269 gene product [Escherichia coli O157:H7]	#N/A
Contig9 from SEQ ID n° 8494 PL-695.1 3088092 to 3090719	p	69%	ref NP_053136.1 orf74 [Escherichia coli] dbj BAA84909.1 (AB024946) orf74 [Escherichia coli]	SEQ ID n-3525
Contig9 from SEQ ID n° 8495 PL-694.1 3090785 to 3091861	p	45%	pir G75064 hypothetical protein PAB1002 - Pyrococcus abyssi (strain Orsay) emb CAB50412.1 (AJ248287) hypothetical protein [Pyrococcus abyssi]	SEQ ID n-3524
Contig9 from SEQ ID n° 8496 PL-693.1 3092017 to 3092640	m	83%	sp Q9XBV2 DSBA_YERPE THIOI:DISULFIDE INTERCHANGE PROTEIN DSBA PRECURSOR gb AAD38401.1 AF155130.1 (AF155130) Dsba [Yersinia pestis]	SEQ ID n-3523
Contig9 from SEQ ID n° 8497 PL-692.1 3092661 to 3093653	m	77%	gb AAD47614.1 AF146615_2 (AF146615) YihE [Pectobacterium carotovorum subsp. carotovorum]	SEQ ID n-3522
Contig9 from SEQ ID n° 8498 PL-691.1 3093862 to 3094461	p	58%	pdb 1E5K A Chain A, Crystal Structure Of The Molybdenum Cofactor Biosynthesis Protein Moba (Protein Fa) From Escherichia Coli At Near Atomic Resolution	SEQ ID n-3521
Contig9 from SEQ ID n° 8499 PL-3718.1 3094458 to 3094976	p	67%	sp P32125 MOBB_ECOLI MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN B	SEQ ID n-3502
Contig9 from SEQ ID n° 8500 PL-690.1 3095057 to 3096709	m	25%	sp Q02171 MYSP_ONCVO PARAMYOSIN gb AAA29431.1 (M95813) paramyosin [Onchocerca volvulus]	SEQ ID n-3520
Contig9 from SEQ ID n° 8501 PL-689.1 3096706 to 3097794	m	No Hits found		SEQ ID n-3518

SEQ ID n° 8502	PL-688.1	Contig9 from 3098060 to 3099430	m	90%	gb AAG58632.1 AE005575_1 (AE005575) glutathione oxidoreductase [Escherichia coli O157:H7] sp P37634 YHIR_ECOLI_HYPOTHETICAL 31.9 KD PROTEIN IN PRLC-GOR INTERGENIC REGION (O280A) pir S47719 hypothetical 31.9K protein (prlc-gor intergenic region) [Escherichia coli gb AAB18475.1 (U00039) No definition line found [Escherichia coli] gb AAC76524.1 (AE000426) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-3516	SEQ ID n-3517
SEQ ID n° 8503	PL-687.1	Contig9 from 3099526 to 3100368	m	79%		
SEQ ID n° 8504	PL-6359.1	Contig9 from 3100289 to 3100441	m	No Hits found	gb AAC32476.1 (AF044503) hcp [Escherichia coli] gb AAG54535.1 AE005199_5 (AE005199) Z0266 gene product [Escherichia coli O157:H7] pir F82498 conserved hypothetical protein VCA0107 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96021.1 (AE004353) conserved hypothetical protein [Vibrio cholerae] pir G82498 conserved hypothetical protein VCA0108 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96022.1 (AE004353) conserved hypothetical protein [Vibrio cholerae] pir H82498 hypothetical protein VCA0109 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96023.1 (AE004353) hypothetical protein [Vibrio cholerae]	SEQ ID n-2901
SEQ ID n° 8506	PL-3714.1	Contig9 from 3102426 to 3102923	p	71%		SEQ ID n-2900
SEQ ID n° 8507	PL-686.1	Contig9 from 3102947 to 3104425	p	84%		SEQ ID n-3515
SEQ ID n° 8508	PL-6357.1	Contig9 from 3104432 to 3104872	p	54%		#N/A
SEQ ID n° 8509	PL-685.1	Contig9 from 3104874 to 3106721	p	66%	gb AAG54529.1 AE005198_10 (AE005198) Z0260 gene product [Escherichia coli O157:H7]	SEQ ID n-3514
SEQ ID n° 8510	PL-684.1	Contig9 from 3106757 to 3107737	p	64%	gb AAG54528.1 AE005198_9 (AE005198) Z0259 gene product [Escherichia coli O157:H7]	SEQ ID n-3513

SEQ ID n° 8511	PL-683.1	Contig9 from 3107743 to 3109029	p	60%	gb AAG54527.1 AE005198_8 (AE005198) Z0258 gene product [Escherichia coli O157:H7]	SEQ ID n-9512
SEQ ID n° 8512	PL-3713.1	Contig9 from 3109029 to 3109595	p	60%	gb AAG54526.1 AE005198_7 (AE005198) Z0257 gene product [Escherichia coli O157:H7]	SEQ ID n-2899
SEQ ID n° 8513	PL-682.1	Contig9 from 3109598 to 3110950	p	68%	gb AAG54525.1 AE005198_6 (AE005198) Z0256 gene product [Escherichia coli O157:H7]	SEQ ID n-9511
SEQ ID n° 8514	PL-681.1	Contig9 from 3110950 to 3111720	p	70%	gb AAG54524.1 AE005198_5 (AE005198) Z0255 gene product [Escherichia coli O157:H7]	SEQ ID n-9510
SEQ ID n° 8515	PL-680.1	Contig9 from 3111731 to 3114376	p	80%	gb AAG54523.1 AE005198_4 (AE005198) putative protease [Escherichia coli O157:H7]	SEQ ID n-9509
SEQ ID n° 8516	PL-679.1	Contig9 from 3114373 to 3115173	p	No. Hits. found		SEQ ID n-9507
SEQ ID n° 8517	PL-678.1	Contig9 from 3115170 to 3115817	p	58%	gb AAG54522.1 AE005198_3 (AE005198) Z0253 gene product [Escherichia coli O157:H7]	SEQ ID n-9506
SEQ ID n° 8518	PL-677.1	Contig9 from 3115823 to 3117256	p	31%	gb AAG54520.1 AE005198_1 (AE005198) Z0251 gene product [Escherichia coli O157:H7]	SEQ ID n-9505
SEQ ID n° 8519	PL-674.1	Contig9 from 3117253 to 3120798	p	68%	gb AAG54519.1 AE005197_8 (AE005197) putative macrophage toxin [Escherichia coli O157:H7]	SEQ ID n-9503
SEQ ID n° 8520	PL-672.1	Contig9 from 3120891 to 3121607	p	58%	gb AAG54518.1 AE005197_7 (AE005197) Z0249 gene product [Escherichia coli O157:H7]	SEQ ID n-9501
SEQ ID n° 8521	PL-671.1	Contig9 from 3121582 to 3122964	m	57%	pdb 1F3I A Chain A, Crystal Structure Of Tn5 Transposase Complexed With End Dna	SEQ ID n-9500
SEQ ID n° 8522	PL-670.1	Contig9 from 3123054 to 3123731	p	46%	gb AAG54518.1 AE005197_7 (AE005197) Z0249 gene product [Escherichia coli O157:H7]	SEQ ID n-9499

SEQ ID n° 8523	PL-669.1	Contig9 from 3123813 to 3125648	p	60%	gb AAC62387.1 (AF044506) VgrG protein [Escherichia coli]	SEQ ID n-3497
SEQ ID n° 8524	PL-3709.1	Contig9 from 3125696 to 3126115	p	37%	gb AAG54902.1 AE005236_2 (AE005236) Z0706 gene product [Escherichia coli O157:H7]	SEQ ID n-2894
SEQ ID n° 8525	PL-667.1	Contig9 from 3126137 to 3130552	p	48%	gb AAG54900.1 AE005236_1 (AE005236) Z0705 gene product [Escherichia coli O157:H7]	SEQ ID n-3495
SEQ ID n° 8526	PL-6341.1	Contig9 from 3130537 to 3130872	p	No Hits found		#N/A
SEQ ID n° 8527	PL-3705.1	Contig9 from 3131440 to 3131991	p	No Hits found		SEQ ID n-2892
SEQ ID n° 8528	PL-6340.1	Contig9 from 3132095 to 3132292	m	No Hits found		#N/A
SEQ ID n° 8529	PL-7143.1	Contig9 from 3132412 to 3132561	p	No Hits found		#N/A
SEQ ID n° 8530	PL-6339.1	Contig9 from 3132583 to 3132963	p	No Hits found		#N/A
SEQ ID n° 8531	PL-3704.1	Contig9 from 3133434 to 3133661	p	No Hits found		SEQ ID n-2891
SEQ ID n° 8532	PL-666.1	Contig9 from 3133968 to 3134675	p	No Hits found		SEQ ID n-3494
SEQ ID n° 8533	PL-665.1	Contig9 from 3134874 to 3135899	m	21%	dbj BAB06239.1 (AF001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-3493
SEQ ID n° 8534	PL-7142.1	Contig9 from 3136340 to 3136507	p	No Hits found		#N/A

[illegible]

SEQ ID n° 8541	PL-662.1	Contig9 from 3142116 to 3142799	p 51%	gb AAG54520.1 AE005198_1 (AE005198) Z0251 gene product [Escherichia coli O157:H7]	SEQ ID n-9490
SEQ ID n° 8542	PL-660.1	Contig9 from 3142796 to 3146341	p 68%	gb AAG54519.1 AE005197_8 (AE005197) putative macrophage toxin [Escherichia coli O157:H7]	SEQ ID n-9489
SEQ ID n° 8543	PL-658.1	Contig9 from 3146437 to 3147330	p 57%	gb AAG54518.1 AE005197_7 (AE005197) Z0249 gene product [Escherichia coli O157:H7]	SEQ ID n-9486
SEQ ID n° 8544	PL-657.1	Contig9 from 3147341 to 3148723	p 57%	pdb 1F3I A Chain A, Crystal Structure of Tn5 Transposase Complexed With End Dna	SEQ ID n-9485
SEQ ID n° 8545	PL-3700.1	Contig9 from 3149120 to 3149554	p 36%	sp P42296 YXID_BACSU HYPOTHETICAL 64.3 KD PROTEIN IN HUTP-BGLP INTERGENIC REGION pir H70076 hypothetical protein J3D [imported] Bacillus subtilis dbj BA006649.1 (D31856) hypothetical protein [Bacillus subtilis] emb CAB15966.1 (Z99124) yxID [Bacillus subtilis]	SEQ ID n-2888
SEQ ID n° 8546	PL-3699.1	Contig9 from 3149556 to 3150035	p No Hits found		SEQ ID n-2885
SEQ ID n° 8547	PL-656.1	Contig9 from 3150341 to 3151048	p No Hits found		SEQ ID n-3484
SEQ ID n° 8548	PL-6324.1	Contig9 from 3151774 to 3151917	p No Hits found		#N/A
SEQ ID n° 8549	PL-3698.1	Contig9 from 3152035 to 3152529	p No Hits found		SEQ ID n-2884
SEQ ID n° 8550	PL-655.1	Contig9 from 3152687 to 3153571	p 59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]	SEQ ID n-3483

SEQ ID n° 8551	PL-6323.1	Contig9 from 3153810 to 3154202	- p -	No Hits found			#N/A
SEQ ID n° 8552	PL-654.1	Contig9 from 3154721 to 3155746	m	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-9482	
SEQ ID n° 8553	PL-6321.1	Contig9 from 3155838 to 3156191	p	No Hits found			#N/A
SEQ ID n° 8554	PL-7141.1	Contig9 from 3156790 to 3156957	p	No Hits found			#N/A
SEQ ID n° 8555	PL-6320.1	Contig9 from 3157445 to 3157642	m	No Hits found			#N/A
SEQ ID n° 8556	PL-6318.1	Contig9 from 3157656 to 3157790	m	No Hits found			#N/A
SEQ ID n° 8557	PL-6317.1	Contig9 from 3157818 to 3158165	m	72%	gb AAG56610.1 AE005386_1 (AE005386) PTS system, maltose and glucose-specific II ABC [Escherichia coli O157:H7] sp P07026 SDIA_ECOLI SDIA REGULATORY PROTEIN pir QEGU1 probable transcription regulator sdia - Escherichia coli dbj BA15736.1 (D90832) Sdia regulatory protein. [Escherichia coli] gb AAC74983.1 (AE000284) transcriptional regulator of ftsQAZ gene cluster [Escherichia coli K12]	SEQ ID n-9481	
SEQ ID n° 8558	PL-653.1	Contig9 from 3158595 to 3159323	m	45%			#N/A
SEQ ID n° 8559	PL-652.1	Contig9 from 3159745 to 3161361	p	29%	gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae]	SEQ ID n-9480	
SEQ ID n° 8560	PL-3697.1	Contig9 from 3161611 to 3162201	p	46%	gb AAC45946.1 (AF021840) Aida [Ralstonia solanacearum]	SEQ ID n-2883	

Contig9 from 3162870 to 3164537	SEQ ID n° 8561 PL-651.1	p 76%	sp P15321 HLYB_SERMA_HEMOLYSIN_ACTIVATOR_PROTEIN PRECURSOR pir B28182 hemolysin B - Serratia marcescens gb AAA50322.1 (M22618) hemolysin determinant [Serratia marcescens]	SEQ ID n-9479
Contig9 from 3164603 to 3169045	SEQ ID n° 8562 PL-650.1	p 56%	sp P15320 HLYA_SERMA_HEMOLYSIN_PRECURSOR pir A28182 hemolysin A - Serratia marcescens gb AAA50323.1 (M22618) hemolysin [Serratia marcescens]	SEQ ID n-9478
Contig9 from 3169384 to 3169932	SEQ ID n° 8563 PL-3695.1	m No Hits found		SEQ ID n-2882
Contig9 from 3170280 to 3170858	SEQ ID n° 8564 PL-649.1	p 50%	gb AAG48301.1 AF310136_1 (AF310136) Tn10 transposase [Plasposon NXBOR]	SEQ ID n-9476
Contig9 from 3170859 to 3171569	SEQ ID n° 8565 PL-648.2	p 58%	ref NP_053090.1 orf28 [Escherichia coli] gb AAB36834.1 (L42638) orf5; open reading frame with no significant homology to any proteins in the database [Escherichia coli] dbj BAA84863.1 (AB024946) orf28 [Escherichia coli]	SEQ ID n-9475
Contig9 from 3171600 to 3172055	SEQ ID n° 8566 PL-3694.1	p 73%	dbj BAB03895.1 (AP001507) transposase (09) [Bacillus halodurans] dbj BAB03988.1 (AP001507) transposase (09) [Bacillus halodurans] dbj BAB05361.1 (AP001512) transposase (09) [Bacillus halodurans] dbj BAB05614.1 (AP001513) transposase (09) [Bacillus halodurans] dbj BAB06561.1 (AP001516) transposase (09) [Bacillus halodurans] dbj BAB06952.1 (AP001518) transposase (09) [Bacillus halodurans] dbj BAB07185.1 (AP001518) transposase (09) [Bacillus halodurans] dbj BAB07197.1 (AP001518) transposase (09) [Bacillus halodurans]	SEQ ID n-2881

Contig9 from SEQ ID n° 8567 PL-647.1 3172203 to 3173597	m	22%	pir [F81045 hemagglutinin/hemolysin-related protein NMB1768 [imported] - Neisseria meningitidis (group B strain MD58) gb AAFA42109.1 (AE002526) hemagglutinin/hemolysin-related protein (Neisseria meningitidis MC58)]	SEQ ID n-3474
Contig9 from SEQ ID n° 8568 PL-646.1 3173998 to 3175050	p	22%	dbj BA06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-3473
Contig9 from SEQ ID n° 8569 PL-7139.1 3175236 to 3175427	m	No Hits found		#N/A
Contig9 from SEQ ID n° 8570 PL-644.1 3175578 to 3176570	p	72%	gb AAG58663.1 AE005577_8 (AE005577) orf, hypothetical protein [Escherichia coli O157:H7] sp P45418 YKDK_ERWCH HYPOTHETICAL 8.1 KD PROTEIN IN KDGK 5'REGION (K2 ORF) pir [B55215'4- oxalocrotonate tautomerase (EC 5.3.2.-) [similarity] - Erwinia chrysanthemi emb CAA52960.1 (X75047) K2 ORF [Erwinia chrysanthemi]	SEQ ID n-3471 #N/A
Contig9 from SEQ ID n° 8571 PL-6315.1 3176626 to 3176832	p	58%	gb AAG58668.1 AE005578_5 (AE005578) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-3470
Contig9 from SEQ ID n° 8572 PL-643.1 3176876 to 3178366	m	67%	sp P37649 YHJK_ECOLI PROTEIN YHJK pir [S47750 hypothetical protein (dctA-dppF intergenic region) - Escherichia coli gb AAB18506.1 (U00039) No definition line found [Escherichia coli] gb AAC76554.1 (AE000429) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-3469 gb AAG58684.1 AE005580_6 (AE005580) putative ATP binding component of dipeptide transport system [Escherichia coli O157:H7]	SEQ ID n-3468
Contig9 from SEQ ID n° 8573 PL-642.1 3178545 to 3179258	m	61%		
Contig9 from SEQ ID n° 8574 PL-641.1 3179615 to 3180595	m	84%		

<p> Contig9 from 3180631 to 3181611 SEQ ID n° 8575 PL-640.1 m 90% </p>	<p> sp P37314 DPPD_ECOLI DIPEPTIDE TRANSPORT ATP-BINDING PROTEIN DPPD_pir S61404 dipeptide transport protein dppd - Escherichia coli gb AAA23705.1 (L08399) peripheral membrane protein [Escherichia coli] gb AAB18519.1 (U00039) dppd [Escherichia coli] gb AAC76566.1 (AE000431) putative ATP-binding component of dipeptide transport system [Escherichia coli K12] gb AAG58685.1 AE005580_7 (AE005580) putative ATP-binding component of dipeptide transport system [Escherichia coli O157:H7] SEQ ID n-3467 sp P37315 DPPC_ECOLI DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC_pir S47764 dipeptide transport system permease protein dppc - Escherichia coli gb AAA23704.1 (L08399) transmembrane protein [Escherichia coli] gb AAB18520.1 (U00039) dppc [Escherichia coli] gb AAC76567.1 (AE000431) dipeptide transport system permease protein 2 [Escherichia coli K12] gb AAG58686.1 AE005580_8 (AE005580) dipeptide transport system permease protein 2 [Escherichia coli O157:H7] SEQ ID n-3465 sp P37316 DPPB_ECOLI DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPB_pir S47765 dipeptide transport system permease protein dppb - Escherichia coli gb AAA23703.1 (L08399) transmembrane protein [Escherichia coli] gb AAB18521.1 (U00039) dppb [Escherichia coli] gb AAC76568.1 (AE000431) dipeptide transport system permease protein 1 [Escherichia coli K12] gb AAG58687.1 AE005580_9 (AE005580) dipeptide transport system permease protein 1 [Escherichia coli O157:H7] SEQ ID n-3464 </p>
<p> Contig9 from 3181624 to 3182523 SEQ ID n° 8576 PL-639.1 m 87% </p>	
<p> Contig9 from 3182534 to 3183553 SEQ ID n° 8577 PL-638.1 m 92% </p>	

SEQ ID n° 8578 PL-637.1	Contig9 from 3183672 to 3185279	m	84%	sp P23847 DPPA_ECOLI PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN PRECURSOR (DIPEPTIDE-BINDING PROTEIN) (DBP) pir A39194 periplasmic dipeptide transport protein precursor dppA - Escherichia coli emb CAA41090.1 (X58051) dipeptide binding protein (DBP) [Escherichia coli] gb AA23707.1 (M35045) dipeptide transporter protein [Escherichia coli] gb AA23702.1 (L08399) dipeptide-binding protein [Escherichia coli] gb AA18522.1 (U00039) dppA [Escherichia coli] gb AAC76569.1 (AE000431) dipeptide transport protein [Escherichia coli K12]	SEQ ID n° 3463
				gb AAG61057.1 AF322013_176 (AF322013) ID870 [Bradyrhizobium japonicum]	
SEQ ID n° 8579 PL-636.1	Contig9 from 3185882 to 3186802	m	46%	sp P37887 CYSK_BACSU CYSTEINE SYNTHASE (O- ACETYL SERINE SULFHYDRYLASE) (O-ACETYL SERINE (THIOL)-LYASE) (CSASE) (SUPEROXIDE-INDUCIBLE PROTEIN 11) (SOI11) pir S66103 cysteine synthase (EC 4.2.99.8) A - Bacillus subtilis dbj BAA05308.1 (D26185) cysteine synthetase A [Bacillus subtilis] emb CAB11849.1 (Z99104) cysteine synthetase A [Bacillus subtilis]	#N/A
				pir A70044 conserved hypothetical protein yvmC Bacillus subtilis gb AAC67279.1 (AF017113) yvmC [Bacillus subtilis] emb CAB15512.1 (Z99121) similar to hypothetical proteins [Bacillus subtilis] emb CAB15524.1 (Z99122) similar to hypothetical proteins [Bacillus subtilis]	
SEQ ID n° 8581 PL-635.1	Contig9 from 3187553 to 3188257	p	51%		SEQ ID n° 3461

SEQ ID n° 8582	PL-634.1	Contig9 from 3188343 to 3189566	p	64%	sp O34926 CYPX_BACSU PUTATIVE CYTOCHROME P450 CYPX pir F69611-cytochrome P450 cypX - Bacillus subtilis gb AAC67280.1 (AF017113) CypB [Bacillus subtilis] emb CAB1511.1 (Z99121) cytochrome P450-like enzyme [Bacillus subtilis] emb CAB1523.1 (Z99122) cytochrome P450-like enzyme [Bacillus subtilis] SEQ ID n-9460
SEQ ID n° 8583	PL-7138.1	Contig9 from 3189707 to 3189835	p	No Hits found	#N/A
SEQ ID n° 8584	PL-6311.1	Contig9 from 3189909 to 3190073	m	76%	ref NP_053144.1 ORF11 [Yersinia pestis] gb AAF05107.1 AF152923_11 (AF152923) ORF11 [Yersinia pestis] #N/A
SEQ ID n° 8585	PL-633.1	Contig9 from 3190184 to 3192253	m	89%	sp P00961 SYGB_ECOLI GLYCYL-TRNA SYNTHETASE BETA CHAIN (GLYCINE--TRNA LIGASE BETA CHAIN) (GLYRS) pir SYECGB glycine--trna ligase (EC 6.1.1.14) beta chain - Escherichia coli gb AA18536.1 (U00039) glycine-trna synthetase, beta subunit [Escherichia coli] gb AAC76583.1 (AE000433) glycine trna synthetase, beta subunit [Escherichia coli K12] SEQ ID n-9459
SEQ ID n° 8586	PL-632.1	Contig9 from 3192263 to 3193177	m	85%	gb AAG58708.1 AE005582_11 (AE005582) glycine trna synthetase, alpha subunit [Escherichia coli O157:H7] SEQ ID n-9458

SEQ ID n° 8587	PL-3693.1	Contig9 from 3193374 to 3193946	p	74%	sp P05100 3MGL_ECOLI_DNA-3-METHYLADEININE GLYCOSYLASE I (3-METHYLADEININE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) (DNA-3-METHYLADEININE GLYCOSIDASE I) pir DGEW1 3-methyladenine-DNA glycosylase (EC 3.2.2.-) I - Escherichia coli emb CAA27472.1 (X03845) TAGI (aa 1-187) [Escherichia coli] gb AA24658.1 (J02606) 3- methyladenine-DNA glycosylase I (tag) [Escherichia coli] gb AB18526.1 (U00039) 3- methyladenine DNA glycosylase I, constitutive [Escherichia coli] gb AAC78573.1 (AE000432) 3- methyl-adenine DNA glycosylase I, constitutive [Escherichia coli K12] gb AAG58721.1 AE005584_3 (AE005584) alanine- alpha-ketoisovalerate (or valine-pyruvate) transaminase, transaminase C [Escherichia coli O157:H7]	SEQ ID n-3880
SEQ ID n° 8588	PL-631.1	Contig9 from 3194152 to 3195405	p	82%	gb AAG58721.1 AE005584_3 (AE005584) alanine- alpha-ketoisovalerate (or valine-pyruvate) transaminase, transaminase C [Escherichia coli O157:H7]	SEQ ID n-3457
SEQ ID n° 8589	PL-6309.1	Contig9 from 3195624 to 3195746	p	No Hits found	#N/A	
SEQ ID n° 8590	PL-3692.1	Contig9 from 3196158 to 3196613	p	40%	gb AAG58890.1 AE005600_8 (AE005600) yldQ gene product [Escherichia coli O157:H7]	SEQ ID n-2879
SEQ ID n° 8591	PL-630.1	Contig9 from 3196676 to 3197965	m	70%	sp P31455 YIDR_ECOLI_HYPOTHETICAL_46.4_KD PROTEIN IN IBPA-GYRB INTERGENIC REGION pir B65171 hypothetical protein yldr - Escherichia coli (strain K-12) gb AAC76712.1 (AE000446) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-3456
SEQ ID n° 8592	PL-629.1	Contig9 from 3198099 to 3198716	p	74%	gb AAG58790.1 AE005592_1 (AE005592) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-3454
SEQ ID n° 8593	PL-628.1	Contig9 from 3198710 to 3200452	m	50%	sp P25772 YICF_ECOLI_HYPOTHETICAL_63.2_KD PROTEIN IN RPH-GMK INTERGENIC REGION	SEQ ID n-3453

SEQ ID n° 8594	PL-6307.1	Contig9 from 3200953 to 3201042	p	No Hits found	pir C82602 hypothetical protein XF2068 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84867.1 AE004023.3 (AE004023) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 8595	PL-3691.1	Contig9 from 3201104 to 3201559	p	40%	ref NP_052451.1 yacB [Plasmid Colib-P9] dbj BAA75090.1 (AB021078) yacB [Plasmid Colib- P9]	SEQ ID n-2878 #N/A
SEQ ID n° 8596	PL-6305.1	Contig9 from 3201873	p	51%	ref NP_046944.1 gp48 [Bacteriophage N15] pir T13135 protein gp48 - phage N15 gb AAC19087.1 (AF064539) gp48 [Bacteriophage N15]	#N/A
SEQ ID n° 8597	PL-6304.1	Contig9 from 3202176 to 3202454	p	43%		#N/A
SEQ ID n° 8598	PL-7137.1	Contig9 from 3202485 to 3202619	p	No Hits found		#N/A
SEQ ID n° 8599	PL-627.1	Contig9 from 3203447 to 3204106	p	No Hits found		#N/A
SEQ ID n° 8600	PL-7136.1	Contig9 from 3204997 to 3205383	m	No Hits found		SEQ ID n-3452 #N/A
SEQ ID n° 8601	PL-626.1	Contig9 from 3205458 to 3206198	p	No Hits found		SEQ ID n-3451
SEQ ID n° 8602	PL-625.1	Contig9 from 3206736 to 3207425	p	No Hits found		SEQ ID n-3450
SEQ ID n° 8603	PL-623.1	Contig9 from 3208192 to 3209415	p	27%	gb AAF50913.2 (AF003571) HERC2 gene product [Drosophila melanogaster]	SEQ ID n-3448
SEQ ID n° 8604	PL-6300.1	Contig9 from 3209500 to 3209676	m	No Hits found		#N/A

Contig9 from SEQ ID n° 8605 PL-622.1	3209652 to 3210947	p 21%	gb AAF50913.2 (AE003571) HERC2 gene product [Drosophila melanogaster]	SEQ ID n-3447
Contig9 from SEQ ID n° 8606 PL-6298.1	3211027 to 3211239	m 54%	emb CAB41498.1 (AJ238399) hypothetical transposase [Escherichia coli]	#N/A
Contig9 from SEQ ID n° 8607 PL-6297.1	3211357 to 3211518	m No Hits found		#N/A
Contig9 from SEQ ID n° 8608 PL-621.1	3211648 to 3212271	p 79%	sp P24234 KGUA_ECOLI GUANYLATE KINASE (GMP KINASE) pif KIECGU guanylate kinase (EC 2.7.4.8) - Escherichia coli gb AAB88711.1 (M84400) GMP kinase [Escherichia coli] gb AAA62001.1 (L10328) 5'guanylate kinase [Escherichia coli] gb AAC76672.1 (AE000442) guanylate kinase [Escherichia coli K12] sp P08374 RPOZ_ECOLI DNA-DIRECTED RNA POLYMERASE OMEGA CHAIN (TRANSCRIPTASE OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT) pif RNECO DNA- directed RNA polymerase (EC 2.7.7.6) omega chain - Escherichia coli gb AAA24229.1 (M15266) omega protein [Escherichia coli] gb AAB00159.1 (M24503) omega protein [Escherichia coli] gb AAA62002.1 (L10328) RNA polymerase omega subunit [Escherichia coli] gb AAC76673.1 (AE000442) RNA polymerase, omega subunit [Escherichia coli K12] gb AAC58793.1 AE005592_4 (AE005592) RNA polymerase, omega subunit [Escherichia coli O157:H7]	SEQ ID n-3446
Contig9 from SEQ ID n° 8609 PL-6296.1	3212326 to 3212601	p 78%		#N/A

855

SEQ ID n° 8610	PL-620.1	Contig9 from 3212619 to 3214736	p	88%	m	No Hits found	sp P17580 SPOT_ECOLI_GUANOSINE-3',5'- BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (PPGPP)ASE (PENTA-PHOSPHATE GUANOSINE-3'-PYROPHOSPHOHYDROLASE) pir SHECGD guanosine 3',5'-bis(diphosphate) 3'- pyrophosphatase (EC 3.1.7.2) - Escherichia coli gb AA62003.1 (U10328) (p)ppGpp 3'-pyrophosphohydrolase [Escherichia coli] gb AAB00160.1 (M24503) (p)ppGpp 3'- pyrophosphohydrolase [Escherichia coli] gb AAC76674.1 (AE000442) (p)ppGpp synthetase II; also guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase [Escherichia coli K12] gb AAG58794.1 AE005592_5 (AE005592) (p)ppGpp synthetase II; also guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase [Escherichia coli O157:H7]	SEQ ID n-9445
SEQ ID n° 8611	PL-3690.1	Contig9 from 3214668 to 3215159	m	31%	m	No Hits found	ref NP_073234.1 orf10 [Salmonella enterica serovar Choleraesuis] dbj BAB20517.1 (AB040415) orf10 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-2877
SEQ ID n° 8612	PL-3689.1	Contig9 from 3215174 to 3215674	m	54%	m	No Hits found	sp P30130 FIMD_ECOLI OUTER MEMBRANE USHER PROTEIN FIMD PRECURSOR pir S56542 outer membrane usher protein fimD precursor - Escherichia coli gb AAA97213.1 (U14003) CG Site No. 18349 [Escherichia coli] gb AAC77273.1 (AE000502) outer membrane protein; export and assembly of type 1 fimbriae, interrupted [Escherichia coli K12]	SEQ ID n-3442
SEQ ID n° 8613	PL-619.1	Contig9 from 3215806 to 3217131	m		m			SEQ ID n-3443
SEQ ID n° 8614	PL-618.1	Contig9 from 3217300 to 3219930	m		m			SEQ ID n-3443

SEQ ID n° 8615	PL-617.1	Contig9 from 3220114 to 3220908	m	47%	gb AAG55424.1 AE005284_2 (AE005284) putative chaperone [Escherichia coli O157:H7]	SEQ ID n-9441
SEQ ID n° 8616	PL-616.1	Contig9 from 3220945 to 3221664	m	50%	gb AAG59498.1 AE005662_10 (AE005662) periplasmic chaperone, required for type 1 fimbriae [Escherichia coli O157:H7]	SEQ ID n-9440
SEQ ID n° 8617	PL-615.1	Contig9 from 3221745 to 3222401	m	No Hits found		SEQ ID n-9439
SEQ ID n° 8618	PL-614.1	Contig9 from 3222491 to 3223213	m	No Hits found		SEQ ID n-9438
SEQ ID n° 8619	PL-613.1	Contig9 from 3223281 to 3223853	m	No Hits found	#N/A	
SEQ ID n° 8620	PL-612.1	Contig9 from 3223891 to 3224631	m	45%	gb AAG58694.1 AE005581_6 (AE005581) putative fimbrial chaperone [Escherichia coli O157:H7]	SEQ ID n-9437
SEQ ID n° 8621	PL-611.1	Contig9 from 3224758 to 3225363	m	36%	gb AAB41914.1 (U31413) FcTA precursor [Escherichia coli]	SEQ ID n-9436
SEQ ID n° 8622	PL-610.1	Contig9 from 3225789 to 3226355	m	70%	sp P04742 FIMB_ECOLI TYPE 1 FIMBRIAE REGULATORY PROTEIN FIMB pir S56537 recombinase fimb (involved in phase variation) - Escherichia coli pir RGECHF type 1 fimbriae regulatory protein fimb - Escherichia coli gb AAA97208.1 (U14003) recombinase involved in phase variation [Escherichia coli] gb AAC77268.1 (AE000502) recombinase involved in phase variation; regulator for fima [Escherichia coli K12] gb AAG59494.1 AE005662_6 (AE005662) recombinase involved in phase variation; regulator for fima [Escherichia coli O157:H7]	SEQ ID n-9435

SEQ ID n° 8623	PL-609.1	Contig9 from 3226767 to 3228878	p	86%	gb AAG58796.1 AE005592.7 (AE005592) DNA helicase, resolution of Holliday junctions, branch migration [Escherichia coli O157:H7]	SEQ ID n-3433
SEQ ID n° 8624	PL-6289.1	Contig9 from 3229534 to 3229812	p	No Hits found		#N/A
SEQ ID n° 8625	PL-6288.1	Contig9 from 3229906 to 3230166	p	No Hits found		#N/A
SEQ ID n° 8626	PL-6287.1	Contig9 from 3230826 to 3231041	m	No Hits found		#N/A
SEQ ID n° 8627	PL-6286.1	Contig9 from 3231155 to 3231445	m	74%	gb AAC84004.1 (AF072126) stability protein stbE [Morganella morganii]	#N/A
SEQ ID n° 8628	PL-6285.1	Contig9 from 3231435 to 3231689	m	51%	sp P07007 RELB_ECOLI RELB PROTEIN pir BVECRB relB protein - Escherichia coli emb CAA26250.1 (X02405) relB protein (aa 1-79) [Escherichia coli] dbj BAA15263.1 (D90798) RelB protein [Escherichia coli] dbj BAA15273.1 (D90799) RelB protein [Escherichia coli] dbj BAA15295.1 (D90800) RelB protein [Escherichia coli] gb AAC74637.1 (AE000253) negative regulator of translation [Escherichia coli K12] pir C81019 hypothetical protein NME1983 [imported] - Neisseria meningitidis (group B strain MD58, group A strain Z2491) gb AAF42311.1 (AE002547) hypothetical protein [Neisseria meningitidis MC58] emb CAB83756.1 (AL162753) hypothetical protein [Neisseria meningitidis Z2491]	#N/A
SEQ ID n° 8629	PL-608.1	Contig9 from 3232096 to 3232863	m	39%		SEQ ID n-3432

SEQ ID n° 8630	PL-6283.1	Contig9 from 3233779 to 3234048	p	42%	pir B82474 hypothetical protein VCA0312 VCA0386 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAC38426.1 (AF055586) unknown [Vibrio cholerae] gb AAF96220.1 (AE004370) hypothetical protein [Vibrio cholerae] gb AAF96292.1 (AE004374) hypothetical protein [Vibrio cholerae] #N/A pir F82466 conserved hypothetical protein VCA0385 VCA0311 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96219.1 (AE004370) hypothetical protein [Vibrio cholerae] gb AAF96291.1 (AE004374) conserved hypothetical protein [Vibrio cholerae] #N/A dbj BAA92862.1 (AB040403) TRP-1 [Burkholderia glumae] SEQ ID n-9431
SEQ ID n° 8631	PL-6282.1	Contig9 from 3234051 to 3234458	p	35%	sp P19933 GLTS_ECOLI SODIUM/GLUTAMATE SYMPORT CARRIER PROTEIN (GLUTAMATE PERMEASE) pir S14031 glts protein - Escherichia coli pir Y0ECNQ sodium--glutamate symport carrier protein - Escherichia coli emb CAA35540.1 (X17499) glts protein [Escherichia coli] gb AAA62006.1 (U10328) glutamate permease [Escherichia coli] gb AAC76677.1 (AE000442) glutamate transport [Escherichia coli K12] emb CAA06472.1 (AJ005325) glutamate permease [synthetic construct] emb CAA06475.1 (AJ005328) glutamate permease [synthetic construct] emb CAA06485.1 (AJ005339) glutamate permease [synthetic construct] SEQ ID n-9430
SEQ ID n° 8632	PL-607.1	Contig9 from 3234734 to 3235477	m	60%	
SEQ ID n° 8633	PL-6281.1	Contig9 from 3236121 to 3236345	m	No Hits found	#N/A
SEQ ID n° 8634	PL-606.1	Contig9 from 3236589 to 3237797	m	89%	

SEQ ID n° 8635	PL-605.1	Contig9 from 3238040 to 3239425	p	86%	sp P27432 YICE_ECOLI PUTATIVE PURINE PERMEASE YICE pir H65166 hypothetical 48.9 kD protein in gltS 3'region - Escherichia coli (strain K-12) gb AAA62007.1 (L10328) o463 [Escherichia coli] gb AAC76678.1 (AE000443) putative transport protein [Escherichia coli K12] gb AAG58799.1 AE005593_1 (AE005593) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-9429
SEQ ID n° 8636	PL-604.1	Contig9 from 3239634 to 3241187	m	70%	gb AAC38324.1 (AF031325) phenol hydroxylase [Bacillus thermoleovorans]	SEQ ID n-9428
SEQ ID n° 8637	PL-603.1	Contig9 from 3241659 to 3243365	p	55%	sp P31433 YICH_ECOLI HYPOTHETICAL 62.3 KD PROTEIN IN GLTS-SELC INTERGENIC REGION pir A65167 hypothetical 62.3K protein (gltS- selc region) - Escherichia coli (strain K-12) gb AAC76679.1 (AE000443) orf, hypothetical protein [Escherichia coli K12] pir F69044 mutator MutT protein homolog - Methanobacterium thermoautotrophicum (strain Delta H) gb AAB85814.1 (AE000897) mutator MutT protein homolog [Methanothermobacter thermautotrophicus]	SEQ ID n-9427
SEQ ID n° 8638	PL-6280.1	Contig9 from 3243536 to 3243958	p	44%	sp P32148 YIID_ECOLI HYPOTHETICAL 37.1 KD PROTEIN IN RBN-FDHE INTERGENIC REGION (O329) pir S40832 hypothetical 37.1K protein (glnA- fdhB intergenic region) - Escherichia coli gb AAB03021.1 (L19201) ORF_o329 [Escherichia coli] gb AAD13450.1 (AE000464) putative acetyltransferase (EC 2.3.1.18) [Escherichia coli K12]	#N/A
SEQ ID n° 8639	PL-602.1	Contig9 from 3243996 to 3244913	m	80%		SEQ ID n-9426

SEQ ID n° 8640	PL-6278.1	Contig9 from 3244986 to 3245423	m	85%	sp P32147 YIHZ_ECOLI_HYPOTHETICAL 15.9 KD PROTEIN IN RBN-FDHE INTERGENIC REGION (O145) pir S40831 hypothetical 15.9K protein (glrA- fdhE intergenic region) - Escherichia coli gb AB03020.1 (L19201) ORF_0145 [Escherichia coli] gb AAD13449.1 (AE000464) orf, hypothetical protein [Escherichia coli K12] gb AAG59077.1 AE005619_10 (AE005619) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8641	PL-601.1	Contig9 from 3245467 to 3246093	m	68%	gb AAG59075.1 AE005619_8 (AE005619) putative phosphatase [Escherichia coli O157:H7]	SEQ ID n-3425
SEQ ID n° 8642	PL-600.1	Contig9 from 3246250 to 3247704	p	77%	gb AAK02216.1 (AE006048) unknown [Pasteurella multocida]	SEQ ID n-3424
SEQ ID n° 8643	PL-599.1	Contig9 from 3248759 to 3249328	p	41%	emb CAB56502.1 (AJ249744) putative membrane protein CjaE [Campylobacter jejuni]	SEQ ID n-3421
SEQ ID n° 8644	PL-598.1	Contig9 from 3249391 to 3251211	m	92%	emb CAC20136.1 (AJ278218) BipA protein [Escherichia coli] gb AAG59060.1 AE005618_1 (AE005618) putative GTP-binding factor [Escherichia coli O157:H7]	SEQ ID n-3420
SEQ ID n° 8645	PL-6275.1	Contig9 from 3251333 to 3251566	m	No Hits found		#N/A
SEQ ID n° 8646	PL-596.1	Contig9 from 3251671 to 3253080	p	86%	sp P28786 GLNA_PROVU GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) pir S23899 glutamate--ammonia ligase (EC 6.3.1.2) - Proteus vulgaris emb CAA48234.1 (X68129) glutamate-- ammonia ligase [Proteus vulgaris]	SEQ ID n-3418
SEQ ID n° 8647	PL-595.1	Contig9 from 3253234 to 3254283	p	83%	sp P06218 NTRB_KLEPN NITROGEN REGULATION PROTEIN II NTRB pir A24114 nitrogen regulation protein II (EC 2.7.3.-) ntrB - Klebsiella pneumoniae emb CAA26923.1 (X03146) ntrB protein (aa 1-349) [Klebsiella pneumoniae]	SEQ ID n-3417

SEQ ID n° 8648	PL-594.1	Contig9 from 3254293 to 3255765	p	83%	sp P41789 NTRC_SALTY_NITROGEN_REGULATION_PROTEIN NR(I) pir S53024 nitrogen regulation protein I ntrC - Salmonella typhimurium emb CAA59425.1 (X85104) nitrogen regulatory protein C [Salmonella typhimurium]	SEQ ID n-9416
SEQ ID n° 8649	PL-593.1	Contig9 from 3255831 to 3257240	m	48%	gb AAC92523.1 (AF027768) TnpA [Serratia marcescens]	SEQ ID n-9415
SEQ ID n° 8650	PL-592.1	Contig9 from 3257144 to 3260350	m	5%	ref NP_051667.1 conserved hypothetical protein [Deinococcus radiodurans] pir D75633 conserved hypothetical protein - Deinococcus radiodurans (strain R1)	
SEQ ID n° 8651	PL-591.1	Contig9 from 3261907 to 3263280	m	86%	gb AAF12566.1 AE001826_35 (AE001826) conserved hypothetical protein [Deinococcus radiodurans] sp P37129 HEMN_SALTY_OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE) gb AAA19690.1 (U06779) putative oxygen- independent coproporphyrinogen III oxidase [Salmonella typhimurium]	SEQ ID n-9414
SEQ ID n° 8652	PL-6269.1	Contig9 from 3263283 to 3263447	m	No Hits found		SEQ ID n-9413
SEQ ID n° 8653	PL-3688.1	Contig9 from 3263474 to 3263983	m	66%	sp P37130 YIHI_SALTY_HYPOTHETICAL_19.2_KD PROTEIN IN POLA-HEMN INTERGENIC REGION gb AAA19691.1 (U06779) putative protein [Salmonella typhimurium]	SEQ ID n-2874
SEQ ID n° 8654	PL-589.1	Contig9 from 3264177 to 3265640	p	24%	pir B70367 hypothetical protein aq_765 - Aquifex aeolicus gb AAC06926.1 (AE000706) putative protein [Aquifex aeolicus]	SEQ ID n-9410
SEQ ID n° 8655	PL-6268.1	Contig9 from 3265685 to 3265795	m	No Hits found		#N/A
SEQ ID n° 8656	PL-588.1	Contig9 from 3266032 to 3267711	p	60%	gb AAC31980.1 (L39897) HecB [Pectobacterium chrysanthemi]	SEQ ID n-3409

SEQ ID n° 8657	PL-587.1	Contig9 from 3267687 to 3272900	p 40%	pir G81044 hemagglutinin/hemolysin-related protein NMB1779 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF42119.1 (AE002527) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	SEQ ID n-3408
SEQ ID n° 8658	PL-3687.1	Contig9 from 3272906 to 3273451	p No Hits found		SEQ ID n-2873
SEQ ID n° 8659	PL-6266.1	Contig9 from 3273582 to 3273866	p No Hits found	#N/A	
SEQ ID n° 8660	PL-3686.1	Contig9 from 3273990 to 3274358	p No Hits found		SEQ ID n-2872
SEQ ID n° 8661	PL-585.1	Contig9 from 3274785 to 3275528	m 71%	pir G83371 probable amino acid permease PA2202 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05590.1 AE004646_11 (AE004646) probable amino acid permease [Pseudomonas aeruginosa]	SEQ ID n-3406
SEQ ID n° 8662	PL-584.1	Contig9 from 3275530 to 3276267	m 69%	pir H83371 probable amino acid permease PA2203 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05591.1 AE004646_12 (AE004646) probable amino acid permease [Pseudomonas aeruginosa]	SEQ ID n-3405
SEQ ID n° 8663	PL-583.1	Contig9 from 3276349 to 3277185	m 70%	pir C83369 probable binding protein component of ABC transporter PA2204 [imported] Pseudomonas aeruginosa (strain PAO1) gb AAG05592.1 AE004647_1 (AE004647) probable binding protein component of ABC transporter [Pseudomonas aeruginosa]	SEQ ID n-3404

SEQ ID n° 8664	PL-582.1	Contig9 from 3277354 to 3278085	m	88%	sp P07656 PHOU_ECOLI PHOSPHATE TRANSPORT SYSTEM PROTEIN PHOU pir BVECFU peripheral membrane protein U - Escherichia coli emb CAA26510.1 (X02723) phoU gene product (aa 1-241) [Escherichia coli] gb AAA24382.1 (K01992) peripheral membrane protein U [Escherichia coli] gb AAC76747.1 (AE000449) negative regulator for pho regulon and putative enzyme in phosphate metabolism [Escherichia coli K12] SEQ ID n-9403
					sp P07655 PSTB_ECOLI PHOSPHATE TRANSPORT ATP- BINDING PROTEIN PSTB pir BVECFU ABC-type phosphate transport system ATP-binding protein pstB [validated] - Escherichia coli emb CAA26509.1 (X02723) pstB gene product (aa 1- 257) [Escherichia coli] gb AAA24381.1 (K01992) peripheral membrane protein B [Escherichia coli] gb AAA62076.1 (U10328) peripheral membrane protein B [Escherichia coli] gb AAC76748.1 (AE000449) ATP-binding component of high- affinity phosphate-specific transport system [Escherichia coli K12] gb AAG58921.1 AE005603_7 (AE005603) ATP-binding component of high-affinity phosphate- specific transport system [Escherichia coli O157:H7] SEQ ID n-9402
SEQ ID n° 8666	PL-580.1	Contig9 from 3278891 to 3279775	m	89%	dbj BAA22863.1 (D89963) integral membrane protein A [Enterobacter cloacae] SEQ ID n-9401
					dbj BAA22862.1 (D89963) peripheral membrane protein C [Enterobacter cloacae] SEQ ID n-9399

SEQ ID n° 8668	PL-577.1	Contig9 from 3280865 to 3281905	m	85%	<p>sp P06128 PSTS_ECOLI PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR (PBP) pir [BYECP phosphate-repressible phosphate-binding protein precursor [validated] - Escherichia coli gb AAA24378.1 (K01992) phosphate-binding protein [Escherichia coli] gb AAC76751.1 (AE000449) high-affinity phosphate-specific transport system; periplasmic phosphate-binding protein [Escherichia coli K12]</p>	SEQ ID n-9398
SEQ ID n° 8669	PL-576.1	Contig9 from 3282244 to 3283575	m	75%	<p>sp P08982 ENVZ_SALTY OSMOLARITY SENSOR PROTEIN ENVZ pir [S01367 inner membrane protein envZ - Salmonella typhimurium emb CAA30935.1 (X12374) envZ inner membrane protein (AA 1 - 450) [Salmonella typhimurium]</p>	SEQ ID n-9397
SEQ ID n° 8670	PL-575.1	Contig9 from 3283572 to 3284291	m	75%	<p>sp P03025 OMPR_ECOLI TRANSCRIPTIONAL REGULATORY PROTEIN OMPR pir [RGEOR osmosensor response regulator ompR - Escherichia coli gb AAA16241.1 (J01656) OmpR protein [Escherichia coli] emb CAA54510.1 (X77305) ompR [Salmonella typhi] gb AAA58202.1 (U18997) CG Site No. 434; alternate name ompB [Escherichia coli] gb AAC76430.1 (AE000416) response regulator (sensor, EnvZ) affecting transcription of ompC and ompF: outer membrane protein synthesis [Escherichia coli K12] gb AAG58506.1 AE005562_9 (AE005562) response regulator (sensor, EnvZ) affecting transcription of ompC and ompF: outer membrane protein synthesis [Escherichia coli O157:H7]</p>	SEQ ID n-9396

Contig9 from 3285145 to 3285618	SEQ ID n° 8671 PL-3684.1	pir A65136 transcription elongation factor greb - Escherichia coli (strain K-12) gb AAAS8203.1 (U18997) ORF_0170 [Escherichia coli] gb AAC76431.1 (AE000416) transcription elongation factor and transcript cleavage [Escherichia coli K12]	SEQ ID n-2871
Contig9 from 3286041 to 3288371	SEQ ID n° 8672 PL-574.1	sp P46837 YHGF_ECOLI 85.1 KDA PROTEIN IN GREB- FEOA INTERGENIC REGION sp P33649 FEOA_ECOLI FERROUS IRON TRANSPORT PROTEIN A pir B36932 iron(II) transport system protein feoA - Escherichia coli emb CAA50386.1 (X71063) feoA [Escherichia coli] gb AAAS8206.1 (U18997) CG Site No. 28964 [Escherichia coli] gb AAC76433.1 (AE000416) ferrous iron transport protein A [Escherichia coli K12] gb AAG58509.1 AE005563_3 (AE005563) ferrous iron transport protein A [Escherichia coli O157:H7]	SEQ ID n-3395
Contig9 from 3288769 to 3289002	SEQ ID n° 8673 PL-6263.1	gb AAG58510.1 AE005563_4 (AE005563) ferrous iron transport protein B [Escherichia coli O157:H7]	#N/A
Contig9 from 3289055 to 3291367	SEQ ID n° 8674 PL-573.1	sp P46845 YHGG_ECOLI HYPOTHETICAL 8.7 KD PROTEIN IN FEOB-BIOH INTERGENIC REGION (O78) pir B65136 hypothetical 8.7 kD protein in feoB- bioH intergenic region - Escherichia coli (strain K-12) gb AAAS8208.1 (U18997) ORF_078 [Escherichia coli] gb AAC76435.1 (AE000416) orf, hypothetical protein [Escherichia coli K12] gb AAG58511.1 AE005563_5 (AE005563) orf, hypothetical protein [Escherichia coli O157:H7] ref NP_046944.1 gp48 [Bacteriophage N15] pir T13135 protein gp48 - phage N15 gb AAC19087.1 (AF064539) gp48 [Bacteriophage N15]	SEQ ID n-3394
Contig9 from 3291377 to 3291616	SEQ ID n° 8675 PL-6262.1		#N/A
Contig9 from 3291739 to 3292041	SEQ ID n° 8676 PL-3683.1		SEQ ID n-2870

Contig9 from SEQ ID n° 8677 PL-6261.1 3292034 to 3292366	m	48%	ref NP_046945.1 gp49 [Bacteriophage N15] pir T13136 protein gp49 - phage N15 gb AAC19088.1 (AF064539) gp49 [Bacteriophage N15] #N/A
Contig9 from SEQ ID n° 8678 PL-572.1 3292443 to 3293228	m	74%	sp P13001 BIOH_ECOLI BIOH PROTEIN pir BVECBH bioh protein - Escherichia coli emb CAA33612.1 (X15587) bioh protein (AA 1-256) [Escherichia coli] gb AA58210.1 (U18997) CG Site No. 954; alternate name bioB [Escherichia coli] gb AAC76437.1 (AE000417) biotin biosynthesis; reaction prior to pimeloyl CoA [Escherichia coli K12] SEQ ID n-9393
Contig9 from SEQ ID n° 8679 PL-6260.1 3293228 to 3293521	p	No Hits found	gb AAC71703.1 (AF060183) putative methyltransferase [Mycobacterium avium] gb AAD20365.1 (AF125999) methyltransferase mtfc [Mycobacterium avium] gb AAD44210.1 AF143772_12 (AF143772) Mtfc [Mycobacterium avium] SEQ ID n-2868 pir S16426 tyrosine--trna ligase (EC 6.1.1.1) TyrZ - Bacillus subtilis emb CAA51565.1 (X73124) ipa-9r [Bacillus subtilis] emb CAB15872.1 (Z99123) tyrosyl-trna synthetase [Bacillus subtilis] SEQ ID n-9392
Contig9 from SEQ ID n° 8681 PL-571.1 3294482 to 3295681	m	61%	gb AAG58513.1 AE005563_7 (AE005563) biotin biosynthesis; reaction prior to pimeloyl CoA [Escherichia coli O157:H7] #N/A
Contig9 from SEQ ID n° 8682 PL-6258.1 3295793 to 3295990	m	43%	pir H65136 hypothetical 27.7 kD protein in bioh- gntt intergenic region - Escherichia coli (strain K-12) gb AA58211.1 (U18997) ORF_0243 [Escherichia coli] gb AAC76438.1 (AE000417) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-9391
Contig9 from SEQ ID n° 8683 PL-570.1 3296009 to 3296713	p	51%	

SEQ ID n° 8684	PL-3680.1	Contig9 from 3296773 to 3297348	p	93%	sp P46847 YHGI_ECOLI PROTEIN YHGI pir A65137 hypothetical 21.0 kD protein in bioh-gntt intergenic region - Escherichia coli (strain K-12) gb AAA58212.1 (U18997) ORF_0191 [Escherichia coli] gb AAC76439.1 (AE000417) orf, hypothetical protein [Escherichia coli K12] gb AAG58515.1 AE005563_9 (AE005563) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2867
SEQ ID n° 8685	PL-6255.1	Contig9 from 3297479 to 3297814	p	53%	gb AAG58529.1 AE005565_4 (AE005565) protein of glp regulon [Escherichia coli O157:H7] #N/A
SEQ ID n° 8686	PL-569.1	Contig9 from 3297823 to 3298671	p	66%	gb AAG58528.1 AE005565_3 (AE005565) protein of glp regulon [Escherichia coli O157:H7] SEQ ID n-9389
SEQ ID n° 8687	PL-568.1	Contig9 from 3298689 to 3299447	p	87%	gb AAG58527.1 AE005565_2 (AE005565) repressor of the glp operon [Escherichia coli O157:H7] SEQ ID n-9388
SEQ ID n° 8688	PL-567.1	Contig9 from 3299688 to 3301190	p	84%	gb AAG58530.1 AE005565_5 (AE005565) sn-glycerol- 3-phosphate dehydrogenase (aerobic) [Escherichia coli O157:H7] SEQ ID n-9387
SEQ ID n° 8689	PL-6253.1	Contig9 from 3301467 to 3301697	m	48%	gb AAG59083.1 AE005620_5 (AE005620) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 8690	PL-566.1	Contig9 from 3302031 to 3302930	p	45%	pir C82284 hypothetical protein VC0764 [Imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93929.1 (AE004161) hypothetical protein [Vibrio cholerae] SEQ ID n-9386
SEQ ID n° 8691	PL-565.1	Contig9 from 3303153 to 3303707	m	No Hits found	SEQ ID n-9385
SEQ ID n° 8692	PL-6252.1	Contig9 from 3303849 to 3304097	p	44%	gb AAG53986.1 AF327444_2 (AF327444) putative transposase B [Erwinia herbicola] #N/A
SEQ ID n° 8693	PL-3679.1	Contig9 from 3304275 to 3304820	m	53%	gb AAD38236.1 (U17224) CarH [Pectobacterium carotovorum] SEQ ID n-2865

868

SEQ ID n° 8694	PL-3678.1	Contig9 from 3304817 to 3305353	m	55%	gb AAD38235.1 (U17224) CarG [Pectobacterium carotovorum]	SEQ ID n-2864
SEQ ID n° 8695	PL-3677.1	Contig9 from 3305343 to 3306191	m	58%	gb AAD38234.1 (U17224) CarF [Pectobacterium carotovorum]	SEQ ID n-2863
SEQ ID n° 8696	PL-6951.1	Contig9 from 3306199 to 3306453	m	62%	gb AAD38233.1 (U17224) CarE [Pectobacterium carotovorum]	#N/A
SEQ ID n° 8697	PL-3101.1	Contig9 from 3306440 to 3307624	m	62%	sp Q9XB58 CARD_ERWCA CARBAPENEM ANTIBIOTICS BIOSYNTHESIS PROTEIN CARD gb AAD38232.1 (U17224) CarD [Pectobacterium carotovorum]	SEQ ID n-2342
SEQ ID n° 8698	PL-3100.1	Contig9 from 3307701 to 3308522	m	89%	gb AAD38231.1 (U17224) CarC [Pectobacterium carotovorum]	SEQ ID n-2341
SEQ ID n° 8699	PL-3099.1	Contig9 from 3308536 to 3309285	m	78%	gb AAD38230.1 (U17224) CarB [Pectobacterium carotovorum]	SEQ ID n-2338
SEQ ID n° 8700	PL-3098.1	Contig9 from 3309288 to 3310793	m	70%	gb AAD38229.1 (U17224) CarA [Pectobacterium carotovorum]	SEQ ID n-2337
SEQ ID n° 8701	PL-6251.1	Contig9 from 3311570 to 3311740	m	No Hits found		#N/A
SEQ ID n° 8702	PL-6250.1	Contig9 from 3311929 to 3312201	p	73%	gb AAG58522.1 AE005564_7 (AE005564) orf; hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8703	PL-3676.1	Contig9 from 3312192 to 3312680	p	66%	gb AAG58523.1 AE005564_8 (AE005564) orf; hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2862

SEQ ID n° 8704	PL-3097.1	3312763 to 3313395	m	75%	<p>Contig9 from</p> <p>sp P44480 ALKH_HAEMIN PUTATIVE KHG/KDPG ALDOLASE [INCLUDES: 4-HYDROXY-2-OXOGLUTARATE ALDOLASE (2-KETO-4-HYDROXYGLUTARATE ALDOLASE) (KHG-ALDOLASE); 2-DEHYDRO-3- DEOXYPHOSPHOGLUCONATE ALDOLASE (PHOSPHO-2-DEHYDRO-3-DEOXYGLUCONATE ALDOLASE) (PHOSPHO-2-KETO-3-DEOXYGLUCONATE ALDOL> pir A64045 KHG-KDPG bifunctional aldolase HI0047 [similarity] - Haemophilus influenzae (strain Rd KW20) gb AAC21725.1 (U32690) 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphoglucuronate aldolase (eda) [Haemophilus influenzae Rd]</p>	SEQ ID n-2336
SEQ ID n° 8705	PL-3096.1	3313410 to 3314354	m	67%	<p>Contig9 from</p> <p>sp P44482 KDGK_HAEMIN 2-DEHYDRO-3- DEOXYGLUCONOKINASE (2-KETO-3-DEOXYGLUCONOKINASE) (3-DEOXY-2-OXO-D-GLUCONATE KINASE) (KDG KINASE) pir C64045 2-dehydro-3-deoxyglucokinase homolog - Haemophilus influenzae (strain Rd KW20) gb AAC21727.1 (U32690) 2- dehydro-3-deoxyglucokinase (kdgK) [Haemophilus influenzae Rd]</p>	SEQ ID n-2335
SEQ ID n° 8706	PL-3095.1	3314351 to 3315775	m	76%	<p>Contig9 from</p> <p>sp P42607 UXAC_ECOLI URONATE ISOMERASE (GLUCURONATE ISOMERASE) (URONIC ISOMERASE) pir A65098 glucuronate isomerase (EC 5.3.1.12) Escherichia coli dbj BA02587.1 (D13328) Uronate isomerase [Escherichia coli] gb AAC76127.1 (AE000391) uronate isomerase [Escherichia coli K12]</p>	SEQ ID n-2334
SEQ ID n° 8707	PL-3094.1	3315772 to 3317253	m	75%	<p>Contig9 from</p> <p>gb AAG59505.1 AE005663_3 (AE005663) mannonate oxidoreductase [Escherichia coli O157:H7]</p>	SEQ ID n-2333
SEQ ID n° 8708	PL-3093.1	3317281 to 3318594	m	79%	<p>Contig9 from</p> <p>sp P40800 YGIK_SALTY HYPOTHETICAL 46.1 KD PROTEIN IN PLSC 3'REGION gb AAA56680.1 (U09309) YgiK [Salmonella typhimurium]</p>	SEQ ID n-2332

SEQ ID n° 8709	PL-3675.1	Contig9 from 3318622 to 3319128	m	51%	gb AAF01413.1 AF186091_1 (AF186091) putative small integral C4-dicarboxylate membrane transport protein DctQ [Klebsiella pneumoniae] dbj BAB04420.1 (AP001509) C4-dicarboxylate transport system (C4-dicarboxylate- binding protein) [Bacillus halodurans] sp P39161 UXUR_ECOLI UXU OPERON TRANSCRIPTIONAL REGULATOR pir S56549 regulatory protein uxur - Escherichia coli gb AAA97220.1 (U14003) CG Site No. 12 [Escherichia coli] dbj BAA02592.1 (D13329) uxu regulon repressor [Escherichia coli] gb AAC77280.1 (AE000503) regulator for uxu operon [Escherichia coli K12] sp P44488 UXUA_HAEIN MANNONATE DEHYDRATASE (D- MANNONATE HYDROLASE) pir EG4045 mannonate dehydratase (EC 4.2.1.8) - Haemophilus influenzae gb AAC21733.1 (U32690) mannonate dehydratase (uxuA) [Haemophilus influenzae Rd] #N/A	SEQ ID n-2861
SEQ ID n° 8710	PL-3092.1	Contig9 from 3319426 to 3320406	p	54%	pir B82354 deoxycytidylate deaminase-related protein VC0175 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93351.1 (AE004108) deoxycytidylate deaminase-related protein [Vibrio cholerae] emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis]	SEQ ID n-2331
SEQ ID n° 8711	PL-3091.1	Contig9 from 3320525 to 3321268	p	71%	emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis]	SEQ ID n-2326
SEQ ID n° 8712	PL-3090.1	Contig9 from 3321306 to 3322493	p	83%	emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis]	SEQ ID n-2325
SEQ ID n° 8713	PL-6247.1	Contig9 from 3322835 to 3323005	m	No Hits found		
SEQ ID n° 8714	PL-3089.1	Contig9 from 3323260 to 3324459	m	51%		
SEQ ID n° 8715	PL-3088.1	Contig9 from 3325119 to 3326708	m	26%		
SEQ ID n° 8716	PL-3087.1	Contig9 from 3326801 to 3328396	m	24%		

871

SEQ ID n° 8717	PL-3086.2	Contig9 from 3328705 to 3330294	m	29%	emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis]	#N/A
SEQ ID n° 8718	PL-3085.1	Contig9 from 3330732 to 3332324	m	31%	emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis]	SEQ ID n-2323
SEQ ID n° 8719	PL-3674.1	Contig9 from 3332817 to 3333320	m	No Hits found		SEQ ID n-2860
SEQ ID n° 8720	PL-3084.1	Contig9 from 3333483 to 3335075	m	29%	emb CAB08016.1 (Z94043) penicillin-binding protein [Bacillus subtilis]	SEQ ID n-2322
SEQ ID n° 8721	PL-3083.1	Contig9 from 3335448 to 3336329	m	64%	pir H83306 hypothetical protein PA2712 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06100.1 AE004699_5 (AE004699) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2321
SEQ ID n° 8722	PL-3082.1	Contig9 from 3336489 to 3337679	m	28%	dbj BAB06652.1 (AP001517) BH2933-unknown [Bacillus halodurans]	SEQ ID n-2320
SEQ ID n° 8723	PL-3080.1	Contig9 from 3338464 to 3339564	m	73%	gb AAD56249.1 AF186235_1 (AF186235) L- arginine:lysine amidinotransferase [Pseudomonas syringae pv. phaseolicola]	SEQ ID n-2318
SEQ ID n° 8724	PL-4066.2	Contig9 from 3340328 to 3340630	m	86%	gb AAC46152.1 (U89925) crystalline inclusion protein [Photorhabdus luminescens]	#N/A
SEQ ID n° 8725	PL-3079.2	Contig9 from 3341566 to 3342504	m	No Hits found		#N/A
SEQ ID n° 8726	PL-3078.3	Contig9 from 3342649 to 3343548	p	32%	pir A48494 3-methyladenine DNA glycosylase - Bacillus subtilis	#N/A
SEQ ID n° 8727	PL-6242.1	Contig9 from 3343937 to 3344362	m	No Hits found		#N/A

SEQ ID n° 8728	PL-1944.1	Contig9 from 3344359 to 3346218	m	24%	emb CAB65593.1 (AL136058) putative helicase [Streptomyces coelicolor A3(2)]	SEQ ID n-3075
SEQ ID n° 8729	PL-1943.1	Contig9 from 3346757 to 3347338	m	No Hits found	pir F81045 hemagglutinin/hemolysin-related protein NMB1768 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF42109.1 (AE002526) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58]	SEQ ID n-3074
SEQ ID n° 8730	PL-6241.1	Contig9 from 3347319 to 3347492	m	44%		#N/A
SEQ ID n° 8731	PL-6240.1	Contig9 from 3347556 to 3347789	p	No Hits found		#N/A
SEQ ID n° 8732	PL-6239.1	Contig9 from 3347838 to 3347978	p	No Hits found		#N/A
SEQ ID n° 8733	PL-6238.1	Contig9 from 3348071 to 3348241	p	No Hits found	pir A83056 hypothetical protein PA4711 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG08097.1 AE004885_2 (AE004885) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 8734	PL-3673.1	Contig9 from 3348230 to 3348616	m	27%		SEQ ID n-2859
SEQ ID n° 8735	PL-6237.1	Contig9 from 3348613 to 3348795	m	No Hits found		#N/A
SEQ ID n° 8736	PL-1941.1	Contig9 from 3348810 to 3350021	m	77%	gb AAG12159.1 (AY007371) beta-ketoadipyl CoA thiolase [Burkholderia pseudomallei]	SEQ ID n-3073

SEQ ID n° 8737	PL-1940.1	Contig9 from 3350079 to 3351143	m	67%	sp Q45072 TFTE_BURCE_MALEYLACETATE_REDUCTASE pir I40177 maleylacetate reductase (EC. 1.3.1.32) [validated] - Pseudomonas cepacia gb AAC43333.1 (U19883) maleylacetate reductase [Burkholderia cepacia] pir C83618 probable CoA transferase, subunit B PA0227 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03616.1 AE004460_9 (AE004460) probable CoA transferase, subunit B [Pseudomonas aeruginosa] SEQ ID n-2072
SEQ ID n° 8738	PL-1939.1	Contig9 from 3351140 to 3351919	m	68%	pir B83618 probable CoA transferase, subunit A PA0226 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03615.1 AE004460_8 (AE004460) probable CoA transferase, subunit A [Pseudomonas aeruginosa] dbj BAB04258.1 (AP001508) NADP-dependent aldehyde dehydrogenase [Bacillus halodurans] SEQ ID n-2069
SEQ ID n° 8740	PL-1937.1	Contig9 from 3352801 to 3354270	m	62%	SEQ ID n-2068
SEQ ID n° 8741	PL-1936.1	Contig9 from 3354290 to 3355141	m	No Hits found	SEQ ID n-2067
SEQ ID n° 8742	PL-3671.1	Contig9 from 3355311 to 3355811	m	No Hits found	SEQ ID n-2858
SEQ ID n° 8743	PL-1935.1	Contig9 from 3355956 to 3356726	p	56%	gb AAC38247.1 (AF003947) Pcar [Rhodococcus opacus] SEQ ID n-2066
SEQ ID n° 8744	PL-6229.1	Contig9 from 3357088 to 3357240	m	60%	gb AAD16952.1 (AF106566) Rhum [Salmonella typhimurium] #N/A
SEQ ID n° 8745	PL-1934.1	Contig9 from 3357391 to 3358038	m	57%	gb AAD16952.1 (AF106566) Rhum [Salmonella typhimurium] SEQ ID n-2065

Contig9 from SEQ ID n° 8746 PL-1933.1 3358516 to 3359349	m 57%	gb AAG55370.1 AE005277_11 (AE005277) unknown [Escherichia coli O157:H7] gb AAG55778.1 AE005314.6 (AE005314) unknown [Escherichia coli O157:H7] sp P77692 YKFI_ECOLI HYPOTHETICAL 12.9 KD PROTEIN IN PROA-PERR INTERGENIC REGION pir E64749 hypothetical protein b0245 - Escherichia coli gb AAB08664.1 (U70214) similar to E. coli ORF_0109 [Escherichia coli] gb AAC73348.1 (AE000132) orf, hypothetical protein [Escherichia coli K12] sp P52141 YFVZ_ECOLI HYPOTHETICAL 11.7 KDA PROTEIN IN ALPA-GABD INTERGENIC REGION (O105) pir T08656 yfiZ protein - Escherichia coli gb AAA79813.1 (U36840) ORF_0105 [Escherichia coli] gb AAC75693.1 (AE000349) orf, hypothetical protein [Escherichia coli K12] dbj BAJ16513.1 (D90889) similar to [SwissProt Accession Number P52141] [Escherichia coli] #N/A	SEQ ID n-3064		
Contig9 from SEQ ID n° 8747 PL-6226.1 3359463 to 3359750	m 84%	sp Q47685 YKFG_ECOLI HYPOTHETICAL 18.1 KD PROTEIN IN PROA-PERR INTERGENIC REGION pir G64749 hypothetical protein b0247 - Escherichia coli gb AAB08667.1 (U70214) similar to E. coli ORF_0160, also similar to radC [Escherichia coli] gb AAC73350.1 (AE000133) putative DNA repair protein [Escherichia coli K12] dbj BAA77916.1 (D83536) Hypothetical 18.0 kd protein in alpa- gabD intergenic region (o160). [Escherichia coli] SEQ ID n-3857			
Contig9 from SEQ ID n° 8748 PL-6224.1 3359825 to 3360151	m 73%	Contig9 from SEQ ID n° 8749 PL-3670.1 3360194 to 3360667	m 56%	Contig9 from SEQ ID n° 8750 PL-1932.1 3360805 to 3361554	m No Hits found

SEQ ID n-3063

sp P28912 YHHI_ECOLI H REPEAT-ASSOCIATED PROTEIN IN RHB-PIT INTERGENIC REGION (ORF-H)			
pir S47703 H repeat-associated protein homolog b3484 - Escherichia coli gb AAC61885.1 (L02370) H repeat-associated protein [Escherichia coli] gb AB18459.1 (U00039) alternate gene name yhhI [Escherichia coli] gb AAC76509.1 (AE000424) putative receptor [Escherichia coli K12]			
SEQ ID n° 8751 PL-1931.1	Contig9 from 3361587 to 3362717	m 60%	SEQ ID n-2062
Contig9 from			
SEQ ID n° 8752 PL-3669.1	3362997 to 3363593	p No Hits found	SEQ ID n-2855
Contig9 from			
SEQ ID n° 8753 PL-6222.1	3363845 to 3363979	p No Hits found	#N/A
Contig9 from			
SEQ ID n° 8754 PL-6219.1	3364127 to 3364393	p 67%	#N/A
Contig9 from			
SEQ ID n° 8755 PL-1930.1	3364576 to 3366192	m 29%	SEQ ID n-2061
Contig9 from			
SEQ ID n° 8756 PL-1929.1	3366381 to 3369632	m No Hits found	SEQ ID n-2060
Contig9 from			
SEQ ID n° 8757 PL-1928.1	3369695 to 3370909	m 86%	SEQ ID n-2059
pir C82470 conserved hypothetical protein VCA0347 VCA0506.[imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96255.1 (AE004372) conserved hypothetical protein [Vibrio cholerae] gb AAF96409.1 (AE004381) conserved hypothetical protein [Vibrio cholerae]			
gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae]			
gb AAD54663.1 AF097520_1 (AF097520) Sal integrase [Shigella flexneri]			

Contig9 from 3371402 to 3373444	p	81%	sp P27298 OPDA_ECOLI_OLIGOPEPTIDASE A pir S47718 oligopeptidase A (EC 3.4.24.-) - Escherichia coli gb AAB18474.1 (U00039) CG Site No. 18031 [Escherichia coli] gb AAC76523.1 (AE000426) oligopeptidase A [Escherichia coli K12] pir S47717 hypothetical protein f285 - Escherichia coli gb AAB18473.1 (U00039) gtg start, alternate starts possible [Escherichia coli] SEQ ID n-2058
Contig9 from 3373451 to 3374194	p	84%	sp P14657 DHE4_UNKP_NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (NADP-GDH) pir S06938 glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - unidentified bacterium emb CAA34434.1 (X16399) glutamate dehydrogenase (AA 1-446) [unidentified bacterium] SEQ ID n-2056 pir S47715 universal stress protein A - Escherichia coli gb AAB18471.1 (U00039) uspa [Escherichia coli] gb AAC76520.1 (AE000425) universal stress protein; broad regulatory function? [Escherichia coli K12] gb AAG58627.1 AE005574_4 (AE005574) universal stress protein; broad regulatory function? [Escherichia coli O157:H7] SEQ ID n-2854
Contig9 from 3375837 to 3376268	m	73%	#N/A
Contig9 from 3376386 to 3376592	m	No Hits found	
Contig9 from 3376733 to 3377068	p	56%	sp P37632 USPB_ECOLI_UNIVERSAL STRESS PROTEIN B pir S47714 hypothetical 13K protein (pit-uspA intergenic region) - Escherichia coli gb AAB18470.1 (U00039) No definition line found [Escherichia coli] gb AAC76519.1 (AE000435) orf, hypothetical protein [Escherichia coli K12] gb AAG58626.1 AE005574_3 (AE005574) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2853

SEQ ID n° 8764	PL-1924.1	Contig9 from 3377123 to 3378613	m	82%	sp P37308 PITA_ECOLI LOW-AFFINITY INORGANIC PHOSPHATE TRANSPORTER 1 pir S47713 pita protein - Escherichia coli gb AA18469.1 (U00039) CG Site No. 385 [Escherichia coli] gb AAC76518.1 (AE000425) low-affinity phosphate transport [Escherichia coli K12] gb AAG58625.1 AE005574_2 (AE005574) low-affinity phosphate transport [Escherichia coli O157:H7]	SEQ ID n-2055
SEQ ID n° 8765	PL-1923.1	Contig9 from 3378883 to 3380067	p	80%	gb AAG58624.1 AE005574_1 (AE005574) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2054
SEQ ID n° 8766	PL-1922.1	Contig9 from 3380348 to 3381559	m	66%	pir P83493 probable MFS transporter PA1212 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04601.1 AE004551_5 (AE004551) probable MFS transporter [Pseudomonas aeruginosa]	SEQ ID n-2053
SEQ ID n° 8767	PL-1921.1	Contig9 from 3381584 to 3382777	m	39%	emb CAB92560.1 (AL356812) putative carboxylase. [Streptomyces coelicolor A3(2)]	SEQ ID n-2052
SEQ ID n° 8768	PL-6211.1	Contig9 from 3383725 to 3383823	m	No Hits found		#N/A
SEQ ID n° 8769	PL-3666.1	Contig9 from 3384630 to 3385103	m	No Hits found		SEQ ID n-2852
SEQ ID n° 8770	PL-3665.1	Contig9 from 3385103 to 3385600	m	No Hits found		SEQ ID n-2851
SEQ ID n° 8771	PL-1920.1	Contig9 from 3386354 to 3387229	p	29%	pir S76456 hypothetical protein - Synecocystis sp. (strain PCC 6803) dbj BAAL8585.1 (D90915) hypothetical protein [Synecocystis sp.] pir C83390 cyanate lyase PA2052 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05440.1 AE004631_9 (AE004631) cyanate lyase [Pseudomonas aeruginosa]	SEQ ID n-2051
SEQ ID n° 8772	PL-3664.1	Contig9 from 3387385 to 3387855	m	80%		SEQ ID n-2850

SEQ ID n° 8773	PL-1919.1	Contig9 from 3387883 to 3388542	m	73%	sp P17582 CYNT_ECOLI CARBONIC ANHYDRASE pir QRETC carbonate dehydratase [EC 4.2.1.1] - Escherichia coli gb AA18063.1 (U73857) cyanate anhydrase [Escherichia coli] gb AAC73442.1 (AB000141) carbonic anhydrase [Escherichia coli K12] gb AG54688.1 AE005213_4 (AE005213) carbonic anhydrase [Escherichia coli O157:H7] SEQ ID n-1049
SEQ ID n° 8774	PL-1918.1	Contig9 from 3388887 to 3389789	p	72%	pir C83388 transcription regulator CynR PA2054 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AG85442.1 AE004632_1 (AE004632) transcriptional regulator CynR [Pseudomonas aeruginosa] SEQ ID n-1048
SEQ ID n° 8775	PL-1917.1	Contig9 from 3389831 to 3391006	m	44%	pir E82521 hypothetical protein XF2735 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85520.1 AE004080_2 (AE004080) hypothetical protein [Xylella fastidiosa] SEQ ID n-1047
SEQ ID n° 8776	PL-1916.1	Contig9 from 3391024 to 3394425	m	44%	pir D82521 hypothetical protein XF2734 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85519.1 AE004080_1 (AE004080) hypothetical protein [Xylella fastidiosa] SEQ ID n-1046
SEQ ID n° 8777	PL-1915.1	Contig9 from 3394433 to 3395326	m	No Hits found	SEQ ID n-1045
SEQ ID n° 8778	PL-1914.1	Contig9 from 3395378 to 3396838	m	42%	pir F82523 hypothetical protein XF2733 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85518.1 AE004079_9 (AE004079) hypothetical protein [Xylella fastidiosa] SEQ ID n-1044
SEQ ID n° 8779	PL-1913.1	Contig9 from 3397193 to 3400465	m	77%	gb AAA25124.1 (M16187) pullulanase precursor [Klebsiella aerogenes] SEQ ID n-1043
SEQ ID n° 8780	PL-3663.1	Contig9 from 3401169 to 3401663	m	46%	emb CAA74718.1 (Y14336) putative extracellular protein containing predicted 35aa signal peptide [Streptomyces reticuli] SEQ ID n-2849

SEQ ID n° 8781	PL-1912.1	Contig9 from 3401771 to 3402397	m	59%	gb AAD12185.1 (U57900) utilizing regulatory protein tutB [Thausera aromatica] sp P23222 FIXL_BRAJA SENSOR PROTEIN FIXL pir S13330 fixL protein - Bradyrhizobium japonicum emb CAA40143.1 (X56808) ttg start codon [Bradyrhizobium japonicum] emb CAA06276.1 (AJ005001) FixL protein [Bradyrhizobium japonicum] sp P46852 YHHW_ECOLI PROTEIN YHHW pir B65140 hypothetical 26.3 kD protein in gntR-ggt intergenic region - Escherichia coli (strain K-12) gb AA58237.1 (U18997) ORF_f231 [Escherichia coli] gb AAC76464.1 (AE000420) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-2040	SEQ ID n-2042
SEQ ID n° 8782	PL-1911.1	Contig9 from 3402397 to 3403761	m	27%	pdh 1AYL Phosphoenolpyruvate Carboxykinase pir D65135 hypothetical 32.8 kD protein in mrca. pckA intergenic region - Escherichia coli (strain K-12) gb AA58198.1 (U18997) ORF_o294 [Escherichia coli] gb AAC76426.1 (AE000415) orf, hypothetical protein [Escherichia coli K12] gb AAG58501.1 AE005562_4 (AE005562) orf, hypothetical protein [Escherichia coli O157:H7] gb AAK03630.1 (AE006191) unknown [Pasteurella multocida]	SEQ ID n-2038
SEQ ID n° 8783	PL-1910.1	Contig9 from 3404452 to 3405147	p	86%	gb AAC28926.1 (U66822) Umob [Proteus mirabilis] gb AAG58497.1 AE005561_10 (AE005561) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2036
SEQ ID n° 8784	PL-1909.1	Contig9 from 3405195 to 3406814	m	90%		SEQ ID n-2037
SEQ ID n° 8785	PL-1908.1	Contig9 from 3407054 to 3407926	m	79%		#N/A
SEQ ID n° 8786	PL-6201.1	Contig9 from 3407949 to 3408365	m	74%		
SEQ ID n° 8787	PL-1907.1	Contig9 from 3408433 to 3410565	m	68%		
SEQ ID n° 8788	PL-1906.1	Contig9 from 3411042 to 3411590	p	73%		

SEQ ID n° 8789	PL-1905.1	Contig9 from 3411634 to 3414162	m	85%	gb AAG58496.1 AE005561_9 (AE005561) peptidoglycan synthetase; penicillin-binding protein 1A [Escherichia coli O157:H7] SEQ ID n-2034
SEQ ID n° 8790	PL-1904.1	Contig9 from 3414282 to 3415112	p	40%	sp P45753 YREF_ECOLI HYPOTHETICAL 29.0 KDA PROTEIN IN HOFQ-MRCA INTERGENIC REGION SEQ ID n-2033
SEQ ID n° 8791	PL-3661.1	Contig9 from 3415112 to 3415666	p	46%	pir G82053 probable fimbrial assembly protein PILN VC2633 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95774.1 (AE004329) fimbrial assembly protein PILN, putative [Vibrio cholerae] SEQ ID n-2848
SEQ ID n° 8792	PL-3660.1	Contig9 from 3415653 to 3416198	p	No Hits found	SEQ ID n-2847
SEQ ID n° 8793	PL-1903.1	Contig9 from 3416191 to 3417225	p	53%	sp P34749 HOFQ_ECOLI PROTEIN TRANSPORT PROTEIN HOFQ PRECURSOR pir B65134 protein transport protein hofq precursor - Escherichia coli (strain K-12) gb AA58188.1 (U18997) hopQ [Escherichia coli] gb AAC76416.1 (AE000414) putative transport portein [Escherichia coli K12] SEQ ID n-2032
SEQ ID n° 8794	PL-3659.1	Contig9 from 3417595 to 3418116	p	94%	gb AAG58490.1 AE005561_3 (AE005561) shikimate kinase I [Escherichia coli O157:H7] SEQ ID n-2845
SEQ ID n° 8795	PL-1902.1	Contig9 from 3418164 to 3419264	p	85%	sp P07639 AROB_ECOLI 3-DEHYDROQUINATE SYNTHASE pir SYECQ 3-dehydroquinatate synthase (EC 4.6.1.3) - Escherichia coli emb CAA27495.1 (X03867) 3-dehydroquinatate synthase (aa 1-362) [Escherichia coli] emb CAA79666.1 (Z19601) ORF, aroB. Millar G., Coggins J.R.; FEBS Lett. 200:11-17(1986) [Escherichia coli] gb AA58186.1 (U18997) 3-dehydroquinatate synthase [Escherichia coli] gb AAC76414.1 (AE000414) 3-dehydroquinatate synthase [Escherichia coli K12] SEQ ID n-2031

SEQ ID n° 8796	PL-1901.1	Contig9 from 3419557 to 3420483	p	55%	gb AAG58488.1 AE005561.1 (AE005561) putative membrane protein; interferes with cell division [Escherichia coli O157:H7]	SEQ ID n-2030
SEQ ID n° 8797	PL-1900.1	Contig9 from 3420568 to 3421380	p	86%	sp P45454 DNA_SERVA DNA ADENINE METHYLASE (DEOXYADENOSYL-METHYLTRANSFERASE) (M.SMADAM) pir S47099 site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) dam Serratia marcescens emb CAA55177.1 (X78412) Deoxyadenosyl-methyltransferase [Serratia marcescens]	SEQ ID n-2029
SEQ ID n° 8798	PL-1899.1	Contig9 from 3421441 to 3422121	p	83%	sp P32661 RPE_ECOLI RIBULOSE-PHOSPHATE 3- EPIMERASE (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (R5P3E) pir E65133 ribulose-phosphate 3- epimerase (EC 5.1.3.1) - Escherichia coli gb AAA58183.1 (U18997) 24 kD protein [Escherichia coli] gb AAC76411.1 (AE000414) D- ribulose-5-phosphate 3-epimerase [Escherichia coli K12] gb AAG58486.1 AE005560.12 (AE005560) D-ribulose-5-phosphate 3-epimerase [Escherichia coli O157:H7]	SEQ ID n-2026
SEQ ID n° 8799	PL-1898.1	Contig9 from 3422111 to 3422815	p	59%	sp P32662 GPH_ECOLI PHOSPHOGLYCOLATE PHOSPHATASE (PGP) pir S5288 phosphoglycolate phosphatase (EC 3.1.3.18) [validated] - Escherichia coli emb CAA79664.1 (Z19601) ORF for 27kD protein. [Escherichia coli] gb AAA58182.1 (U18997) 27 kD protein in ECDAMOPRA [Escherichia coli] gb AAC76410.1 (AE000414) phosphoglycolate phosphatase [Escherichia coli K12]	SEQ ID n-2025
SEQ ID n° 8800	PL-1897.1	Contig9 from 3422820 to 3423857	p	84%	gb AAG42458.1 AF308467_4 (AF308467) tryptophanyl- tRNA synthetase [Klebsiella aerogenes]	SEQ ID n-2024
SEQ ID n° 8801	PL-6198.1	Contig9 from 3424123 to 3424344	m	No Hits found		#N/A

SEQ ID n° 8802	PL-6197.1	Contig9 from 3424560 to 3424853	p	No Hits found	#N/A
SEQ ID n° 8803	PL-1896.1	Contig9 from 3424881 to 3425804	p	50%	gb AAK02295.1 (AE006055) unknown [Pasteurella multocida]
SEQ ID n° 8804	PL-1895.1	Contig9 from 3425773 to 3426522	p	No Hits found	SEQ ID n-1022
SEQ ID n° 8805	PL-3658.1	Contig9 from 3426524 to 3427003	p	28%	sp P44270 YG02_HAEMIN_HYPOTHETICAL_PROTEIN_H11602 pir A64038 hypothetical protein H11602 - Haemophilus influenzae (strain Rd KW20) gb AAC23261.1 (U32834) H. influenzae predicted coding region H11602 [Haemophilus influenzae Rd]
SEQ ID n° 8806	PL-6196.1	Contig9 from 3427014 to 3427187	m	No Hits found	SEQ ID n-2844
SEQ ID n° 8807	PL-1894.1	Contig9 from 3427207 to 3427797	m	54%	sp P45215 YE59_HAEMIN_PROBABLE_RNA_POLYMERASE SIGMA_FACTOR_H11459 pir G64124 transcription initiation factor sigma homolog H11459 - Haemophilus influenzae (strain Rd KW20) gb AAC23107.1 (U32824) sigma factor, putative [Haemophilus influenzae Rd]
SEQ ID n° 8808	PL-1893.1	Contig9 from 3428182 to 3428853	m	77%	gb AA059104.1 AE005622_6 (AE005622) orf, hypothetical protein [Escherichia coli O157:H7]
SEQ ID n° 8809	PL-1892.1	Contig9 from 3428972 to 3429598	m	81%	sp P53655 SODM_YEREN_SUPEROXIDE_DISMUTASE [MN] emb CAA55596.1 (X96852) soda [Yersinia enterocolitica]

SEQ ID n° 8810	PL-1891.1	Contig9 from 3429972 to 3431927	p 90%	sp P27550 ACSA_ECOLI_ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) pir D65215 acetate--CoA ligase (EC 6.2.1.1) - Escherichia coli gb AAC43163.1 (U00006) acetyl-CoA sythetase [Escherichia coli] gb AAC77039.1 (AE000480) acetyl-CoA synthetase [Escherichia coli K12]	SEQ ID n-2018
SEQ ID n° 8811	PL-1890.2	Contig9 from 3431992 to 3432303	p 75%	gb AAG59266.1 AE005639_10 (AE005639) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8812	PL-6906.1	Contig9 from 3432300 to 3433949	p 86%	pir F83241 probable sodium:solute symporter PA3234 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06522.1 AE004746_6 (AE004746) probable sodium:solute symporter [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 8813	PL-3657.1	Contig9 from 3434198 to 3434737	p No Hits found		#N/A
SEQ ID n° 8814	PL-1888.1	Contig9 from 3434737 to 3435810	p 56%	gb AAA96312.1 (U50906) outer membrane adherence protein-associated protein [Escherichia coli]	SEQ ID n-2014
SEQ ID n° 8815	PL-3656.1	Contig9 from 3436141 to 3436653	p 62%	gb AAF65225.1 AF249895_1 (AF249895) putative transposase [Xanthomonas pv. mangiferaeindicae]	SEQ ID n-2843
SEQ ID n° 8816	PL-3655.1	Contig9 from 3436569 to 3437084	p 56%	gb AAF61102.1 AF225215_1 (AF225215) putative transposase [Xanthomonas oryzae pv. oryzae]	SEQ ID n-2842

Contig9 from 3437364 to 3437618	m	69%	<p>ref NP_047570.1 unknown [Yersinia pestis] pir T42852 hypothetical protein Y0012 - Yersinia pestis plasmid pCD1 gb AAC69767.1 (AF074612) unknown [Yersinia pestis] emb CAB54945.1 (AL117189) YPCD1.68c, Y0012, hypothetical protein, len: 68 aa; identical to corresponding CDS from Y.pestis KIMS pCD1 (EMBL:AF074612) (68 aa), fasta scores, opt: 453 z-score: 678.5 E(): 2e-30 98.5% identity in 68 aa overlap. Similar to parts of hypothe> gb AAC31494.1 (AF071034) L0015 [Escherichia coli] gb AAG54625.1 AE005206_13 (AE005206) unknown protein encoded in ISEC8 [Escherichia coli O157:H7] gb AAG56018.1 AE005334_5 (AE005334) unknown protein encoded by ISEC8 in prophage CP-933X [Escherichia coli O157:H7] gb AAG56196.1 AE005348_13 (AE005348) putative IS encoded protein encoded within prophage CP-9330 [Escherichia coli O157:H7] gb AAG57057.1 AE005425_7 (AE005425) unknown protein encoded by ISEC8 [Escherichia coli O157:H7] gb AAG58121.1 AE005528_11 (AE005528) unknown protein encoded by ISEC8 [Escherichia coli O157:H7] gb AAG58813.1 AE005594_8 (AE005594) unknown protein encoded by ISEC8 within prophage CP-933L [Escherichia coli O157:H7] gb AAG55308.1 AE005273_1 (AE005273) unknown in ISEC8 [Escherichia coli O157:H7] gb AAG55717.1 AE005309_7 (AE005309) unknown in ISEC8 [Escherichia coli O157:H7]</p>	SEQ ID n-3013 #N/A
Contig9 from 3437603 to 3438868	m	50%	<p>gb AAG56196.1 AE005348_13 (AE005348) putative IS encoded protein encoded within prophage CP-9330 [Escherichia coli O157:H7] gb AAG57057.1 AE005425_7 (AE005425) unknown protein encoded by ISEC8 [Escherichia coli O157:H7] gb AAG58121.1 AE005528_11 (AE005528) unknown protein encoded by ISEC8 [Escherichia coli O157:H7] gb AAG58813.1 AE005594_8 (AE005594) unknown protein encoded by ISEC8 within prophage CP-933L [Escherichia coli O157:H7] gb AAG55308.1 AE005273_1 (AE005273) unknown in ISEC8 [Escherichia coli O157:H7] gb AAG55717.1 AE005309_7 (AE005309) unknown in ISEC8 [Escherichia coli O157:H7]</p>	SEQ ID n-3013 #N/A
Contig9 from 3438932 to 3439267	m	73%	<p>gb AAG56196.1 AE005348_13 (AE005348) putative IS encoded protein encoded within prophage CP-9330 [Escherichia coli O157:H7] gb AAG57057.1 AE005425_7 (AE005425) unknown protein encoded by ISEC8 [Escherichia coli O157:H7] gb AAG58121.1 AE005528_11 (AE005528) unknown protein encoded by ISEC8 [Escherichia coli O157:H7] gb AAG58813.1 AE005594_8 (AE005594) unknown protein encoded by ISEC8 within prophage CP-933L [Escherichia coli O157:H7] gb AAG55308.1 AE005273_1 (AE005273) unknown in ISEC8 [Escherichia coli O157:H7] gb AAG55717.1 AE005309_7 (AE005309) unknown in ISEC8 [Escherichia coli O157:H7]</p>	SEQ ID n-3013 #N/A
Contig9 from 3439261 to 3439563	m	No Hits found	<p>gb AAG56196.1 AE005348_13 (AE005348) putative IS encoded protein encoded within prophage CP-9330 [Escherichia coli O157:H7] gb AAG57057.1 AE005425_7 (AE005425) unknown protein encoded by ISEC8 [Escherichia coli O157:H7] gb AAG58121.1 AE005528_11 (AE005528) unknown protein encoded by ISEC8 [Escherichia coli O157:H7] gb AAG58813.1 AE005594_8 (AE005594) unknown protein encoded by ISEC8 within prophage CP-933L [Escherichia coli O157:H7] gb AAG55308.1 AE005273_1 (AE005273) unknown in ISEC8 [Escherichia coli O157:H7] gb AAG55717.1 AE005309_7 (AE005309) unknown in ISEC8 [Escherichia coli O157:H7]</p>	SEQ ID n-3013 #N/A

885

SEQ ID n° 8821	PL-7386.1	Contig9 from 3442463 to 3442597	m	No Hits found		#N/A
SEQ ID n° 8822	PL-6164.1	Contig9 from 3445247 to 3445468	p	63%	gb AAG58958.1 AE005607_4 (AE005607) yieP gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8823	PL-6163.1	Contig9 from 3445449 to 3445694	p	52%	gb AAG58958.1 AE005607_4 (AE005607) yieP gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8824	PL-805.1	Contig9 from 3445764 to 3447155	p	84%	gb AAG58957.1 AE005607_3 (AE005607) putative transport protein [Escherichia coli O157:H7] sp P25551 RBSR_ECOLI_RIBOSE_OPERON_REPRESSOR pir B65179 ribose operon repressor - Escherichia coli dbj BA01259.1 (D10466) rbs repressor [Escherichia coli] gb AAC76776.1 (AB000452) regulator for rbs operon [Escherichia coli K12] gb AAG58956.1 AE005607_2 (AE005607) regulator for rbs operon [Escherichia coli O157:H7]	SEQ ID n-9644
SEQ ID n° 8825	PL-806.1	Contig9 from 3447152 to 3448153	m	79%		SEQ ID n-9645

SEQ ID n° 8826	PL-807.1	Contig9 from 3448156 to 3449085	m	79%	<p>sp P05054 RBSK_ECOLI_RIBOKINASE_pir KIECRB ribokinase (EC 2.7.1.15) [validated] - Escherichia coli pdb 1RK2 B Chain B, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 pdb 1RKD E. Coli Ribokinase Complexed With Ribose And Adp pdb 1RK2 C Chain C, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 pdb 1RK2 A Chain A, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 pdb 1RK2 D Chain D, E. Coli Ribokinase Complexed With Ribose And Adp, Solved In Space Group P212121 pdb 1RKA A Chain A, The Apo Form Of E. Coli Ribokinase pdb 1RKS A Chain A, E. Coli Ribokinase In Complex With D-Ribose gb AA51476.1 (M13169) ribokinase [Escherichia coli] gb AA62105.1 (L10328) ribokinase [Escherichia coli] gb AAC76775.1 (AE000452) ribokinase [Escherichia coli K12] gb AAG58955.1 AE005607_1 (AE005607) ribokinase [Escherichia coli O157:H7] gb AAG58954.1 AE005606_10 (AE005606) D-ribose periplasmic binding protein [Escherichia coli O157:H7] sp P04984 RBSK_ECOLI_RIBOSE_TRANSPORT_SYSTEM PERMEASE PROTEIN RBSC pir G65178 high affinity ribose transport protein rbSC - Escherichia coli gb AA62103.1 (L10328) high affinity ribose transport protein [Escherichia coli] gb AAC76773.1 (AE000452) D-ribose high-affinity transport system [Escherichia coli K12]</p>	SEQ ID n-9646
SEQ ID n° 8827	PL-808.1	Contig9 from 3449149 to 3450039	m	86%		SEQ ID n-9647
SEQ ID n° 8828	PL-809.1	Contig9 from 3450064 to 3451035	m	89%		

887

SEQ ID n° 8829	PL-810.1	Contig9 from 3451042 to 3452547	m	86%	sp P04983 RBSA_ECOLI_RIBOSE_TRANSPORT_ATP- BINDING_PROTEIN_RBSA_pir B26304 ribose transport protein rbsa - Escherichia coli gb AA51473.1 (M13169) high affinity ribose transport protein [Escherichia coli] gb AAC76772.1 (AE000452) ATP-binding component of D-ribose high-affinity transport system [Escherichia coli K12] gb AAG58951.1 AE005606_7 (AE005606) D-ribose high-affinity transport system; membrane-associated protein [Escherichia coli O157:H7] #N/A	SEQ ID n-3650
SEQ ID n° 8830	PL-6161.1	Contig9 from 3452555 to 3452974	m	78%	gb AAG58949.1 AE005606_5 (AE005606) putative 2- component regulator [Escherichia coli O157:H7] SEQ ID n-3651	
SEQ ID n° 8831	PL-811.1	Contig9 from 3453227 to 3454738	p	71%	gb AAG58948.1 AE005606_4 (AE005606) ylem gene product [Escherichia coli O157:H7] SEQ ID n-3652	
SEQ ID n° 8832	PL-812.1	Contig9 from 3454743 to 3456200	p	76%	gb AAG58947.1 AE005606_3 (AE005606) asparagine synthetase A [Escherichia coli O157:H7] SEQ ID n-3653	
SEQ ID n° 8833	PL-813.1	Contig9 from 3456207 to 3457199	m	78%	sp P03809 ASNC_ECOLI_REGULATORY_PROTEIN_ASNC pir Q0ECE1 regulatory protein asnC - Escherichia coli gb AA62095.1 (L10328) regulatory protein [Escherichia coli] gb AA24252.1 (K00826) 17K protein [Escherichia coli] gb AAC7676.1 (AE000451) regulator for asnA, asnC and gldA [Escherichia coli K12] gb AAG58946.1 AE005606_2 (AE005606) regulator for asnA, asnC and gldA [Escherichia coli O157:H7] prf 1002215B protein 17KD [Escherichia coli] SEQ ID n-2841	
SEQ ID n° 8834	PL-3652.1	Contig9 from 3457366 to 3457827	p	85%		

SEQ ID n° 8835	PL-3651.1	Contig9 from 3457919 to 3458359	p 73%	sp P03817 MIOC_ECOLI MIOC PROTEIN pir Q08C16 mioc protein - Escherichia coli gb AAA62094.1 (L10328) involved in modulation of initiation at oric [Escherichia coli] gb AAA24251.1 (X00826) 16K protein [Escherichia coli] gb AAC76765.1 (AE000451) initiation of chromosome replication [Escherichia coli] K12] prf 1002215A protein 16kD [Escherichia coli] SEQ ID n~2840
SEQ ID n° 8836	PL-814.2	Contig9 from 3458740 to 3460629	p 90%	sp P17112 GIDA_ECOLI GLUCOSE INHIBITED DIVISION PROTEIN A pir BVECOA glucose inhibited division protein - Escherichia coli gb AAC76764.1 (AE000451) glucose-inhibited division; chromosome replication? [Escherichia coli K12] SEQ ID n~3654
SEQ ID n° 8837	PL-815.1	Contig9 from 3460643 to 3461263	p 81%	sp P17113 GIDB_ECOLI GLUCOSE INHIBITED DIVISION PROTEIN B pir BVECOB gidB protein - Escherichia coli gb AAA62092.1 (L10328) glucose inhibited division protein [Escherichia coli] emb CAA25774.1 (X01631) gidB protein [Escherichia coli] gb AAC76763.1 (AE000451) glucose-inhibited division; chromosome replication? [Escherichia coli K12] gb AAG58943.1 AE005605_11 (AE005605) glucose- inhibited division; chromosome replication? [Escherichia coli O157:H7] SEQ ID n~3655

pir||BVECU1 uncI protein - Escherichia coli
 gb|AAA24730.1| (J01594) ATP synthase uncI
 polypeptide (atp-1; gtg start codon)
 [Escherichia coli] gb|AA62091.1| (L10328) ATP
 synthase subunit? [Escherichia coli]
 emb|CAA25640.1| (X01383) atpJ gene product (AA 1-
 128) [Escherichia coli] emb|CAA23513.1|
 (V00264) reading frame gene 1 (A) [Escherichia
 coli] emb|CAA25775.1| (X01631) uncI protein
 [Escherichia coli] gb|AAC76762.1| (AE000450)
 membrane-bound ATP synthase, dispensable
 protein, affects expression of atpB
 [Escherichia coli K12] gb|AAF19355.1|AF188265_1
 (AF188265) ATP synthase subunit i [Salmonella
 typhimurium] gb|AAG58942.1|AE005605_10
 (AE005605) membrane-bound ATP synthase,
 dispensable protein, affects
 expression of atpB [Escherichia coli O157:H7] SEQ ID n-2839
 sp|P00855|ATP6_ECOLI ATP SYNTHASE A CHAIN
 (PROTEIN 6) pir||LWEC6 H+-transporting ATP
 synthase (EC 3.6.1.34) protein 6 - Escherichia
 coli emb|CAA23514.1| (V00264) reading frame
 gene 2 (A) [Escherichia coli] emb|CAA25776.1|
 (X01631) uncB protein [Escherichia coli]
 gb|AAA24731.1| (J01594) ATP synthase a subunit
 (atp-2) [Escherichia coli] gb|AA62090.1|
 (L10328) ATP synthase F0 subunit a [Escherichia
 coli] emb|CAA23520.1| (V00266) alternate atpB
 CDS [Escherichia coli] gb|AAC76761.1|
 (AE000450) membrane-bound ATP synthase, F0
 sector, subunit a [Escherichia coli
 K12] gb|AAG58941.1|AE005605_9 (AE005605)
 membrane-bound ATP synthase, F0 sector, subunit
 a [Escherichia coli O157:H7] SEQ ID n-3656

Contig9 from
 SEQ ID n° 8838 PL-3650.1 3461874 to 524
 3462251

Contig9 from
 SEQ ID n° 8839 PL-816.1 3462282 to 874
 3463106

sp|P00844|ATPL_ECOLI ATP SYNTHASE C CHAIN (LIPID-
 BINDING PROTEIN)
 (DICYCLOHEXYLCARBODIIMIDE-BINDING PROTEIN)
 pir||LWECA H+-transporting ATP synthase (EC
 3.6.1.34) lipid-binding protein -
 Escherichia coli pdb|1C17|A Chain A, A1C12
 Subcomplex Of F1Fo Atp Synthase pdb|1C17|B
 Chain B, A1C12 Subcomplex Of F1Fo Atp Synthase
 pdb|1C17|C Chain C, A1C12 Subcomplex Of F1Fo Atp
 Synthase pdb|1C17|D Chain D, A1C12 Subcomplex
 Of F1Fo Atp Synthase pdb|1C17|E Chain E, A1C12
 Subcomplex Of F1Fo Atp Synthase pdb|1C17|F
 Chain F, A1C12 Subcomplex Of F1Fo Atp Synthase
 pdb|1C17|G Chain G, A1C12 Subcomplex Of F1Fo Atp
 Synthase pdb|1C17|H Chain H, A1C12 Subcomplex
 Of F1Fo Atp Synthase pdb|1C17|I Chain I, A1C12
 Subcomplex Of F1Fo Atp Synthase pdb|1C17|J
 Chain J, A1C12 Subcomplex Of F1Fo Atp Synthase
 pdb|1C17|K Chain K, A1C12 Subcomplex Of F1Fo Atp
 Synthase pdb|1C17|L Chain L, A1C12 Subcomplex
 Of F1Fo Atp Synthase pdb|1A91| Subunit C Of
 The F1Fo Atp Synthase Of Escherichia Coli; Nmr,
 10 Structures pdb|1C99|A Chain A,
 #N/A

Contigs from
 SEQ ID n° 8840 PL-6159.1 3463160 to 3463399
 p 91%

sp|P00859|ATPF_ECOLI ATP SYNTHASE B CHAIN
 pir||LWECB H+-transporting ATP synthase (EC
 3.6.1.34) chain b - Escherichia coli
 gb|AAA83871.1| (M25464) integral membrane proton
 channel F0 subunit B [Escherichia
 coli] gb|AAA24733.1| (J01594) ATP synthase b
 subunit (atp-4; gtc start codon)
 [Escherichia coli] gb|AA62088.1| (L10328) ATP
 synthase F0 subunit b [Escherichia coli]
 emb|CAA23516.1| (V00264) reading frame gene 4
 (B) [Escherichia coli] emb|CAA23523.1| (V00266)
 atpF [Escherichia coli] emb|CAA25778.1|
 (X01631) uncF protein [Escherichia coli]
 gb|AAC76759.1| (AE000450) membrane-bound ATP
 synthase, F0 sector, subunit b
 [Escherichia coli K12] gb|AAG58939.1|AE005605_7
 (AE005605) membrane-bound ATP synthase, F0
 sector, subunit b [Escherichia coli]

SEQ ID n-2837

Contigs from
 SEQ ID n° 8841 PL-3649.1 3463458 to 93%
 3463928

O157:H7]

SEQ ID n° 8842	PL-3648.1	Contig9 from 3463941 to 3464474	p 87%	<p>sp P00831 ATPD_ECOLI ATP SYNTHASE DELTA CHAIN pir PWECD H+-transporting ATP synthase (EC 3.6.1.34) delta chain - Escherichia coli emb CAA23517.1 (V00264) reading frame gene 5 (delta) [Escherichia coli] emb CAA23524.1 (V00266) atpH [Escherichia coli] emb CAA25779.1 (X01631) uncH protein [Escherichia coli] gb AAA83872.1 (M25464) H+ ATPase F0 delta subunit [Escherichia coli] gb AA24734.1 (J01594) ATP synthase delta subunit (atp-5) [Escherichia coli] gb AA62087.1 (L10328) ATP synthase F1 delta subunit [Escherichia coli] gb AAC76758.1 (AE000450) membrane-bound ATP synthase, F1 sector, delta-subunit [Escherichia coli K12] gb AAG58938.1 AE005605_6 (AE005605) membrane-bound ATP synthase, F1 sector, delta- subunit [Escherichia coli O157:H7] sp P00822 ATPA_ECOLI ATP SYNTHASE ALPHA CHAIN pir PWECA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - Escherichia coli gb AA62086.1 (L10328) ATP synthase F1 alpha subunit [Escherichia coli] gb AAC76757.1 (AE000450) membrane-bound ATP synthase, F1 sector, alpha-subunit [Escherichia coli K12] gb AAG58937.1 AE005605_5 (AE005605) membrane-bound ATP synthase, F1 sector, alpha- subunit [Escherichia coli O157:H7] gb AA19361.1 AF188265_7 (AF188265) ATP synthase subunit gamma [Salmonella typhimurium]</p>	SEQ ID n-2836 SEQ ID n-9657 SEQ ID n-3658
SEQ ID n° 8843	PL-817.1	Contig9 from 3464489 to 3466030	p 92%		
SEQ ID n° 8844	PL-818.1	Contig9 from 3466089 to 3466952	p 93%		

SEQ ID n°	8846 PL-819.1	<div>Contig9 from 3466987 to 3468369</div>	P 95%	sp P00824 ATPB_ECOLI ATP SYNTHASE BETA CHAIN <u>p1r FWECH H+-transporting ATP synthase (EC 3.6.1.34) beta chain - Escherichia coli emb CAA23527.1 (V00267) reading frame beta [Escherichia coli] emb CAA23594.1 (V00311) reading frame papB [Escherichia coli] gb AA83875.1 (M25464) H+ ATPase F1 beta subunit [Escherichia coli] gb AAA24737.1 (J01594) ATP synthase beta subunit (atp-8) [Escherichia coli] gb AA62084.1 (L10328) ATP synthase F1 beta subunit [Escherichia coli] emb CAA25782.1 (X01631) uncD protein [Escherichia coli] gb AAC76755.1 (AE000450) membrane-bound ATP synthase, F1 sector, beta-subunit [Escherichia coli K12]AAG58935.1 AE005605_3 (AE005605) membrane-bound ATP synthase, F1 sector, beta-subunit pdb 1BSH A Chain A, Solution Structure Of The Epsilon Subunit Of The F1-Atpsynthase From Escherichia Coli And Orientation Of The Subunit Relative To The Beta Subunits Of The Complex pdb IBSN A Chain A, Solution Structure Of The Epsilon Subunit Of The F1-Atpsynthase From Escherichia Coli And Orientation Of The Subunit Relative To The Beta Subunits Of The Complex sp P17114 GLMU_ECOLI UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (N-ACETYLGLUCOSAMINE-1-PHOSPHATE URIDYLYTRANSFERASE)</u>
SEQ ID n°	8847 PL-820.1	<div>Contig9 from 3468942 to 3470315</div>	P 86%	

#N/A

SEQ ID n~3659

SEQ ID n~3661

SEQ ID n° 8848	PL-822.1	Contig9 from 3470423 to 3472252	p	85%	sp P17169 GLMS_ECOLI GLUCOSAMINE--FRUCTOSE-6- PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D- FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) PHOSPHATE SYNTHASE) pir XNECGM glutamine-- fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Escherichia coli gb AAC76752.1 (AE000450) L-glutamine:D-fructose- 6-phosphate aminotransferase [Escherichia coli K12]	SEQ ID n-3662
SEQ ID n° 8849	PL-6156.1	Contig9 from 3472401 to 3472655	p	62%	gb AAB18024.1 (U73857) hypothetical protein [Escherichia coli]	#N/A
SEQ ID n° 8850	PL-6155.1	Contig9 from 3472675 to 3472815	p	37%	pir D82269 probable ribosomal protein L36 VC0879 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94041.1 (AE004172) ribosomal protein L36, putative [Vibrio cholerae]	#N/A
SEQ ID n° 8851	PL-823.1	Contig9 from 3473230 to 3474285	p	22%	pir S18689 sc/svp protein - Escherichia coli plasmid p15B emb CAA44052.1 (X62121) DNA inversion product [Escherichia coli]	SEQ ID n-3663
SEQ ID n° 8852	PL-824.1	Contig9 from 3474333 to 3474917	p	57%	HOMOLOG pir S18684 gene T protein - Escherichia coli plasmid p15B emb CAA44047.1 (X62121) T [Escherichia coli]	SEQ ID n-3664
SEQ ID n° 8853	PL-6154.1	Contig9 from 3475336 to 3475677	m	37%	sp P40784 YCDD_SALTY HYPOTHETICAL PROTEIN IN NANH 3'REGION	#N/A
SEQ ID n° 8854	PL-825.1	Contig9 from 3475687 to 3476697	m	20%	dbj BAA76527.2 (AB017338) tail fiber [Pectobacterium carotovorum]	SEQ ID n-3665

895

SEQ ID n° 8855	PL-3647.1	3476777 to 3477349	p	83%	Contig9 from	sp P03013 HIN_SALTY DNA-INVERTASE HIN pir JWBET DNA-invertase - Salmonella sp emb CAA24652.1 (V01369) reading frame (HIN) [Salmonella typhimurium] emb CAA24654.1 (V01370) hin gene [Salmonella typhimurium] gb AA27073.1 (J01801) hin protein [Salmonella typhimurium] gb AA27140.1 (M12293) flagellar protein [Salmonella typhimurium] sp P21323 VR7I_ECOLI HYPOTHETICAL 21.9 KD PROTEIN (ORF1) (RETRON EC67) pir JQ0864 hypothetical: 21.9K protein - Escherichia coli retron Ec67 gb AA23390.1 (M55249) unknown [Escherichia coli]	SEQ ID n-2835
SEQ ID n° 8856	PL-826.2	3477632 to 3478246	m	52%	Contig9 from	sp NP_046763.1 gpX [Bacteriophage P2] sp P51772 VPX_BPP2 TAIL PROTEIN X (GPX) pir BS5855 tail protein - phage P2 gb AAD03274.1 (AF063097) gpX [Bacteriophage P2] ref NP_046771.1 gpV [Bacteriophage P2] sp P31340 VPV_BPP2 BASEPLATE ASSEMBLY PROTEIN V (GPV) gb AAD03282.1 (AF063097) gpV [Bacteriophage P2] ref NP_052264.1 M protein [Enterobacteria phage 186] gb AAC34161.1 (U32222) M protein [Enterobacteria phage 186] ref NP_046773.1 gpJ [Bacteriophage P2] sp P51767 VPJ_BPP2 BASEPLATE ASSEMBLY PROTEIN J (GPJ) gb AAD03284.1 (AF063097) gpJ [Bacteriophage P2] ref NP_046774.1 gpI [Bacteriophage P2] sp P26701 VPI_BPP2 TAIL PROTEIN I (GPI) gb AAD03285.1 (AF063097) gpI [Bacteriophage P2]	SEQ ID n-9666
SEQ ID n° 8857	PL-6152.1	3478628 to 3478810	p	No Hits found	Contig9 from		
SEQ ID n° 8858	PL-6151.1	3479093 to 3479296	p	65%	Contig9 from	ref NP_046763.1 gpX [Bacteriophage P2] sp P51772 VPX_BPP2 TAIL PROTEIN X (GPX) pir BS5855 tail protein - phage P2 gb AAD03274.1 (AF063097) gpX [Bacteriophage P2] ref NP_046771.1 gpV [Bacteriophage P2] sp P31340 VPV_BPP2 BASEPLATE ASSEMBLY PROTEIN V (GPV) gb AAD03282.1 (AF063097) gpV [Bacteriophage P2] ref NP_052264.1 M protein [Enterobacteria phage 186] gb AAC34161.1 (U32222) M protein [Enterobacteria phage 186] ref NP_046773.1 gpJ [Bacteriophage P2] sp P51767 VPJ_BPP2 BASEPLATE ASSEMBLY PROTEIN J (GPJ) gb AAD03284.1 (AF063097) gpJ [Bacteriophage P2] ref NP_046774.1 gpI [Bacteriophage P2] sp P26701 VPI_BPP2 TAIL PROTEIN I (GPI) gb AAD03285.1 (AF063097) gpI [Bacteriophage P2]	#N/A
SEQ ID n° 8859	PL-827.1	3479793 to 3480635	p	43%	Contig9 from		#N/A
SEQ ID n° 8860	PL-6150.1	3480635 to 3480976	p	52%	Contig9 from	ref NP_052264.1 M protein [Enterobacteria phage 186] gb AAC34161.1 (U32222) M protein [Enterobacteria phage 186] ref NP_046773.1 gpJ [Bacteriophage P2] sp P51767 VPJ_BPP2 BASEPLATE ASSEMBLY PROTEIN J (GPJ) gb AAD03284.1 (AF063097) gpJ [Bacteriophage P2] ref NP_046774.1 gpI [Bacteriophage P2] sp P26701 VPI_BPP2 TAIL PROTEIN I (GPI) gb AAD03285.1 (AF063097) gpI [Bacteriophage P2]	SEQ ID n-9667
SEQ ID n° 8861	PL-828.1	3480981 to 3481979	p	68%	Contig9 from		#N/A
SEQ ID n° 8862	PL-829.1	3481972 to 3482586	p	66%	Contig9 from	ref NP_052264.1 M protein [Enterobacteria phage 186] gb AAC34161.1 (U32222) M protein [Enterobacteria phage 186] ref NP_046773.1 gpJ [Bacteriophage P2] sp P51767 VPJ_BPP2 BASEPLATE ASSEMBLY PROTEIN J (GPJ) gb AAD03284.1 (AF063097) gpJ [Bacteriophage P2] ref NP_046774.1 gpI [Bacteriophage P2] sp P26701 VPI_BPP2 TAIL PROTEIN I (GPI) gb AAD03285.1 (AF063097) gpI [Bacteriophage P2]	SEQ ID n-9668
SEQ ID n° 8863	PL-830.1	3482586 to 3483190	p	66%	Contig9 from	ref NP_052264.1 M protein [Enterobacteria phage 186] gb AAC34161.1 (U32222) M protein [Enterobacteria phage 186] ref NP_046773.1 gpJ [Bacteriophage P2] sp P51767 VPJ_BPP2 BASEPLATE ASSEMBLY PROTEIN J (GPJ) gb AAD03284.1 (AF063097) gpJ [Bacteriophage P2] ref NP_046774.1 gpI [Bacteriophage P2] sp P26701 VPI_BPP2 TAIL PROTEIN I (GPI) gb AAD03285.1 (AF063097) gpI [Bacteriophage P2]	SEQ ID n-9669

Contig9 from 3482583 to 3483710	SEQ ID n° 8863 PL-830.1	ref[NP_052267.1] similar to P2 tail fiber protein H, PIR Accession Number B42291 (Enterobacteria phage 186] gb AAC34164.1 (U32222) similar to P2 tail fiber protein H, PIR Accession Number B42291	SEQ ID n-3671
Contig9 from 3483710 to 3484198	SEQ ID n° 8864 PL-3645.1	pir s18687 Sc/SVN protein [Escherichia coli plasmid p15B emb CAA44050.1 (X62121) DNA inversion product [Escherichia coli] sp P09153 TFAB_ECOLI TAIL FIBER ASSEMBLY PROTEIN HOMOLOG FROM LAMBDOID PHAGE E14 pir A64861 ycfa protein, phage protein-related - Escherichia coli gb AAC74240.1 (AE000214) orf, hypothetical protein [Escherichia coli K12] ref[NP_046776.1] gpG [Bacteriophage P2] sp P26699 TFA_BPP2 PROBABLE TAIL FIBER ASSEMBLY PROTEIN (GPG) pir C42291 tail fiber assembly protein G - phage P2 gb AAD03287.1 (AF063097) gpG [Bacteriophage P2] pir A42463 hypothetical protein Bcv (pinB 5' region) - Shigella boydii (fragment) dbj BAA00552.1 (D00660) Bcv gene product [Shigella boydii]	SEQ ID n-2834 SEQ ID n-3672 SEQ ID n-2833
Contig9 from 3485024 to 3485554	SEQ ID n° 8866 PL-3644.1	gpG [Bacteriophage P2] pir A42463 hypothetical protein Bcv (pinB 5' region) - Shigella boydii (fragment) dbj BAA00552.1 (D00660) Bcv gene product [Shigella boydii]	SEQ ID n-3673
Contig9 from 3485570 to 3486121	SEQ ID n° 8867 PL-832.1	gpG [Bacteriophage P2] pir A42463 hypothetical protein Bcv (pinB 5' region) - Shigella boydii (fragment) dbj BAA00552.1 (D00660) Bcv gene product [Shigella boydii]	SEQ ID n-3673
Contig9 from 3486118 to 3486324	SEQ ID n° 8868 PL-6148.1	gpG [Bacteriophage P2] pir A42463 hypothetical protein Bcv (pinB 5' region) - Shigella boydii (fragment) dbj BAA00552.1 (D00660) Bcv gene product [Shigella boydii]	SEQ ID n-3673
Contig9 from 3486539 to 3487711	SEQ ID n° 8869 PL-833.1	gpG [Bacteriophage P2] pir A42463 hypothetical protein Bcv (pinB 5' region) - Shigella boydii (fragment) dbj BAA00552.1 (D00660) Bcv gene product [Shigella boydii]	SEQ ID n-3673

#N/A

897

SEQ ID n° 8870	PL-3643.1	Contig9 from 3487722 to 3488237	p 75%	ref NP_052270.1 similar to P2 tail tube protein FII, Swiss-Prot Accession Number P22502 [Enterobacteria phage 186] gb AAC34167.1 (U32222) similar to P2 tail tube protein FII, Swiss-Prot Accession Number P22502 [Enterobacteria phage 186] prf 2122413B tail tube protein [Bacteriophage 186] SEQ ID n-2832
SEQ ID n° 8871	PL-6145.1	Contig9 from 3488264 to 3488581	p 64%	gb AAC02075.1 (AF043239) unknown [Salmonella typhimurium] #N/A
SEQ ID n° 8872	PL-6144.1	Contig9 from 3488596 to 3488715	p 65%	ref NP_046780.1 gpE+E' [Bacteriophage P2] gb AAD03292.1 (AF063097) gpE+E' [Bacteriophage P2] #N/A
SEQ ID n° 8873	PL-834.1	Contig9 from 3488696 to 3491134	p 33%	gb AAG56919.1 AE005413_13 (AE005413) putative tail fiber component of prophage CP-933T [Escherichia coli O157:H7] SEQ ID n-3675
SEQ ID n° 8874	PL-3641.1	Contig9 from 3491137 to 3491601	p 70%	ref NP_052274.1 F protein [Enterobacteria phage 186] gb AAC34171.1 (U32222) F protein [Enterobacteria phage 186] SEQ ID n-2831
SEQ ID n° 8875	PL-835.1	Contig9 from 3491598 to 3492683	p 66%	ref NP_052275.1 D protein [Enterobacteria phage 186] sp P21679 VPD_BP186 LATE CONTROL GENE D PROTEIN (GPD) gb AAC34172.1 (U32222) D protein [Enterobacteria phage 186] SEQ ID n-3676
SEQ ID n° 8876	PL-6143.1	Contig9 from 3492760 to 3492981	p 61%	gb AAC48864.1 (U49731) late gene activator Pag [Bacteriophage PSP3] #N/A
SEQ ID n° 8877	PL-836.1	Contig9 from 3493188 to 3494297	p 87%	gb AAG22005.1 AF282316_1 (AF282316) aspartate semialdehyde dehydrogenase [Yersinia pseudotuberculosis] gb AAG22006.1 AF282317_1 (AF282317) aspartate semialdehyde dehydrogenase [Yersinia pseudotuberculosis] gb AAG22007.1 AF282318_1 (AF282318) aspartate semialdehyde dehydrogenase [Yersinia pestis] SEQ ID n-3677

SEQ ID n° 8878	PL-837.1	Contig9 from 3494464 to 3495219	p	31%	gb AAG58551.1 AE005568_1 (AE005568) orf; hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-3678
SEQ ID n° 8879	PL-3640.1	Contig9 from 3496338 to 3496817	m	66%	gb AAG54517.1 AE005197_6 (AE005197) Z0248 gene product [Escherichia coli O157:H7]	SEQ ID n-2830
SEQ ID n° 8880	PL-838.1	Contig9 from 3496958 to 3499372	m	90%	sp P06982 GYRB_ECOLI DNA GYRASE SUBUNIT B emb CAA27871.1 (X04341) gyrase B (AA 1-804) [Escherichia coli]	SEQ ID n-3679
SEQ ID n° 8881	PL-839.1	Contig9 from 3499392 to 3500483	m	83%	sp P22839 RECF_PROMI RECF PROTEIN pir JQ0735 recf protein - Proteus mirabilis gb AA083960.1 (M58352) putative [Proteus mirabilis] sp P00583 DP3B_ECOLI DNA POLYMERASE III, BETA CHAIN pir DJE33B DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Escherichia coli pdb 2POL A chain A, Pol Iii (Beta Subunit) (E.C.2.7.7.7) pdb 2POL B chain B, Pol Iii (Beta Subunit) (E.C.2.7.7.7) gb AAB59150.1 (J01602) DNA polymerase III beta- subunit [Escherichia coli] gb AA062052.1 (U10328) DNA polymerase III beta-subunit [Escherichia coli] gb AAC76724.1 (AE000447) DNA polymerase III, beta-subunit [Escherichia coli K12] gb AAG58898.1 AE005601_4 (AE005601) DNA polymerase III, beta-subunit [Escherichia coli O157:H7]	SEQ ID n-3680
SEQ ID n° 8882	PL-840.1	Contig9 from 3500505 to 3501605	m	91%	sp P29440 DNAA_SERMA CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA gb AA02924.1 AA02924 (M17353) DnaA [Serratia marcescens]	SEQ ID n-3682
SEQ ID n° 8883	PL-841.1	Contig9 from 3501610 to 3502998	m	93%		SEQ ID n-3683

SEQ ID n° 8884	PL-6138.1	Contig9 from 3503687 to 3503827	p 88%	<p>sp P02437 RL34_ECOLI 50S RIBOSOMAL PROTEIN L34 pir R5EC34 ribosomal protein L34 [validated] - Escherichia coli emb CAA25982.1 (X01861) L34 (rpmH) (aa 1-46) [Escherichia coli] gb AAB59148.1 (J01602) ribosomal protein L34 [Escherichia coli] gb AA24566.1 (M11056) ribosomal protein L34 [Escherichia coli] gb AA62054.1 (L10328) 50S ribosomal subunit protein L34 [Escherichia coli] gb AAC76726.1 (AE000447) 50S ribosomal subunit protein L34 [Escherichia coli] K12 gb AAG58900.1 AE005601_6 (AE005601) 50S ribosomal subunit protein L34 [Escherichia coli O157:H7] prf 763072A ribosomal protein L34 [Escherichia coli]</p>	#N/A
SEQ ID n° 8885	PL-6137.1	Contig9 from 3503844 to 3504203	p 85%	<p>sp P22835 RNPA_PROMI RIBONUCLEASE P PROTEIN COMPONENT (PROTEIN C5) (RNASE P) pir JQ0731 ribonuclease P (EC 3.1.26.5) protein component - Proteus mirabilis gb AAA83956.1 (M58352) RNaseP C5 subunit [Proteus mirabilis] sp P22834 YIDD_PROMI HYPOTHETICAL 9.6 KD PROTEIN IN RNPA 3'REGION pir JQ0730 9K protein - Proteus mirabilis gb AAA83955.1 (M58352) ORF2; 9 kDa protein; putative [Proteus mirabilis]</p>	#N/A
SEQ ID n° 8887	PL-842.1	Contig9 from 3504430 to 3506070	p 85%	<p>gb AAG58902.1 AE005601_8 (AE005601) 60 KD inner- membrane protein [Escherichia coli O157:H7] sp P25522 THDP_ECOLI THIOPHENE AND FURAN OXIDATION PROTEIN THDF pir C65173 thiophene and furan oxidation 50 kD protein thdf - Escherichia coli (strain K-12) gb AAC76729.1 (AE000447) GTP-binding protein in thiophene and furan oxidation [Escherichia coli K12]</p>	SEQ ID n-3684
SEQ ID n° 8888	PL-843.1	Contig9 from 3506317 to 3507681	p 90%		SEQ ID n-3685

SEQ ID n° 8889	PL-844.1	Contig9 from 3507915 to 3509135	m	28%	sp 050224 RECQ_THIFE ATP-DEPENDENT DNA HELICASE RECQ pir T45499 probable DNA recombinase recg [imported] - Thiobacillus ferrooxidans gb AAC21662.1 (AF032884) RecQ [Acidithiobacillus ferrooxidans] ref NP_053136.1 orf74 [Escherichia coli] dbj BA084909.1 (AB024946) orf74 [Escherichia coli] SEQ ID n-3686
SEQ ID n° 8890	PL-845.1	Contig9 from 3509162 to 3511825	m	43%	gb AAG57162.1 AE005436_9 (AE005436) Z3269 gene product [Escherichia coli O157:H7] SEQ ID n-3687
SEQ ID n° 8891	PL-6132.1	Contig9 from 3511894 to 3512136	m	47%	sp P23873 HIPB_ECOLI HIPB PROTEIN pir A38112 hipB protein - Escherichia coli gb AAA56877.1 (M61242) hipB [Escherichia coli] dbj BAA15180.1 (D90792) HipB protein [Escherichia coli] dbj BAA15188.1 (D90793) HipB protein [Escherichia coli] dbj BAA15195.1 (D90794) HipB protein [Escherichia coli] gb AAC74581.1 (AE000248) persistence to inhibition of murein or DNA biosynthesis; regulatory protein [Escherichia coli K12] #N/A
SEQ ID n° 8892	PL-6131.1	Contig9 from 3512486 to 3512791	p	43%	
SEQ ID n° 8893	PL-846.1	Contig9 from 3512791 to 3514110	p	67%	pir F64904 hipA protein - Escherichia coli gb AAC74580.1 (AE000248) persistence to inhibition of murein or DNA biosynthesis, DNA-binding regulator [Escherichia coli K12] pir C81957 probable integral membrane protein NMA0408 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB83707.1 (AL162753) putative integral membrane protein [Neisseria meningitidis Z2491] SEQ ID n-3688
SEQ ID n° 8894	PL-847.1	Contig9 from 3514307 to 3515956	m	53%	SEQ ID n-3689

SEQ ID n° 8895	PL-848.1	Contig9 from 3516064 to 3517923	m	73%	sp P14081 SELB_ECOLI SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR (SELB TRANSLATION FACTOR) pir EFECB translation elongation factor EF- selb - Escherichia coli emb CAA34637.1 (X16644) SEL B (AA 1-614) [Escherichia coli] gb AAC76614.1 (AE000436) selenocysteinyl-trna- specific translation factor [Escherichia coli K12] prf 1602238A translation factor [Escherichia coli] SEQ ID n-9690
SEQ ID n° 8896	PL-849.1	Contig9 from 3517957 to 3519348	m	71%	sp P23328 SELA_ECOLI L-SERYL-TRNA(SEC) SELENIUM TRANSFERASE (CYSTEINYL-TRNA(SEC)) SELENIUM TRANSFERASE (SELENOCYSTEINE SYNTHASE) (SELENOCYSTEINYL-TRNA(SEC) SYNTHASE) pir A38730 sela protein - Escherichia coli gb AA24624.1 (M64177) selenocysteine synthase [Escherichia coli] SEQ ID n-9691
SEQ ID n° 8897	PL-850.1	Contig9 from 3519359 to 3520288	m	80%	gb AAG59084.1 AE005620_6. (AE005620) affects formate dehydrogenase-N [Escherichia coli O157:H7] SEQ ID n-9693
SEQ ID n° 8898	PL-851.1	Contig9 from 3520802 to 3521755	p	33%	sp P16559 TCMN_STRGA MULTIFUNCTIONAL CYCLASE- DEHYDRATASE-3-O-METHYL TRANSFERASE TCMN pir S27696 tcmN protein - Streptomyces glaucescens gb AAG67518.1 (M80674) possible internal translational start site at position 9950; SAM binding site at position 10617 to 10636 [Streptomyces glaucescens] gb AAG51616.1 AC010795_20 (AC010795) caffeic O- methyltransferase, putative; 68744-70102 [Arabidopsis thaliana] SEQ ID n-9694
SEQ ID n° 8899	PL-852.3	Contig9 from 3522468 to 3523421	p	38%	#N/A

SEQ ID n° 8900 PL-6129.1	Contig9 from 3523710 to 3524678	p	58%	pir C81839 probable transposase for IS1655 NMA1481 [imported] - Neisseria meningitidis (group B strain MD58, group A strain Z2491) emb CAB84714.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] emb CAB84719.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] #N/A	#N/A
SEQ ID n° 8901 PL-4030.2	Contig9 from 3525387 to 3526340	p	38%	gb AAG51676.1 AC010704.20 (AC010704) putative caffeic acid 3-O-methyltransferase; 41078-42528 [Arabidopsis thaliana] #N/A	#N/A
SEQ ID n° 8902 PL-2730.2	Contig9 from 3526970 to 3527923	p	38%	gb AAG51676.1 AC010704.20 (AC010704) putative caffeic acid 3-O-methyltransferase; 41078-42528 [Arabidopsis thaliana] SEQ ID n-1933	SEQ ID n-1933
SEQ ID n° 8903 PL-2729.1	Contig9 from 3528845 to 3529840	p	31%	gb AAG51616.1 AC010795_20 (AC010795) caffeic O-methyltransferase, putative; 68744-70102 [Arabidopsis thaliana] SEQ ID n-1931	SEQ ID n-1931
SEQ ID n° 8904 PL-2728.1	Contig9 from 3530241 to 3530882	m	74%	sp P32174 FDOI_ECOLI FORMATE DEHYDROGENASE, CYTOCHROME B556 (FDO) SUBUNIT (FORMATE DEHYDROGENASE-O GAMMA SUBUNIT) (FDH-Z GAMMA SUBUNIT) (AEROBIC FORMATE DEHYDROGENASE CYTOCHROME B556 SUBUNIT) pir S40836 formate dehydrogenase (EC 1.2.1.2) O (aerobic) gamma chain - Escherichia coli gb AAB03025.1 (L19201) formate dehydrogenase-O gamma subunit [Escherichia coli] gb AAD13454.1 (AB000464) formate dehydrogenase, cytochrome B556 (FDO) subunit [Escherichia coli K12] gb AAG59085.1 AE005620_7 (AE005620) formate dehydrogenase, cytochrome B556 (FDO) subunit [Escherichia coli O157:H7] SEQ ID n-1930	SEQ ID n-1930

SEQ ID n° 8905	PL-2727.1	Contig9 from 3530879 to 3531808	m	86%	sp P32175 FDOH_ECOLI FORMATE DEHYDROGENASE-O, IRON-SULFUR SUBUNIT (FORMATE DEHYDROGENASE-O BETA SUBUNIT) (FDH-Z BETA SUBUNIT) (AEROBIC FORMATE DEHYDROGENASE IRON-SULFUR SUBUNIT) pir S40837 formate dehydrogenase (EC 1.2.1.2) O (aerobic) beta chain - Escherichia coli	SEQ ID n° 1929
SEQ ID n° 8906	PL-2726.1	Contig9 from 3531819 to 3534278	m	91%	gb AA03026.1 (L19201) formate dehydrogenase-O beta subunit [Escherichia coli] gb AAD13455.1 (AE000464) formate dehydrogenase-O, iron-sulfur subunit [Escherichia coli K12] gb AAD13456.1 (AE000464) formate dehydrogenase- O, major subunit [Escherichia coli K12]	SEQ ID n° 1928
SEQ ID n° 8907	PL-2725.1	Contig9 from 3534279 to 3534866	m	91%	gb AAD13456.1 (AE000464) formate dehydrogenase- O, major subunit [Escherichia coli K12]	SEQ ID n° 1927
SEQ ID n° 8908	PL-2724.1	Contig9 from 3535064 to 3535894	p	73%	gb AAG59088.1 AE005620_10 (AE005620) affects formate dehydrogenase-N [Escherichia coli O157:H7]	SEQ ID n° 1926
SEQ ID n° 8909	PL-2723.1	Contig9 from 3536006 to 3536773	m	38%	emb CAB67714.1 (AJ271405) putative transferase enzyme [Streptomyces rochei]	SEQ ID n° 1925
SEQ ID n° 8910	PL-2722.1	Contig9 from 3537384 to 3538304	p	51%	gb AAG57157.1 AE005436_4 (AE005436) putative kinase [Escherichia coli O157:H7]	SEQ ID n° 1924
SEQ ID n° 8911	PL-2721.1	Contig9 from 3538352 to 3539569	p	52%	emb CAA63510.1 (X92946) macrolide efflux protein [Lactococcus lactis]	SEQ ID n° 1923
SEQ ID n° 8912	PL-6127.1	Contig9 from 3539671 to 3539832	p	45%	pir H70559 hypothetical protein Rv1634 - Mycobacterium tuberculosis (strain H37RV) emb CAB08887.1 (Z95554) hypothetical protein Rv1634 [Mycobacterium tuberculosis]	#N/A

SEQ ID n° 8913	PL-2720.2	Contig9 from 3540052 to 3540993	p	58%	pir G81857 hypothetical protein NMA1635 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB84863.1 (AL162756) hypothetical protein [Neisseria meningitidis Z2491]	#N/A
SEQ ID n° 8914	PL-6126.1	Contig9 from 3541039 to 3541158	p	71%	pir G81857 hypothetical protein NMA1635 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB84863.1 (AL162756) hypothetical protein [Neisseria meningitidis Z2491]	#N/A
SEQ ID n° 8915	PL-2719.1	Contig9 from 3541685 to 3542635	p	No Hits found		SEQ ID n-2920
SEQ ID n° 8916	PL-7127.1	Contig9 from 3542676 to 3542843	m	No Hits found		#N/A
SEQ ID n° 8917	PL-4029.1	Contig9 from 3543347 to 3543814	m	No Hits found		SEQ ID n-3178
SEQ ID n° 8918	PL-2718.1	Contig9 from 3543866 to 3545047	m	51%	gb AAB70880.1 (U66703) reverse transcriptase [Escherichia coli]	SEQ ID n-2919
SEQ ID n° 8919	PL-6125.1	Contig9 from 3545097 to 3545285	p	No Hits found		#N/A
SEQ ID n° 8920	PL-6124.1	Contig9 from 3545536 to 3545730	p	36%	gb AAG55936.1 AE005327_6 (AE005327) unknown protein encoded by prophage CP-933C [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8921	PL-4028.1	Contig9 from 3545958 to 3546389	p	46%	ref NP_046805.1 unknown [Pantoea citrea] gb AAC17959.1 (AF022806) unknown [Pantoea citrea]	SEQ ID n-9177
SEQ ID n° 8922	PL-6123.1	Contig9 from 3546650 to 3546823	m	No Hits found		#N/A

SEQ ID n° 8929	PL-2713.1	Contig9 from 3550871 to 3552088	m	78%	sp P24285 DPP_ECOLI_DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN pir A65165 pantothenate metabolism flavoprotein dfp - Escherichia coli (strain K-12) gb AAC76663.1 (AE000441) flavoprotein affecting synthesis of DNA and pantothenate metabolism [Escherichia coli K12] gb AAG58783.1 AE005591_7 (AE005591) flavoprotein affecting synthesis of DNA and pantothenate metabolism [Escherichia coli O157:H7]	SEQ ID n-3914
SEQ ID n° 8930	PL-2712.1	Contig9 from 3552287 to 3552979	p	68%	gb AAG58782.1 AE005591_6 (AE005591) DNA repair protein [Escherichia coli O157:H7]	SEQ ID n-3913
SEQ ID n° 8931	PL-6118.1	Contig9 from 3553219 to 3553455	p	87%	sp P02428 RL28_ECOLI_50S_RIBOSOMAL PROTEIN L28 pir R5EC28 ribosomal protein L28 [validated] - Escherichia coli gb AAA74099.1 (J01677) ribosomal protein L28 [Escherichia coli] gb AAA61990.1 (L10328) 50S ribosomal subunit protein L28 [Escherichia coli] gb AAC76661.1 (AE000441) 50S ribosomal subunit protein L28 [Escherichia coli K12] gb AAG58781.1 AE005591_5 (AE005591) 50S ribosomal subunit protein L28 [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8932	PL-6117.1	Contig9 from 3553467 to 3553634	p	94%	sp P02436 RL33_ECOLI_50S_RIBOSOMAL PROTEIN L33 pir R5EC33 ribosomal protein L33 [validated] - Escherichia coli gb AAA74100.1 (J01677) ribosomal protein L33 [Escherichia coli] gb AAA61989.1 (L10328) 50S ribosomal subunit protein L33 [Escherichia coli] gb AAC76660.1 (AE000441) 50S ribosomal subunit protein L33 [Escherichia coli K12] gb AAC01772.1 (U23405) L33 [Salmonella typhimurium] gb AAG58780.1 AE005591_4 (AE005591) 50S ribosomal subunit protein L33 [Escherichia coli O157:H7]	#N/A

SEQ ID n° 8933	PL-2711.1	Contig9 from 3553805 to 3554926	p	44%	pir A82676 conserved hypothetical protein XF1470 [imported] - Xylella fastidiosia (strain 9a5c) gb AF84279.1 AE003977_2 (AE003977) conserved hypothetical protein [Xylella fastidiosia] gb AAD37767.1 AF146532.7 (AF146532) putative heptosyl III transferase waaQ [Klebsiella pneumoniae] pir F71196 probable hexosyltransferase (EC 2.4.1.-) PH1844 - Pyrococcus horikoshii dbj BAA30965.1 (AP000007) 381aa long hypothetical protein [Pyrococcus horikoshii] emb CAE58324.1 (AL121855) hypothetical protein SCF62.09 [Streptomyces coelicolor A3(2)] sp P26471 RFAL_SALTY O-ANTIGEN LIGASE pir B41317 O-antigen ligase complex protein rfal - Salmonella typhimurium gb AAA27206.1 (M73826) O-antigen ligase [Salmonella typhimurium] gb AAG58779.1 AE005591_3 (AE005591) formamidopyrimidine DNA glycosylase [Escherichia coli O157:H7] sp Q9X980 COORD_SERMA PHOSPHOPANTETHEINE ADENYLTRANSFERASE (PANTETHEINE-PHOSPHATE ADENYLTRANSFERASE) (PPAT) (DEPHOSPHO-COA PYROPHOSPHORYLASE) gb AAD28804.1 (U52844) KdtB [Serratia marcescens] sp Q54435 KDTX_SERMA LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS GLYCOSYL TRANSFERASE KDTX gb AAC44433.1 (U52844) glucosyl transferase [Serratia marcescens] gb AAC44432.1 (U52844) 3-deoxy-manno- octulosonic acid transferase [Serratia marcescens]	SEQ ID n-2912
SEQ ID n° 8934	PL-2710.1	Contig9 from 3555114 to 3556136	p	39%		SEQ ID n-2911
SEQ ID n° 8935	PL-2709.1	Contig9 from 3556117 to 3557235	p	33%		
SEQ ID n° 8936	PL-2708.1	Contig9 from 3557216 to 3558391	p	31%		SEQ ID n-2909
SEQ ID n° 8937	PL-2707.1	Contig9 from 3558425 to 3559651	m	57%		SEQ ID n-2908
SEQ ID n° 8938	PL-2706.1	Contig9 from 3559762 to 3560571	p	83%		SEQ ID n-2907
SEQ ID n° 8939	PL-4024.1	Contig9 from 3560650 to 3561135	m	75%		SEQ ID n-2906
SEQ ID n° 8940	PL-2705.1	Contig9 from 3561132 to 3561905	m	75%		SEQ ID n-3175
SEQ ID n° 8941	PL-2704.1	Contig9 from 3561906 to 3563183	m	83%		SEQ ID n-2905
						SEQ ID n-2904

SEQ ID n° 8942	PL-2703.1	Contig9 from 3563412 to 3564476	p	63%	gb AAD37767.1 AF146532_7 (AF146532) putative heptosyl III transferase WaaQ [Klebsiella pneumoniae]	SEQ ID n-1903
SEQ ID n° 8943	PL-2702.1	Contig9 from 3564473 to 3565603	p	80%	gb AAD28801.1 (U52844) putative glycosyltransferase [Serratia marcescens]	SEQ ID n-1902
SEQ ID n° 8944	PL-2701.1	Contig9 from 3565600 to 3566703	p	60%	gb AAD28802.1 (U52844) putative glycosyltransferase [Serratia marcescens]	SEQ ID n-1901
SEQ ID n° 8945	PL-2700.1	Contig9 from 3566971 to 3567930	p	No Hits found	sp P24173 RFAC_ECOLI LIPOPOLYSACCHARID3 HEPTOSYLTRANSFERASE-1 pir A40619 lipopolysaccharide heptosyltransferase (EC 2.4.99.-) I rfaC [similarity] - Escherichia coli emb CAA44391.1 (X62530) rfa-2 [Escherichia coli] gb AAB18598.1 (U00039) alternate gene name rfa2 [Escherichia coli] gb AAC76645.1 (AE000440) heptosyl transferase I; lipopolysaccharide core biosynthesis [Escherichia coli K12]	SEQ ID n-1900
SEQ ID n° 8946	PL-2699.1	Contig9 from 3568055 to 3569020	m	72%		
SEQ ID n° 8947	PL-2698.1	Contig9 from 3569020 to 3570069	m	83%	gb AAD37762.1 AF146532_2 (AF146532) heptosyl II transferase WaaF [Klebsiella pneumoniae]	SEQ ID n-1896

sp P17963 RFAD_ECOLI ADP-L-GLYCERO-D-MANNO- HEPTOSE-6-EPIMERASE (ADP-GLYCEROMANNO-HEPTOSE 6-EPIMERASE) pir [JU0299 ADPqlyceromanno- heptose 6-epimerase (EC 5.1.3.20) rfad [validated] - Escherichia coli emb CAA38364.1 (X54492) acidic 34,893Da Htrm protein [Escherichia coli] gb AA24525.1 (M33577) rfad protein [Escherichia coli] gb AAB18596.1 (U00039) ADP-L-Glycero-D- mannoheptose-6-epimerase [Escherichia coli] gb AAC76643.1 (AE000440) ADP-L-glycero-D- mannoheptose-6-epimerase [Escherichia coli K12] gb AAG58766.1 AE005590_1 (AE005590) ADP-L-glycero-D-mannoheptose-6-epimerase [Escherichia coli O157:H7] SEQ ID n-2895					
sp P07912 KBL_ECOLI 2-AMINO-3-KETO BUTYRATE COENZYME A LIGASE (AKB LIGASE) (GLYCINE ACETYLTRANSFERASE) pir [XUECGA glycine C- acetyltransferase (EC 2.3.1.29) - Escherichia coli gb AAB18594.1 (U00039) glycine acetyltransferase [Escherichia coli] gb AAC76641.1 (AE000439) 2-amino-3-ketobutyrate CoA ligase [glycine acetyltransferase] [Escherichia coli K12] gb AAG58764.1 AE005589_4 (AE005589) 2-amino-3- ketobutyrate CoA ligase [glycine acetyltransferase] [Escherichia coli O157:H7] sp P07913 TDH_ECOLI THREONINE 3-DEHYDROGENASE pir [DEECTH L-threonine 3-dehydrogenase (EC 1.1.1.103) - Escherichia coli emb CAA29884.1 (X06690) tdh gene [Escherichia coli] gb AAB18593.1 (U00039) threonine dehydrogenase [Escherichia coli] gb AAC76640.1 (AE000439) threonine dehydrogenase [Escherichia coli K12] SEQ ID n-2893					
Contig9 from 3570080 to 3571018	SEQ ID n° 8948 PL-2697.1	m	79%		
Contig9 from 3571253 to 3572449	SEQ ID n° 8949 PL-2696.1	p	90%		
Contig9 from 3572459 to 3573484	SEQ ID n° 8950 PL-2695.1	p	95%		

Contigs from SEQ ID n° 8951 PL-2694.1 3573773 to 3574834	m	42%	pir H82128 3-oxoacyl-(acyl-carrier-protein) synthase III VC2023 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95171.1 (AE004276) 3-oxoacyl-(acyl- carrier-protein) synthase III [Vibrio cholerae] SEQ ID n-1892
Contigs from SEQ ID n° 8952 PL-6115.1 3575483 to 3575587	m	No Hits found	#N/A
Contigs from SEQ ID n° 8953 PL-4023.1 3575707 to 3576135	p	62%	pir F75337 transposase - Deinococcus radiodurans (strain R1) gb AAF11477.1 AE002031_6 (AE002031) transposase [Deinococcus radiodurans] SEQ ID n-18174
Contigs from SEQ ID n° 8954 PL-2693.1 3576182 to 3576997	m	61%	gb AAG58761.1 AE005589_1 (AE005589) ylbQ gene product [Escherichia coli O157:H7] SEQ ID n-1891
Contigs from SEQ ID n° 8955 PL-2692.1 3576987 to 3578294	m	71%	sp P37690 YIBP_ECOLI HYPOTHETICAL 46.6 KD PROTEIN IN SECB-TDH INTERGENIC REGION SEQ ID n-1890 sp P37688 YIBN_ECOLI HYPOTHETICAL 15.6 KDA PROTEIN IN SECB-TDH INTERGENIC REGION
Contigs from SEQ ID n° 8956 PL-4021.1 3578843 to 3579280	p	71%	pir S47832 hypothetical 15.6K protein (secb-tdh intergenic region) - Escherichia coli gb AAB18588.1 (U00039) No definition line found [Escherichia coli] gb AAC76635.1 (AE000439) orf, hypothetical protein [Escherichia coli K12] gb AAG58758.1 AE005588_9 (AE005588) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-9173

sp|P15040|SECB_ECOLI PROTEIN-EXPORT PROTEIN SECB
 pir||VXKCS protein-export protein seCB -
 Escherichia coli gb|AA83907.1| (M24489) export
 protein [Escherichia coli] gb|AAB18586.1|
 (U00039) CG Site No. 17896 [Escherichia coli]
 gb|AAC76633.1| (AE000439) protein export;
 molecular chaperone; may bind to signal
 sequence [Escherichia coli K12]
 gb|AAG58756.1|AE005588_7 (AE005588) protein
 export; molecular chaperone; may bind to signal
 sequence [Escherichia coli O157:H7]
 sp|P37606|CPDA_ECOLI GLYCEROL-3-PHOSPHATE
 DEHYDROGENASE [NAD+] pir||S47829 glycerol-3-
 phosphate dehydrogenase (NAD+) (EC 1.1.1.8) -
 Escherichia coli gb|AAB18585.1| (U00039) L-
 glycerol 3-phosphate dehydrogenase [Escherichia
 coli] gb|AAC76632.1| (AE000439) glycerol-3-
 phosphate dehydrogenase (NAD+) [Escherichia
 coli K12] gb|AAG58755.1|AE005588_6 (AE005588)
 glycerol-3-phosphate dehydrogenase (NAD+)
 [Escherichia coli O157:H7]
 sp|P05796|CYSE_ECOLI SERINE ACETYLTRANSFERASE
 (SAT) pir||XVECSA serine O-acetyltransferase
 (EC 2.3.1.30) - Escherichia coli gb|AA23648.1|
 (M15745) serine acetyltransferase [Escherichia
 coli] gb|AA23659.1| (M34333) 33 Kd protein
 (cyse) [Escherichia coli] gb|AAB18584.1|
 (U00039) serine acetyltransferase [Escherichia
 coli] gb|AAC76631.1| (AE000438) serine
 acetyltransferase [Escherichia coli K12]
 gb|AAG58754.1|AE005588_5 (AE005588) serine
 acetyltransferase [Escherichia coli O157:H7]

Contig9 from
 SEQ ID n° 8957 PL-4020.1 3579350 to p 86%
 3579826

Contig9 from
 SEQ ID n° 8958 PL-2691.1 3579826 to p 86%
 3580848

Contig9 from
 SEQ ID n° 8959 PL-2690.1 3580892 to p 88%
 3581713

SEQ ID n-9172
 SEQ ID n-2889
 SEQ ID n-2888

SEQ ID n° 8960 PL-2689.1	Contig9 from 3581938 to 3582657	m 33%	pir C64572 conserved hypothetical protein HP0419 - Helicobacter pylori (strain 26695) gb AAD07484.1 (AE000557) conserved hypothetical protein [Helicobacter pylori 26695]	SEQ ID n-3886
SEQ ID n° 8961 PL-6112.1	Contig9 from 3582935 to 3583165	m No Hits found	#N/A	
SEQ ID n° 8962 PL-4019.1	Contig9 from 3583204 to 3583710	m 74%	sp P33899 YIBK_ECOLI_HYPOTHETICAL_TRNA/RRNA METHYLTRANSFERASE YIBK pir S47827 yibk protein - Escherichia coli gb AAB18583.1 (U00039) alternate gene name yibk [Escherichia coli] gb AAC76630.1 (AE000438) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-3170
SEQ ID n° 8963 PL-2688.1	Contig9 from 3583891 to 3584589	m No Hits found		SEQ ID n-3885
SEQ ID n° 8964 PL-6111.1	Contig9 from 3584809 to 3585060	m 40%	gb AAG54897.1 AE005235_4 (AE005235) putative receptor [Escherichia coli O157:H7]	#N/A
SEQ ID n° 8965 PL-2687.1	Contig9 from 3585202 to 3586224	m 80%	gb AAK02370.1 (AE006063) GalB [Pasteurella multocida]	SEQ ID n-3884
SEQ ID n° 8966 PL-2686.1	Contig9 from 3586425 to 3587597	m 32%	pir H82888 methionyl-tRNA formyltransferase UU463 [imported] - Ureaplasma urealyticum gb AAF30875.1 AE002142_9 (AE002142) methionyl-tRNA formyltransferase [Ureaplasma urealyticum]	SEQ ID n-3883
SEQ ID n° 8967 PL-6108.1	Contig9 from 3588134 to 3588475	m 54%	pir C81839 probable transposase for IS1655 NMA1481 [imported] - Neisseria meningitidis (group B strain MD58, group A strain Z2491) emb CAB84714.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491] emb CAB84719.1 (AL162756) putative transposase for IS1655 [Neisseria meningitidis Z2491]	#N/A

SEQ ID n° 8968	PL-7123.1	Contig9 from 358877 to 358908	m	51%	gb AAC98740.1 (AF052750) transposase [Pseudomonas putida]	#N/A
SEQ ID n° 8969	PL-4018.1	Contig9 from 3589056 to 3589526	m	63%	gb AAC98740.1 (AF052750) transposase [Pseudomonas putida]	SEQ ID n-3169
SEQ ID n° 8970	PL-6107.1	Contig9 from 3589638 to 3589817	m	56%	gb AAD29044.1 AF130439_4 (AF130439) transposase [Pseudomonas putida]	#N/A
SEQ ID n° 8971	PL-4017.1	Contig9 from 3589869 to 3590420	m	58%	gb AAK03811.1 (AB006210) unknown [Pasteurella multocida]	SEQ ID n-3168
SEQ ID n° 8972	PL-2685.1	Contig9 from 3590402 to 3591079	m	62%	pir [G81287 probable sugar-phosphate nucleotidyltransferase Cj1423c [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB73847.1 (AL139078) putative sugar- phosphate nucleotidyltransferase [Campylobacter jejuni] pir [H81287 probable phosphoheptose isomerase Cj1424c [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB73848.1 (AL139078) putative phosphoheptose isomerase [Campylobacter jejuni]	SEQ ID n-3882
SEQ ID n° 8973	PL-2684.1	Contig9 from 3591083 to 3591673	m	72%	pir [A81288 probable sugar kinase Cj1425c [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB73849.1 (AL139078) putative sugar kinase [Campylobacter jejuni] gb AAG35360.1 AF317224_2 (AF317224) GDP-mannose 4,6-dehydratase [Aneurinibacillus thermoaerophilus]	SEQ ID n-3881
SEQ ID n° 8974	PL-2683.1	Contig9 from 3591661 to 3592689	m	62%	gb AAD50490.1 AF172324_8 (AF172324) Wbne [Escherichia coli]	#N/A
SEQ ID n° 8975	PL-6105.1	Contig9 from 3593313 to 3593558	m	43%	dbj BAB07433.1 (AF001519) exopolysaccharide biosynthesis [Bacillus halodurans]	SEQ ID n-3879
SEQ ID n° 8976	PL-2682.1	Contig9 from 3593566 to 3594675	m	38%		#N/A
SEQ ID n° 8977	PL-2681.2	Contig9 from 3594685 to 3595533	m	37%		#N/A

SEQ ID n° 8978	PL-6998.1	Contig9 from 3595987 to 3596988	m	58%	gb AAC60769.1 (U46859) WbcF [Yersinia enterocolitica (type 0:8)]	#N/A
SEQ ID n° 8979	PL-4635.1	Contig9 from 3596985 to 3598013	m	50%	gb AAC60768.1 (U46859) WbcE [Yersinia enterocolitica (type 0:8)]	#N/A
SEQ ID n° 8980	PL-4636.1	Contig9 from 3597991 to 3599271	m	35%	pir A44396 P-type cation-translocating ATPase - malaria parasite (Plasmodium falciparum)	#N/A
SEQ ID n° 8981	PL-2493.3	Contig9 from 3599413 to 3600438	m	20%	dbj BAB06239.1 (AF001515) transposase related protein (20) [Bacillus halodurans]	#N/A
SEQ ID n° 8982	PL-2494.1	Contig9 from 3600752 to 3601957	m	49%	gb AAF33461.1 (AF233324) 89% identity with E. coli lipopolysaccharide biosynthesis protein (WXXE) (SP:P2783) [Salmonella typhimurium LT2]	SEQ ID n-1678
SEQ ID n° 8983	PL-2495.1	Contig9 from 3602002 to 3603129	m	74%	gb AAB81632.1 (AF025396) putative amino transferase [Vibrio anguillarum]	SEQ ID n-1679
SEQ ID n° 8984	PL-2496.1	Contig9 from 3603585 to 3604457	m	82%	sp P27831 REFL_ECOLI GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (DTDP-GLUCOSE SYNTHASE) (DTDP-GLUCOSE PYROPHOSPHORYLASE) pir H65182 glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) - Escherichia coli gb AAC76794.1 (AF000455) glucose-1-phosphate thymidyltransferase [Escherichia coli K12]	SEQ ID n-1680
SEQ ID n° 8985	PL-2497.1	Contig9 from 3605233 to 3606192	m	52%	sp P14182 LICB_HAEMIN LICB PROTEIN pir C64128 lic-1 operon protein (LICB) homolog - Haemophilus influenzae KW20) gb AAC23188.1 (U32829) lic-1 operon protein (LICB) [Haemophilus influenzae Rd]	SEQ ID n-1681

SEQ ID n° 8986	PL-2498.1	Contig9 from 3606602 to 3608476	m	73%	pir T44517 trsg protein homolog [imported] - Plesiomonas shigelloides dbj BAA85014.1 (AB025970) ORF9P [Plesiomonas shigelloides] gb AAG17416.1 AF285970_10 (AF285970) Wbgz [Plesiomonas shigelloides]	SEQ ID n-1682
SEQ ID n° 8987	PL-2499.1	Contig9 from 3608486 to 3609097	m	76%	gb AAG17415.1 AF285970_9 (AF285970)-Wbgx [Plesiomonas shigelloides]	SEQ ID n-1683
SEQ ID n° 8988	PL-2500.1	Contig9 from 3609098 to 3610255	m	84%	gb AAG17414.1 AF285970_8 (AF285970) Wbgx [Plesiomonas shigelloides]	SEQ ID n-1686
SEQ ID n° 8989	PL-2501.1	Contig9 from 3610266 to 3611276	m	53%	gb AAG17423.1 AF285971_7 (AF285971) Wbgw [Shigella sonnei]	SEQ ID n-1687
SEQ ID n° 8990	PL-2502.1	Contig9 from 3611446 to 3612684	m	61%	emb CAA07667.1 (AJ007747) putative transferase [Bordetella bronchiseptica]	SEQ ID n-1688
SEQ ID n° 8991	PL-2503.1	Contig9 from 3612681 to 3613751	m	72%	pir C83253 probable UDP-N-acetylglucosamine 2- epimerase Wbpi PA3148 [imported] Pseudomonas aeruginosa (strain PA01) gb AAG06536.1 AE004738_10 (AE004738) probable UDP-N-acetylglucosamine 2-epimerase Wbpi [Pseudomonas aeruginosa]	SEQ ID n-1689
SEQ ID n° 8992	PL-2504.1	Contig9 from 3613757 to 3614860	m	75%	pir D83253 probable glycosyltransferase Wbph PA3149 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAC45862.1 (U50396) Wbph [Pseudomonas aeruginosa] gb AAG06537.1 AE004738_11 (AE004738) probable glycosyltransferase Wbph [Pseudomonas aeruginosa]	SEQ ID n-1690
SEQ ID n° 8993	PL-2505.1	Contig9 from 3614857 to 3616086	m	No Hits found		SEQ ID n-1691

SEQ ID n° 8994	PL-2506.1	Contig9 from 3616076 to 3617182	m	22%	sp P46555 YKG5_CAEEL_HYPOTHETICAL_71.9_KD PROTEIN_B0285.5_IN_CHROMOSOME_III_pir T18692 hypothetical protein_B0285.5 - Caenorhabditis elegans emb CAA84297.1 (Z34533) cDNA EST yk96a2.5 comes from this gene [Caenorhabditis elegans]	SEQ ID n-1692
SEQ ID n° 8995	PL-2507.1	Contig9 from 3617190 to 3618407	m	48%	pir C83251 O-antigen translocase PA3153 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAC45858.1 (U50396) WbpF [Pseudomonas aeruginosa] gb AAG06541.1 AE004739_3 (AE004739) O-antigen translocase [Pseudomonas aeruginosa] pir E83251 probable aminotransferase WbpE PA3155 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06543.1 AE004739_5 (AE004739) probable aminotransferase WbpE [Pseudomonas aeruginosa] pir S70673 acetyl transferase homolog - Bordetella pertussis emb CAA62246.1 (X90711) gene referred to as bplB in Mol. Microbiol. 19:37-52(1996) [Bordetella pertussis] emb CAA07670.1 (AJ007747) putative acetyltransferase [Bordetella bronchiseptica] prf 2210367D bplB gene [Bordetella pertussis]	SEQ ID n-1693
SEQ ID n° 8996	PL-2508.1	Contig9 from 3618413 to 3619483	m	82%	gb AAD45293.1 AF156256_1 (AF156256) putative dehydrogenase [Vibrio anguillarum] pir A83252 probable UDP-glucose/GDP-mannose dehydrogenase WbpA PA3159 [imported] Pseudomonas aeruginosa (strain PA01) gb AAC45852.1 (U50396) WbpA [Pseudomonas aeruginosa] gb AAG06547.1 AE004739_9 (AE004739) probable UDP-glucose/GDP-mannose dehydrogenase WbpA [Pseudomonas aeruginosa]	SEQ ID n-1694
SEQ ID n° 8997	PL-3217.1	Contig9 from 3619498 to 3620085	m	77%		SEQ ID n-1695
SEQ ID n° 8998	PL-2509.1	Contig9 from 3620104 to 3621153	m	71%		SEQ ID n-1696
SEQ ID n° 8999	PL-2510.1	Contig9 from 3621168 to 3622478	m	82%		SEQ ID n-1697

Contig9 from SEQ ID n° 9000 PL-2511.1 3622880 to 3624250	m	87%	sp P08336 CPXA_ECOLI SENSOR PROTEIN CPXA pir S40855 chemotaxis protein cpxA (EC 2.7.3.-) - Escherichia coli gb AAB03044.1 (L19201) CG Site No. 908 [Escherichia coli] gb AAC76893.1 (AE000466) probable sensor protein (histidine protein kinase), acting on arca [Escherichia coli K12] SEQ ID n° 1698
Contig9 from SEQ ID n° 9001 PL-2512.1 3624247 to 3624942	m	92%	sp P16244 CPXR_ECOLI TRANSCRIPTIONAL REGULATORY PROTEIN CPXR pir IS3679 transcription factor - Escherichia coli pir C65197 transcription regulator cpxR - Escherichia coli (strain K-12) gb AAC36868.1 (L14579) transcription factor [Escherichia coli] gb AAC76894.1 (AE000466) transcriptional regulator in 2-component system [Escherichia coli K12] gb AAG59106.1 AE005622_8 (AE005622) transcriptional regulator in 2- component system [Escherichia coli O157:H7] prf 2004283A membrane sensor regulator [Escherichia coli] SEQ ID n° 1699
Contig9 from SEQ ID n° 9002 PL-3218.1 3625100 to 3625594	p	52%	pir S40857 hypothetical protein o167 - Escherichia coli gb AAB03046.1 (L19201) ORF o167 [Escherichia coli] gb AAG59107.1 AE005622_9 (AE005622) y10 gene product [Escherichia coli O157:H7] SEQ ID n° 2471
Contig9 from SEQ ID n° 9003 PL-3219.1 3625837 to 3626271	m	65%	emb CAB54522.1 (AJ245959) Int protein [Bacteriophage WPhi] SEQ ID n° 2472
Contig9 from SEQ ID n° 9004 PL-6997.1 3626284 to 3626460	p	54%	gb AAG58617.1 AE005572_15 (AE005572) Z4883 gene product [Escherichia coli O157:H7 EDL933] dbj BAB37780.1 (AP002565) Hica-like protein [Escherichia coli O157:H7] #N/A
Contig9 from SEQ ID n° 9005 PL-4645.1 3626453 to 3626800	p	65%	gb AAG58616.1 AE005572_14 (AE005572) Z4882 gene product [Escherichia coli O157:H7] #N/A

SEQ ID n° 9006	PL-4646.1	Contig9 from 3627288 to 3627710	m	83%	emb CAB54522.1 (AJ245959) Int protein [Bacteriophage WPhi1]	#N/A
SEQ ID n° 9007	PL-4648.1	Contig9 from 3627732 to 3627920	m	46%	ref NP_046787.1 gpc [Bacteriophage P2] gb AAD03298.1 (AF063097) gpc [Bacteriophage P2]	#N/A
SEQ ID n° 9008	PL-4649.1	Contig9 from 3627945 to 3628259	m	75%	pir JC4694 proteic killer active protein hig B plasmid Rts1 gb AAC43983.1 (U43847) antidote protein [Plasmid Rts1] gb AAD00516.1 (U81366) antidote protein [Plasmid Rts1] prf 2210234B higA gene [Escherichia coli]	#N/A
SEQ ID n° 9009	PL-4650.1	Contig9 from 3628259 to 3628411	m	78%	pir JC4693 proteic killer suppression protein hig A - plasmid Rts1 gb AAC43982.1 (U43847) killer protein [Plasmid Rts1] gb AAD00515.1 (U81366) killer protein [Plasmid Rts1]	#N/A
SEQ ID n° 9010	PL-4651.1	Contig9 from 3628353 to 3628538	m	62%	pir JC4693 proteic killer suppression protein hig A - plasmid Rts1 gb AAC43982.1 (U43847) killer protein [Plasmid Rts1] gb AAD00515.1 (U81366) killer protein [Plasmid Rts1]	#N/A
SEQ ID n° 9011	PL-4653.1	Contig9 from 3629323 to 3629625	m	61%	prf 2210234A higB gene [Escherichia coli] gb AAG54758.1 AE005220_7 (AE005220) unknown [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9012	PL-4654.1	Contig9 from 3629618 to 3629860	m	85%	gb AAG54757.1 AE005220_6 (AE005220) unknown [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9013	PL-7121.1	Contig9 from 3629961 to 3630095	p	No Hits found		#N/A
SEQ ID n° 9014	PL-4655.1	Contig9 from 3630174 to 3630308	p	42%	gb AAG55936.1 AE005327_6 (AE005327) unknown protein encoded by prophage CP-933C [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9015	PL-4656.1	Contig9 from 3630386 to 3630724	m	75%	gb AAF33487.1 (AF233324) hypothetical protein predicted by Glimmer [Salmonella typhimurium LT2]	#N/A

SEQ ID n° 9016	PL-4657.1	Contig9 from 3630721 to 3631038	m 75%	gb AAF33478.1 (AF233324) contains similarity to Bacteriophage N15 (GP49) (GB:AF064539) and Yersinia pestis unfinished genomic sequence (TBLASTX) [Salmonella typhimurium LT2]	#N/A
SEQ ID n° 9017	PL-3220.1	Contig9 from 3631318 to 3631725	p 71%	gb AAD54236.1 AF153829_2 (AF153829) unknown [Salmonella typhi]	SEQ ID n-2474
SEQ ID n° 9018	PL-4659.1	Contig9 from 3631925 to 3632218	m 42%	ref NP_046944.1 gp48 [Bacteriophage N15] pir T13135 protein gp48 - phage N15 gb AAC19087.1 (AF064539) gp48 [Bacteriophage N15]	#N/A
SEQ ID n° 9019	PL-4660.1	Contig9 from 3632227 to 3632577	m 47%	ref NP_046945.1 gp49 [Bacteriophage N15] pir T13136 protein gp49 - phage N15 gb AAC19088.1 (AF064539) gp49 [Bacteriophage N15]	#N/A
SEQ ID n° 9020	PL-2513.1	Contig9 from 3633062 to 3633736	p 48%	pir G82138 CDP-diacylglycerol--glycerol-3- phosphate 3-phosphatidyltransferase- related protein VC1935 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95083.1 (AE004269) CDP-diacylglycerol-- glycerol-3-phosphate phosphatidyltransferase-related protein [Vibrio cholerae]	SEQ ID n-2700
SEQ ID n° 9021	PL-2514.1	Contig9 from 3633729 to 3634370	p 56%	pir B83329 probable acyltransferase PA2537 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05925.1 AE004681_7 (AE004681) probable acyltransferase [Pseudomonas aeruginosa]	SEQ ID n-2701
SEQ ID n° 9022	PL-2515.1	Contig9 from 3634367 to 3635311	p 72%	pir A83329 probable phosphatidate cytidyltransferase PA2536 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05924.1 AE004681_6 (AE004681) probable phosphatidate cytidyltransferase [Pseudomonas aeruginosa]	SEQ ID n-2702

SEQ ID n° 9023	PL-2516.1	Contig9 from 3635693 to 3636664	p	86%	gb AAD16179.1 (AF098509) phosphofructokinase [Enterobacter cloacae]	SEQ ID n-1703
SEQ ID n° 9024	PL-2517.1	Contig9 from 3636836 to 3637831	p	82%	pir S40860 periplasmic sulphate binding protein - Escherichia coli pir BYEC sulfate binding protein precursor, periplasmic - Escherichia coli gb AAB03049.1 (U19201) periplasmic sulphate binding protein [Escherichia coli] gb AAC76899.1 (AE000466) periplasmic sulfate- binding protein [Escherichia coli K12]	SEQ ID n-1704
SEQ ID n° 9025	PL-2518.1	Contig9 from 3637884 to 3638651	m	85%	sp Q9Z6B9 TPIS_ENTCL TRIOSEPHOSPHATE ISOMERASE (TIM) gb AAD16183.1 (AF098509) triose phosphate isomerase [Enterobacter cloacae] sp P32160 YTIQ_ECOLI HYPOTHETICAL 21.8 KD PROTEIN IN TPIA-FPR INTERGENIC REGION PRECURSOR pir S40863 hypothetical.21.8K protein (tpia 3'region) precursor - Escherichia coli gb AAB03052.1 (U19201) ORF_f199 [Escherichia coli] gb AAC76902.1 (AE000466) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-1705
SEQ ID n° 9026	PL-2519.1	Contig9 from 3638786 to 3639388	m	53%	sp P32161 YIIR_ECOLI HYPOTHETICAL 16.5 KD PROTEIN IN TPIA-FPR INTERGENIC REGION (O146) pir S40864 hypothetical 16.5K protein (tpia-fpr intergenic region) - Escherichia coli gb AAB03053.1 (U19201) ORF_o146 [Escherichia coli] gb AAC76903.1 (AE000466) orf, hypothetical protein [Escherichia coli K12] gb AAG59114.1 AE005623_5 (AE005623) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-1706
SEQ ID n° 9027	PL-4661.1	Contig9 from 3639456 to 3639890	p	68%	gb AAG59117.1 AE005623_8 (AE005623) ferredoxin- NADP reductase [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9028	PL-2520.1	Contig9 from 3639893 to 3640639	m	85%	gb AAG59119.1 AE005623_10 (AE005623) glycerol kinase [Escherichia coli O157:H7]	SEQ ID n-1708
SEQ ID n° 9029	PL-2521.1	Contig9 from 3641048 to 3642571	m	89%		SEQ ID n-1709

SEQ ID n° 9030	PL-2522.1	Contig9 from 3642602 to 3643432	m	80%	sp P31140 GLPF_SHIFL GLYCEROL UPTAKE FACILITATOR PROTEIN	SEQ ID n-3710
SEQ ID n° 9031	PL-4663.1	Contig9 from 3643738 to 3643980	p	58%	sp P32164 YIUU_ECOLI HYPOTHETICAL 9.6 KD PROTEIN IN GLPF-HSLU INTERGENIC REGION (O81) pir S40871 hypothetical_9.6K protein (glpf-hslu intergenic region) - Escherichia coli gb AB03060.1 (L19201) ORF_081 [Escherichia coli] gb AAC76910.1 (AE000467) orf, hypothetical protein [Escherichia coli K12] gb AAG59121.1 AE005623_12 (AE005623) orf, hypothetical protein [Escherichia coli O157:H7] sp P32165 MENG_ECOLI S-ADENOSYLMETHIONINE:2- DEMETHYLMENAQUINONE METHYLTRANSFERASE pir S40872 2-demethylmenaquinone 2-C- methyltransferase (EC 2.1.1.-) meng [validated] - Escherichia coli gb AB03061.1 (L19201) ORF_f161 [Escherichia coli] gb AB01208.1 (U56082) S-adenosylmethionine:2- demethylmenaquinone methyltransferase [Escherichia coli] gb AAC76911.1 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli K12] gb AAG59124.1 AE005623_15 (AE005623) menaquinone biosynthesis, unknown [Escherichia coli O157:H7] gb AAG59125.1 AE005624_1 (AE005624) 1,4- dihydroxy-2-naphthoate --> dimethylmenaquinone [Escherichia coli O157:H7]	SEQ ID n-2476
SEQ ID n° 9032	PL-3222.1	Contig9 from 3644041 to 3644550	m	84%		
SEQ ID n° 9033	PL-2523.1	Contig9 from 3644700 to 3645617	m	74%		SEQ ID n-3711

<p>sp P32168 HSLU_ECOLI ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT HSLU (HEAT SHOCK PROTEIN HSLU) pir JT0761 heat-shock-protein hslu - Escherichia coli gb AA03063.1 (L19201) matches PS00017: ATP_GTP_A; similar to Pasteurella haemolytica hypoth. protein ORF1; heat shock induced [Escherichia coli] gb AAC76913.1 (AE000467) heat shock protein hslvu, ATPase subunit, homologous to chaperones [Escherichia coli K12] gb AAG59126.1 AE005624_2 (AE005624) heat shock protein hslvu, ATPase subunit, homologous to chaperones [Escherichia coli O157:H7]</p>	<p>Contig9 from SEQ ID n° 9034 PL-2524.1 3645713 to 3647044</p>	<p>m 91%</p>	<p>SEQ ID n-2712</p>
<p>emb CAC00719.1 (AJ295709) heat shock protein [Salmonella typhimurium]</p>	<p>Contig9 from SEQ ID n° 9035 PL-3223.1 3647056 to 3647586</p>	<p>m 80%</p>	<p>SEQ ID n-2477</p>
<p>sp P29131 FTSN_ECOLI CELL DIVISION PROTEIN FTSN pir A47122 cell division protein FTSN - Escherichia coli gb AA23814.1 (L14281) cell division protein [Escherichia coli]</p>	<p>Contig9 from SEQ ID n° 9036 PL-2525.1 3647710 to 3648537</p>	<p>m 56%</p>	<p>SEQ ID n-2713</p>
<p>sp P06964 CYTR_ECOLI TRANSCRIPTIONAL REPRESSOR CYTR pir RPECCT cyt transcription repressor cytr - Escherichia coli gb AA03066.1 (L19201) CG Site No. 887 [Escherichia coli]</p>	<p>Contig9 from SEQ ID n° 9037 PL-2526.1 3648607 to 3649635</p>	<p>m 78%</p>	<p>SEQ ID n-2714</p>
<p>emb CAA27318.1 (X03683) put. Cyt repressor (aa 1-341) [Escherichia coli] gb AAC76916.1 (AE000467) regulator for deo operon, udp, cdd, tsx, nupC, and nupG [Escherichia coli K12] gb AAG59129.1 AE005624_5 (AE005624) regulator for deo operon, udp, cdd, tsx, nupC, and nupG [Escherichia coli O157:H7] gb AAG59130.1 AE005624_6 (AE005624) primosomal protein N' (= factor Y) (putative helicase) [Escherichia coli O157:H7]</p>	<p>Contig9 from SEQ ID n° 9038 PL-2527.1 3649962 to 3652181</p>	<p>m 76%</p>	<p>SEQ ID n-2715</p>

SEQ ID n° 9039	PL-4667.1	Contig9 from 3652370 to 3652585	p	77%	<p>sp P02432 RL31_ECOLI 50S RIBOSOMAL PROTEIN' L31 pir RSEC31 ribosomal protein L31 [validated] - Escherichia.coli gb AAB03068.1 (L19201) 50S ribosomal protein L31 [Escherichia coli] emb CAA55286.1 (X78541) ribosomal protein L31 [Escherichia.coli] gb AAC76918.1 (AE000467) 50S ribosomal subunit protein L31 [Escherichia coli K12] gb AAG59131.1 AE005624_7 (AE005624) 50S ribosomal subunit protein L31 [Escherichia coli O157:H7] #N/A</p>
SEQ ID n° 9040	PL-4669.1	Contig9 from 3652713 to 3653030	m	91%	<p>sp P06203 METJ_SALTY MET REPRESSOR (MET REGULON REGULATORY PROTEIN METJ) pir A23081 regulatory protein metJ - Salmonella typhimurium emb CAA25997.1 (X01961) metJ gene pot. repressor (aa 1-104) [Salmonella typhimurium] #N/A</p>
SEQ ID n° 9041	PL-2528.1	Contig9 from 3653306 to 3654478	p	84%	<p>sp P00935 METB_ECOLI CYSTATHIONINE GAMMA- SYNTHASE (CGS) (O-SUCCINYLMOMOSERINE (THIOL)-LYASE) pir SYECG O-succinylhomoserine (thiol)-lyase (EC 4.2.99.9) - Escherichia coli gb AA24167.1 (K01547) cystathione gamma- synthase [Escherichia coli] gb AAB03071.1 (L19201) cystathionine gamma-synthase [Escherichia coli] gb AAC76921.1 (AE000468) cystathionine gamma-synthase [Escherichia coli K12] SEQ ID n-3716</p>

sp P00562 AK2H_ECOLI BIFUNCTIONAL ASPARTOKINASE/HOMOSERINE DEHYDROGENASE II (AKII- HDII) [INCLUDES: ASPARTOKINASE II ; HOMOSERINE DEHYDROGENASE II]		SEQ ID n~2717	
Contig9 from			
SEQ ID n° 9042 PL-2529.1	3654481 to p 86% 3656916		
pir S03169 5,10-methylenetetrahydrofolate reductase (FADH2) (EC 1.7.99.5) - Salmonella typhimurium		SEQ ID n~2719	
Contig9 from			
SEQ ID n° 9043 PL-2530.1	3657261 to p 87% 3658145		
Contig9 from			
SEQ ID n° 9044 PL-6947.1	3658524 to p No Hits found 3658856		#N/A
Contig9 from			
SEQ ID n° 9045 PL-6946.1	3658914 to p 35% 3659069		#N/A
Contig9 from			
SEQ ID n° 9046 PL-2531.2	3659604 to p 22% 3660563		SEQ ID n~2720
Contig9 from			
SEQ ID n° 9047 PL-2533.1	3661575 to p No Hits found 3662525		SEQ ID n~2722
Contig9 from			
SEQ ID n° 9048 PL-4680.1	3662528 to p No Hits found 3662923		#N/A
Contig9 from			
SEQ ID n° 9049 PL-3225.1	3663217 to m No Hits found 3663798		SEQ ID n~2478
Contig9 from			
SEQ ID n° 9050 PL-4682.1	3663915 to m No Hits found 3664019		#N/A

sp|P00864|CAPP_ECOLI PHOSPHOENOLPYRUVATE
 CARBOXYLASE (PEPCASE) (PEPC) pir||QYEC
 phosphoenolpyruvate carboxylase (EC 4.1.1.31) -
 Escherichia coli pdb|1FY| Three-Dimensional
 Structure Of Phosphoenolpyruvate Carboxylase
 From Escherichia Coli At 2.8 A Resolution
 emb|CAA29332.1| (X05903) PEP carboxylase (AA 1-
 883) [Escherichia coli] gb|AAC43062.1| (U000006)
 phosphoenolpyruvate carboxylase [Escherichia
 coli] gb|AAC76938.1| (AE000469)
 phosphoenolpyruvate carboxylase [Escherichia
 coli K12] prf||1005219A
 carboxylase, phosphoenolpyruvate [Escherichia
 coli] SEQ ID n-1723
 sp|P23908|ARGE_ECOLI ACETYLORNITHINE DEACETYLASE
 (ACETYLORNITHINASE) (AO) (N-
 ACETYLORNITHINASE) (NRO) pir||B42377
 acetylornithine deacetylase (EC 3.5.1.16) -
 Escherichia coli emb|CAA44625.1| (X62807)
 acetylornithine deacetylase subunit a2
 [Escherichia coli] emb|CAA39076.1| (X55417) N-
 acetylornithinase [Escherichia coli]
 gb|AAC43063.1| (U00006) acetylornithine
 deacetylase [Escherichia coli] gb|AAC76939.1|
 (AE000470) acetylornithine deacetylase
 [Escherichia coli K12] SEQ ID n-1724

Contig9 from
 SEQ ID n° 9051 PL-2534.1 3664113 to m 84%
 3666749

Contig9 from
 SEQ ID n° 9052 PL-2535.1 3667032 to m 85%
 3668189

SEQ ID n° 9053	PL-2536.1	Contig9 from 3668292 to 3669296	p 82%	sp P11446 ARGC_ECOLI N-ACETYL-GAMMA-GLUTAMYL- PHOSPHATE REDUCTASE (AGPR) (N-ACETYL- GLUTAMATE SEMIALDEHYDE DEHYDROGENASE) (NAGSA DEHYDROGENASE) pir RDECEP N-acetyl-gamma- glutamyl-phosphate reductase (EC 1.2.1.38) - Escherichia coli gb AAA23477.1 (M21446) argC (EC 1.2.1.38) [Escherichia coli] gb AAC43064.1 (U00006) N-acetyl-gamma-glutamyl-phosphate reductase [Escherichia coli] gb AAC76940.1 (AE000470) N-acetyl-gamma- glutamylphosphate reductase [Escherichia coli K12] SEQ ID n-1725
SEQ ID n° 9054	PL-2537.1	Contig9 from 3669322 to 3670095	p 85%	sp P11445 ARGB_ECOLI ACETYLGLUTAMATE KINASE (NAG KINASE) (AGK) (N-ACETYL-L-GLUTAMATE PHOSPHOTRANSFERASE) pir KIECAE acetylglutamate kinase (EC 2.7.2.8) - Escherichia coli gb AAA23478.1 (M21446) argB (EC 2.7.2.8) [Escherichia coli] gb AAC43065.1 (U00006) acetylglutamate kinase [Escherichia coli] gb AAC76941.1 (AE000470) acetylglutamate kinase [Escherichia coli K12] gb AGS9161.1 (AE005627_5 (AE005627) acetylglutamate kinase [Escherichia coli O157:H7] SEQ ID n-1726
SEQ ID n° 9055	PL-2538.1	Contig9 from 3670164 to 3671378	p 81%	pir A82052 argininosuccinate synthase VC2642 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95783.1 (AE004330) argininosuccinate synthase [Vibrio cholerae] gb AAG59162.1 (AE005627_6 (AE005627) argininosuccinate lyase [Escherichia coli O157:H7] SEQ ID n-1727
SEQ ID n° 9056	PL-2539.1	Contig9 from 3671531 to 3672910	p 83%	sp P71318 OXYR_ERWCA HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR gb AAC72241.1 (U74302) oxidative stress transcriptional regulator [Pectobacterium carotovorum] SEQ ID n-1728
SEQ ID n° 9057	PL-2540.1	Contig9 from 3673190 to 3674095	p 84%	

SEQ ID n° 9058	PL-2541.1	Contig9 from 3674087 to 3675484	m	87%	sp P27306 STHA_ECOLI SOLUBLE PYRIDINE NUCLEOTIDE TRANSHYDROGENASE (STH) (NAD(P) (+) TRANSYDROGENASE, [B-SPECIFIC])	SEQ ID n-1731
SEQ ID n° 9059	PL-3227.1	Contig9 from 3675859 to 3676407	p	91%	gb AAG59167.1 AE005628_3 (AE005628) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2479
SEQ ID n° 9060	PL-4686.1	Contig9 from 3676524 to 3676895	p	69%	sp P27308 YJUD_ECOLI HYPOTHETICAL 13.0 KD PROTEIN IN UDHA-TRMA INTERGENIC REGION (ORFB) pir G65203 yijD protein - Escherichia coli (strain K-12) gb AAC43070.1 (U00006) alternate name yijD [Escherichia coli] gb AAC76946.1 (AE000470) orf, hypothetical protein [Escherichia coli K12] gb AAG59168.1 AE005628_4 (AE005628) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9061	PL-2542.1	Contig9 from 3676958 to 3678058	m	79%	gb AAG59169.1 AE005628_5 (AE005628) tRNA (uracil- 5-) -methyltransferase [Escherichia coli O157:H7]	SEQ ID n-1732
SEQ ID n° 9062	PL-2543.1	Contig9 from 3678242 to 3680101	p	73%	gb AAG59170.1 AE005628_6 (AE005628) outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23 [Escherichia coli O157:H7]	SEQ ID n-1733
SEQ ID n° 9063	PL-2544.1	Contig9 from 3680046 to 3680909	p	77%	gb AAG59171.1 AE005628_7 (AE005628) glutamate racemase, required for biosynthesis of D-glutamate and peptidoglycan [Escherichia coli O157:H7]	SEQ ID n-1734
SEQ ID n° 9064	PL-3060.1	Contig9 from 3686724 to 3687749	p	76%	sp P37417 MURB_SALTY UDP-N- ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (UDP-N- ACETYL MURAMATE DEHYDROGENASE) gb AA27163.1 (L14816) UDP-N- acetylenolpyruvoylglucosamine reductase [Salmonella typhimurium] gb AAP33492.1 (AF170176) Salmonella typhimurium UDP-N-acetylenolpyruvoylglucosamine reductase (MURB) (SW:P37417) [Salmonella typhimurium LT2]	SEQ ID n-2296

SEQ ID n° 9065	PL-3061.1	Contig9 from 3687746 to 3688705	p	81%	gb AAF33493.1 (AF170176) Salmonella typhimurium - bifunctional protein (BIRA) (SW:P37416) [Salmonella typhimurium LT2] SEQ ID n-2297 sp Q9L9K3 COAA_SALTY PANTOTHENATE KINASE (PANTOTHENIC ACID KINASE) gb AAF33512.1 (AF170176) 96% identity over 316 amino acids with E. coli pantothenate kinase (SW:P15044) [Salmonella typhimurium LT2] SEQ ID n-2298
SEQ ID n° 9066	PL-3062.1	Contig9 from 3688749 to 3689699	m	80%	
SEQ ID n° 9067	PL-4709.1	Contig9 from 3690503 to 3690682	p	No Hits found	#N/A
SEQ ID n° 9068	PL-3063.1	Contig9 from 3690675 to 3691859	p	96%	sp P21694 EFTU_SALTY ELONGATION FACTOR TU (EF-TU) pir S13561 translation elongation factor EF-Tu.B - Salmonella typhimurium emb CAA38913.1 (X55117) elongation factor Tu [Salmonella typhimurium] emb CAA38912.1 (X55116) elongation factor Tu [Salmonella typhimurium] gb AAF33513.1 (AF170176) Salmonella typhimurium translation elongation factors TU (EF-TU) (SW:P21694); contains similarity to Pfam domain PF00009 (GTP_EFTU, Score=541.8 E=4.6e-159, N=1 [Salmonella typhimurium LT2] SEQ ID n-2299
SEQ ID n° 9069	PL-4710.1	Contig9 from 3692613 to 3692807	p	63%	#N/A
SEQ ID n° 9070	PL-3229.1	Contig9 from 3692884 to 3693360	p	93%	sp O68934 BFD_SERMA BACTERIOFERRITIN-ASSOCIATED FERREDOXIN gb AAC14292.1 (AF058451) YheAp [Serratia marcescens] sp O68935 BFR_SERMA BACTERIOFERRITIN (BFR) (CYTOCHROME B-1) (CYTOCHROME B-557) gb AAC14293.1 (AF058451) bacterioferritin [Serratia marcescens] SEQ ID n-2481
SEQ ID n° 9071	PL-4711.1	Contig9 from 3693664 to 3693975	p	97%	sp P44378 RE10_HAEIN 30S RIBOSOMAL PROTEIN S10 pir D64092 ribosomal protein S10 - Haemophilus influenzae (strain Rd KW20) gb AAC22435.1 (U32761) ribosomal protein S10 (rpS10) [Haemophilus influenzae Rd] #N/A

<p> SEQ ID n° 9072 PL-3064.1 Contig9 from 3694008 to p 94% 3694637 </p>	<p> sp P02386 RL3_ECOLI 50S RIBOSOMAL PROTEIN L3 pir R5EC3 ribosomal protein L3 [validated] - Escherichia coli emb CAA26460.1 (X02613) ribosomal protein L3 (rplC) (aa 1-209) [Escherichia coli] gb AAAS8117.1 (U18997) 50S ribosomal subunit protein L3 [Escherichia coli] gb AAC76345.1 (AE000408) 50S ribosomal subunit protein L3 [Escherichia coli K12] gb AAG58441.1 AE005557_10 (AE005557) 50S ribosomal subunit protein L3 [Escherichia coli O157:H7] prf 0509226A protein L3 [Escherichia coli] SEQ ID n-2300 </p>
<p> SEQ ID n° 9073 PL-3065.1 Contig9 from 3694654 to p 92% 3695259 </p>	<p> sp P11253 RL4_YERPS 50S RIBOSOMAL PROTEIN L4 pir R5EB4Y ribosomal protein L4 - Yersinia pseudotuberculosis emb CAA32543.1 (X14363) ribosomal protein L4 (AA 1 - 201) [Yersinia pseudotuberculosis] sp P02424 RL23_ECOLI 50S RIBOSOMAL PROTEIN L23 pir R5EC23 ribosomal protein L23 [validated] - Escherichia coli emb CAA26462.1 (X02613) ribosomal protein L23 (rplW) (aa 1-100) [Escherichia coli] gb AAAS8115.1 (U18997) 50S ribosomal subunit protein L23 [Escherichia coli] gb AAC76343.1 (AE000408) 50S ribosomal subunit protein L23 [Escherichia coli K12] gb AAG58439.1 AE005557_8 (AE005557) 50S ribosomal subunit protein L23 [Escherichia coli O157:H7] #N/A </p>
<p> SEQ ID n° 9074 PL-4713.1 Contig9 from 3695256 to p 92% 3695558 </p>	<p> sp P49239 RL2_YEREN 50S RIBOSOMAL PROTEIN L2 gb AAC43513.1 (U11251) ribosomal protein L2 [Yersinia enterocolitica] SEQ ID n-2302 </p>

SEQ ID n° 9076 PL-4714.1	Contig9 from 3696417 to 3696695	p 97%	<p>sp P02375 RS19_ECOLI 30S RIBOSOMAL PROTEIN S19 pir R3EC19 ribosomal protein S19 [validated] - Escherichia coli emb CAA26464.1 (X02613) ribosomal protein S19 (rpsS) (aa 1-273) [Escherichia coli] gb AA58113.1 (U18997) 30S ribosomal subunit protein S19 [Escherichia coli] gb AAC76341.1 (AE000408) 30S ribosomal subunit protein S19 [Escherichia coli K12] gb AAG58437.1 AE005557.6 (AE005557) 30S ribosomal subunit protein S19 [Escherichia coli O157:H7] sp P02423 RL22_ECOLI 50S RIBOSOMAL PROTEIN L22 pir R5EC22 ribosomal protein L22 [validated] - Escherichia coli emb CAA26465.1 (X02613) ribosomal protein L22 (rplV) (aa 1-110) [Escherichia coli] gb AA58112.1 (U18997) 50S ribosomal subunit protein L22 [Escherichia coli] gb AAC76340.1 (AE000408) 50S ribosomal subunit protein L22 [Escherichia coli K12] gb AAG58436.1 AE005557.5 (AE005557) 50S ribosomal subunit protein L22 [Escherichia coli O157:H7]</p>	#N/A
SEQ ID n° 9077 PL-4715.1	Contig9 from 3696710 to 3697042	p 94%	<p>sp P02352 RS3_ECOLI 30S RIBOSOMAL PROTEIN S3 pir R3EC3 ribosomal protein S3 [validated] - Escherichia coli emb CAA26466.1 (X02613) ribosomal protein S3 (rpsC) (aa 1-233) [Escherichia coli] gb AA58111.1 (U18997) 30S ribosomal subunit protein S3 [Escherichia coli] gb AAC76339.1 (AE000408) 30S ribosomal subunit protein S3 [Escherichia coli K12]</p>	#N/A
SEQ ID n° 9078 PL-3067.1	Contig9 from 3697060 to 3697761	p 80%	<p>sp P02352 RS3_ECOLI 30S RIBOSOMAL PROTEIN S3 pir R3EC3 ribosomal protein S3 [validated] - Escherichia coli emb CAA26466.1 (X02613) ribosomal protein S3 (rpsC) (aa 1-233) [Escherichia coli] gb AA58111.1 (U18997) 30S ribosomal subunit protein S3 [Escherichia coli] gb AAC76339.1 (AE000408) 30S ribosomal subunit protein S3 [Escherichia coli K12]</p>	SEQ ID n-2303

<p>SEQ ID n° 9079 PL-4716.1</p> <p>Contig9 from 3697774 to 3698184</p>	p 94%	<p>sp P02414 RL16_ECOLI 50S RIBOSOMAL PROTEIN L16 pir R5EC16 ribosomal protein L16 [validated] - Escherichia coli emb CAA26467.1 (X02613) ribosomal protein L16 (rplP) (aa 1-136) [Escherichia coli] gb AA58110.1 (U18997) 50S ribosomal subunit protein L16 [Escherichia coli] gb AAC76338.1 (AE000408) 50S ribosomal subunit protein L16 [Escherichia coli K12] gb AAG58434.1 AE005557_3 (AE005557) 50S ribosomal subunit protein L16 [Escherichia coli O157:H7]</p>	#N/A
<p>SEQ ID n° 9080 PL-4717.1</p> <p>Contig9 from 3698184 to 3698375</p>	p 88%	<p>sp P02429 RL29_ECOLI 50S RIBOSOMAL PROTEIN L29 pir R5EC29 ribosomal protein L29 [validated] - Escherichia coli emb CAA26468.1 (X02613) ribosomal protein L29 (rplM) (aa 1-63) [Escherichia coli] gb AA58109.1 (U18997) 50S ribosomal subunit protein L29 [Escherichia coli] gb AAC76337.1 (AE000408) 50S ribosomal subunit protein L29 [Escherichia coli K12] gb AAG58433.1 AE005557_2 (AE005557) 50S ribosomal subunit protein L29 [Escherichia coli O157:H7] prf 0612186A ribosomal protein L29 [Escherichia coli]</p>	#N/A
<p>SEQ ID n° 9081 PL-4718.1</p> <p>Contig9 from 3698375 to 3698629</p>	p 91%	<p>sp P02373 RS17_ECOLI 30S RIBOSOMAL PROTEIN S17 pir R3EC17 ribosomal protein S17 [validated] - Escherichia coli emb CAA26469.1 (X02613) ribosomal protein S17 (rpsQ) (aa 1-84) [Escherichia coli] gb AA58108.1 (U18997) 30S ribosomal subunit protein S17 [Escherichia coli] gb AAC76336.1 (AE000408) 30S ribosomal subunit protein S17 [Escherichia coli K12] gb AAG58432.1 AE005557_1 (AE005557) 30S ribosomal subunit protein S17 [Escherichia coli O157:H7]</p>	#N/A

SEQ ID n° 9082 PL-4720.1	Contig9 from 3698809 to 3699180	p 93%	sp P02411 RL14_ECOLI 50S RIBOSOMAL PROTEIN L14 pir R5EC14 ribosomal protein L14 [validated] - Escherichia coli emb CAA25715.1 (X01563) L14 (xpIN) (aa 1-123) [Escherichia coli]
			gb AAA58107.1 (U18997) 50S ribosomal subunit protein L14 [Escherichia coli] gb AAC76335.1 (AE000408) 50S ribosomal subunit protein L14 [Escherichia coli K12]
SEQ ID n° 9083 PL-4721.1	Contig9 from 3699191 to 3699505	p 86%	gb AGS58431.1 AE005556_24 (AE005556) 50S ribosomal subunit protein L14 [Escherichia coli O157:H7] prf 0806153A_ribosomal protein L14 [Escherichia coli]
			sp P02425 RL24_ECOLI 50S RIBOSOMAL PROTEIN L24 pir R5EC24 ribosomal protein L24 [validated] - Escherichia coli emb CAA25716.1 (X01563) L24 (xpIX) (aa 1-104) [Escherichia coli]
SEQ ID n° 9084 PL-3232.1	Contig9 from 3699520 to 3700059	p 92%	gb AAA58106.1 (U18997) 50S ribosomal subunit protein L24 [Escherichia coli] gb AAC76334.1 (AE000408) 50S ribosomal subunit protein L24 [Escherichia coli K12]
			gb AGS58430.1 AE005556_23 (AE005556) 50S ribosomal subunit protein L24 [Escherichia coli O157:H7]
SEQ ID n° 9085 PL-4722.1	Contig9 from 3700072 to 3700377	p 89%	sp P46178 RL5_BUCAR 50S RIBOSOMAL PROTEIN L5 pir JC2278 ribosomal protein L5 - pea aphid symbiont bacterium dbj BAA06587.1 (D31786) ribosomal protein L5 [Acyrtosiphon kondoi endosymbiont]
			gb AAK03486.1 (AE006177) Rps14 [Pasteurella multocida]

SEQ ID n-2484

#N/A

#N/A

#N/A

SEQ ID n° 9086 PL-4724.1	Contig9 from 3700411 to 3700803	p 94%	<p>sp P02361 RS8_ECOLI 30S RIBOSOMAL PROTEIN S8 pir R3EC8 ribosomal protein S8 [validated] - Escherichia coli gb AA58103.1 (U18997) 30S ribosomal subunit protein S8 [Escherichia coli] gb AAC76331.1 (AE000408) 30S ribosomal subunit protein S8, and regulator [Escherichia coli K12]</p> <p>gb AAG58427.1 AE005556_20 (AE005556) 30S ribosomal subunit protein S8, and regulator [Escherichia coli O157:H7]</p>	#N/A
SEQ ID n° 9087 PL-3068.1	Contig9 from 3700818 to 3701351	p 84%	<p>sp P02390 RL6_ECOLI 50S RIBOSOMAL PROTEIN L6 pir R5EC6 ribosomal protein L6 [validated] - Escherichia coli gb AA58102.1 (U18997) 50S ribosomal subunit protein L6 [Escherichia coli] gb AAC76330.1 (AE000408) 50S ribosomal subunit protein L6 [Escherichia coli K12]</p> <p>gb AAG58426.1 AE005556_19 (AE005556) 50S ribosomal subunit protein L6 [Escherichia coli O157:H7]</p>	SEQ ID n° 2304
SEQ ID n° 9088 PL-4725.1	Contig9 from 3701361 to 3701714	p 94%	<p>sp P02419 RL18_ECOLI 50S RIBOSOMAL PROTEIN L18 pir R5EC18 ribosomal protein L18 [validated] - Escherichia coli emb CAA25721.1 (X01563) L18 (irplR) (aa 1-117) [Escherichia coli] gb AA58101.1 (U18997) 50S ribosomal subunit protein L18 [Escherichia coli] gb AAC76329.1 (AE000408) 50S ribosomal subunit protein L18 [Escherichia coli K12]</p> <p>gb AAG58425.1 AE005556_18 (AE005556) 50S ribosomal subunit protein L18 [Escherichia coli O157:H7]</p>	#N/A

SEQ ID n° 9089	PL-3234.1	Contig9 from 3701729 to 3702229	p 92%	sp P02356 RS5_ECOLI 30S RIBOSOMAL PROTEIN S5 pir R3EC5 ribosomal protein S5 [validated] - Escherichia coli emb CAA25722.1 (X01563) S5 (rpSE) (aa 1-167) [Escherichia coli] gb AA58100.1 (U18997) 30S ribosomal subunit protein S5 [Escherichia coli] gb AAC76328.1 (AE000408) 30S ribosomal subunit protein S5 [Escherichia coli K12] gb AAG58424.1 AE005556_17 (AE005556) 30S ribosomal subunit protein S5 [Escherichia coli O157:H7]	SEQ ID n-2485
SEQ ID n° 9090	PL-4726.1	Contig9 from 3702235 to 3702414	p 84%	sp P46184 RL30_BUCAK 50S RIBOSOMAL PROTEIN L30 pir JC2284 ribosomal protein L30 - pea aphid symbiont bacterium dbj BAA03985.1 (D16555) ribosomal protein L30 [Acyrtosiphon kondoi endosymbiont] dbj BAA06593.1 (D31786) ribosomal protein L30 [Acyrtosiphon kondoi endosymbiont]	#N/A
SEQ ID n° 9091	PL-4727.1	Contig9 from 3702418 to 3702852	p 93%	sp P46185 RL15_BUCAK 50S RIBOSOMAL PROTEIN L15 pir JC2272 ribosomal protein L15 - pea aphid symbiont bacterium dbj BAA03986.1 (D16555) ribosomal protein L15 [Acyrtosiphon kondoi endosymbiont] dbj BAA06594.1 (D31786) ribosomal protein L15 [Acyrtosiphon kondoi endosymbiont]	#N/A
SEQ ID n° 9092	PL-3059.1	Contig9 from 3702860 to 3704191	p 98%	sp P03844 SECY_ECOLI PREPROTEIN TRANSLOCASE SECY SUBUNIT pir QOEGSY preprotein translocase secy [validated] - Escherichia coli emb CAA25725.1 (X01563) SecY (Pr1A) polypeptide (aa 1-443) [Escherichia coli] gb AA58097.1 (U18997) secy [Escherichia coli] gb AAC76325.1 (AE000408) putative ATPase subunit of translocase [Escherichia coli K12] gb AAG58421.1 AE005556_14 (AE005556) putative ATPase subunit of translocase [Escherichia coli O157:H7]	SEQ ID n-2305

SEQ ID n° 9093	PL-4730.1	Contig9 from 3704490 to 3704846	p	91%	gb AAK03477.1 (AE006177) Rps13 [Pasteurella multocida]	#N/A
SEQ ID n° 9094	PL-4732.1	Contig9 from 3704862 to 3705251	p	95%	sp P02366 RS11_ECOLI_30S_RIBOSOMAL_PROTEIN_S11 pir R3EC11 ribosomal protein S11 [validated] - Escherichia coli emb CAA26393.1 (X02543) ribosomal protein S11 (aa 1-129) [Escherichia coli] gb AA58095.1 (U18997) 30S ribosomal subunit protein S11 [Escherichia coli] gb AAC76322.1 (AE000407) 30S ribosomal subunit protein S11 [Escherichia coli K12] gb AAG58418.1 AE005556_11 (AE005556) 30S ribosomal subunit protein S11 [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9095	PL-3070.1	Contig9 from 3705289 to 3705909	p	85%	sp P02354 RS4_ECOLI_30S_RIBOSOMAL_PROTEIN_S4 pir R3EC4 ribosomal protein S4 [validated] - Escherichia coli emb CAA26394.1 (X02543) ribosomal protein S4 (aa 1-206) [Escherichia coli] gb AA58094.1 (U18997) 30S ribosomal subunit protein S4 [Escherichia coli] gb AAC76321.1 (AE000407) 30S ribosomal subunit protein S4 [Escherichia coli K12] gb AAG58417.1 AE005556_10 (AE005556) 30S ribosomal subunit protein S4 [Escherichia coli O157:H7]	SEQ ID n-2307

sp|P00574|RPOA_ECOLI DNA-DIRECTED RNA POLYMERASE
 ALPHA CHAIN (TRANSCRIPTASE ALPHA CHAIN)
 (RNA POLYMERASE ALPHA SUBUNIT) pir|[RNECA DNA-
 directed RNA polymerase (EC 2.7.7.6) alpha chain
 - Escherichia coli pir|[A41658 DNA-
 directed RNA polymerase (EC 2.7.7.6) alpha chain
 - Salmonella typhimurium
 emb|CAA25337.1|(X00766) RNA polymerase alpha
 subunit [Escherichia coli] gb|AA24577.1|
 (J01685) RNA polymerase alpha subunit
 [Escherichia coli] gb|AA27214.1|(M77750) RNA
 polymerase alpha-subunit [Salmonella
 typhimurium] gb|AA58092.1|(U18997) CG site
 No. 234 [Escherichia coli] gb|AAC76320.1|
 (AE000407) RNA polymerase, alpha subunit
 [Escherichia coli K12] gb|AAG58416.1|AE005556_9
 (AE005556) RNA polymerase, alpha subunit
 [Escherichia coli O157:H7] SEQ ID n-2308
 sp|P02416|RL17_ECOLI 50S RIBOSOMAL PROTEIN L17
 pir|[RSEC17 ribosomal protein L17 [validated] -
 Escherichia coli emb|CAA26396.1|(X02543)
 ribosomal protein L17 (aa 1-127) [Escherichia
 coli] emb|CAA25338.1|(X00766) ribosomal
 component L17 [Escherichia coli] gb|AA24578.1|
 (J01685) ribosomal protein L17 [Escherichia
 coli] gb|AA58091.1|(U18997) 50S ribosomal
 subunit protein L17 [Escherichia coli]
 gb|AAC76319.1|(AE000407) 50S ribosomal subunit
 protein L17 [Escherichia coli K12]
 gb|AAG58415.1|AE005556_8 (AE005556) 50S
 ribosomal subunit protein L17 [Escherichia coli
 O157:H7] prf|[0901236A protein L17 [Escherichia
 coli]

Contig9 from
 SEQ ID n° 9096 PL-3071.1 3705935 to 97%
 3706924

Contig9 from
 SEQ ID n° 9097 PL-4734.1 3706965 to 86%
 3707357

#N/A

SEQ ID n° 9098	PL-3236.1	3707492 to 3707908	p	73%	<p>Contig9 from</p> <p>sp P36676 ZNR_ECOLI_ZN(II)-RESPONSIVE REGULATOR OF ZNTA pir I67892 hypothetical transcription regulator mscl-rplQ intergenic region - Escherichia coli gb AAA24773.1 (L29458) similar to merr (Hg resistance) proteins [Escherichia coli] gb AA58089.1 (U18997) yhm [Escherichia coli] gb AAC76317.1 (AE000407) putative transcriptional regulator [Escherichia coli K12]</p>	SEQ ID n-2487
SEQ ID n° 9099	PL-4735.1	3707988 to 3708188	p	61%	<p>Contig9 from</p> <p>sp P36675 YHDL_ECOLI_HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENIC REGION pir I67891 yhdl protein - Escherichia coli gb AAA24772.1 (L29458) yhdl [Escherichia coli]</p>	#N/A
SEQ ID n° 9100	PL-3072.1	3708525 to 3709901	m	90%	<p>Contig9 from</p> <p>sp P23868 TRKA_ECOLI_TRK_SYSTEM POTASSIUM UPTAKE PROTEIN TRKA pir S36252 potassium transport system trkG/trkH protein trka [validated] - Escherichia coli emb CAA36359.1 (X52114) Trka protein of the constitutive K⁺ -transport system Trk [Escherichia coli] gb CAA54371.1 (X77091) trka [Escherichia coli] gb AA58087.1 (U18997) Trka protein of the constitutive K⁺ transport system Trk [Escherichia coli] gb AAC76315.1 (AE000407) transport of potassium [Escherichia coli K12] gb AAG58411.1 AE005556_4 (AE005556) transport of potassium [Escherichia coli O157:H7]</p>	SEQ ID n-2309
SEQ ID n° 9101	PL-3073.1	3709958 to 3711247	m	77%	<p>Contig9 from</p> <p>sp P36929 SUN_ECOLI_SUN_PROTEIN (FMU PROTEIN) pir D65121 fmu protein - Escherichia coli emb CAA71359.1 (Y10307) sun [Escherichia coli] gb AAC76314.1 (AE000407) orf, hypothetical protein [Escherichia coli K12]</p>	SEQ ID n-2310

SEQ ID n° 9102 PL-3074.1	Contig9 from 3711318 to 3712265	m	82%	sp P23882 FMT_ECOLI METHIONYL-TRNA FORMYLTRANSFERASE pir S23108 methionyl-trna formyltransferase (EC 2.1.1.2.9) - Escherichia coli emb CAA45207.1 (X63666) methionyl-trna formyltransferase [Escherichia coli] emb CAA54368.1 (X77091) methionyl-trnaMetf formyltransferase [Escherichia coli] gb AAC76313.1 (AE000407) 10- formyltetrahydrofolate:1-methionyl-trna (FMet) N-formyltransferase [Escherichia coli K12] sp P27251 DEF_ECOLI POLYPEPTIDE DEFORMYLASE (PDF) (FORMYLMETHIONINE DEFORMYLASE) pir S23107 N-formylmethionylaminoacyl-trna deformylase (EC 3.5.1.27) - Escherichia coli emb CAA45206.1 (X63666) fms [Escherichia coli] emb CAA54367.1 (X77091) peptide deformylase [Escherichia coli] emb CAA54826.1 (X77800) deformylase [Escherichia coli] gb AA58084.1 (U18997) N- formylmethionylaminoacyl-trna deformylase [Escherichia coli] gb AAC76312.1 (AE000407) peptide deformylase [Escherichia coli K12] gb AAG58408.1 AE005556_1 (AE005556) peptide deformylase [Escherichia coli O157:H7]	SEQ ID n-2311
				gb AAG58407.1 AE005555_7 (AE005555) smf gene product [Escherichia coli O157:H7]	
SEQ ID n° 9103 PL-3237.1	Contig9 from 3712290 to 3712802	m	92%	gb AAG58405.1 AE005555_5 (AE005555) putative DNA topoisomerase [Escherichia coli O157:H7]	SEQ ID n-2312
				gb AAG58404.1 AE005555_4 (AE005555) orf, hypothetical protein [Escherichia coli O157:H7]	
SEQ ID n° 9104 PL-3075.1	Contig9 from 3714021	p	59%		SEQ ID n-2488
SEQ ID n° 9105 PL-3076.1	Contig9 from 3714095 to 3714625	p	66%		SEQ ID n-2489
SEQ ID n° 9106 PL-3238.1	Contig9 from 3714639 to 3715208	p	75%		SEQ ID n-2489

SEQ ID n° 9107	PL-3077.1	Contig9 from 3715221 to 3716039	p	71%	sp P15770 AROE_ECOLI_SHIKIMATE_5-DEHYDROGENASE pir S00252 shikimate 5-dehydrogenase (EC 1.1.1.25).- Escherichia coli emb CAA68700.1 (Y00710) shikimate dehydrogenase [Escherichia coli] gb AA58078.1 (U18997) shikimate dehydrogenase [Escherichia coli] gb AAC76306.1 (AE000406) dehydroshikimate reductase [Escherichia coli K12] sp P45795 YRDB_ECOLI_HYPOTHETICAL_10.0_KD PROTEIN_IN_RND-AROE_INTERGENIC_REGION (F85) pir C65120 hypothetical 10.0 kD protein in rnd aroe intergenic region - Escherichia coli (strain K-12) gb AA58077.1 (U18997) ORF_f85 [Escherichia coli] gb AAC76305.1 (AE000406) orf, hypothetical protein [Escherichia coli K12] #N/A SEQ ID n-2314
SEQ ID n° 9108	PL-4738.1	Contig9 from 3716036 to 3716299	p	55%	gb AAG58401.1 AE005555_1 (AE005555) putative transferase [Escherichia coli O157:H7] gb AAF33488.1 (AF233324) 83% identity with E. coli hypothetical protein (YIFA) (SP:P22788) and 95% identity with amino acids 1- 80 of E. coli possible regulatory protein (PSSR) (SP:P27826) [Salmonella typhimurium LT2] sp P27827 YIFE_ECOLI_PROTEIN_YIFE pir G65179 hypothetical 13.1 kD protein in pssr-ilvL intergenic region - Escherichia coli (strain K-12) gb AAC77485.1 (AE000453) orf, hypothetical protein [Escherichia coli K12] gb AAG58960.1 AE005608_1 (AE005608) orf, hypothetical protein [Escherichia coli O157:H7] pir S30663 hypothetical protein f516 - Escherichia coli gb AAA67569.1 (M87049) similar to Mg chelatase subunit of Rhodobacter capsulata [Escherichia coli] #N/A SEQ ID n-2434
SEQ ID n° 9109	PL-3239.1	Contig9 from 3716275 to 3716820	m	82%	
SEQ ID n° 9110	PL-3184.1	Contig9 from 3723408 to 3724244	m	73%	
SEQ ID n° 9111	PL-4762.1	Contig9 from 3724370 to 3724708	p	73%	
SEQ ID n° 9112	PL-3185.1	Contig9 from 3724755 to 3726278	m	77%	

SEQ ID n° 9113	PL-4763.1	Contig9 from 3727267 to 3727350	p	No Hits found	#N/A
SEQ ID n° 9114	PL-1954.2	Contig9 from 3727301 to 3728947	p	84%	gb AAG58963.1 AE005608_4 (AE005608) acetohydroxy acid synthase II [Escherichia coli O157:H7] SEQ ID n-1086
SEQ ID n° 9115	PL-4764.1	Contig9 from 3728944 to 3729201	p	68%	gb AAF33482.1 (AF233324) 93% identity with E. coli acetolactate synthase (ILVM) (SP:P13048) [Salmonella typhimurium LT2] pdb 1A3G A Chain A, Branched-Chain Amino Acid Aminotransferase From Escherichia Coli pdb 1A3G B Chain B, Branched-Chain Amino Acid Aminotransferase From Escherichia Coli pdb 1A3G C Chain C, Branched- Chain Amino Acid Aminotransferase From Escherichia Coli SEQ ID n-1087
SEQ ID n° 9116	PL-1955.1	Contig9 from 3729225 to 3730151	p	92%	sp P05791 ILVD_ECOLI DIHYDROXY-ACID DEHYDRATASE (DAD) pir DWECDI dihydroxy-acid dehydratase (EC 4.2.1.9) - Escherichia coli gb AAB59053.1 (M10313) dihydroxyacid dehydrase [Escherichia coli] emb CAA28576.1 (X04890) dihydroxy acid [Escherichia coli] prf 1312306A gene ilvGMEDA cluster [Escherichia coli] gb AAF33479.1 (AF233324) S. typhimurium threonine deaminase (ILVA) (SP:P20506); contains similarity to Pfam families PF00291 (Pyridoxal-phosphate dependent enzyme, score=467.9, E=8.4e-137, N=1) and PF00585 (C-terminal domain of Threonine dehydratase, score=329.2, E=> #N/A
SEQ ID n° 9117	PL-1956.1	Contig9 from 3730344 to 3732194	p	84%	
SEQ ID n° 9118	PL-1957.2	Contig9 from 3732199 to 3733599	p	89%	

SEQ ID n° 9119	PL-1958.1	Contig9 from 3733939 to 3735456	m	78%	sp P27304 EMRB_ECOLI_MULTIDRUG_RESISTANCE PROTEIN B pir [G65048 multidrug resistance protein B - Escherichia coli gb AAC75733.1 (AE000353) multidrug resistance; probably membrane translocase [Escherichia coli K12] dbj BAAL6548.1 (D90891) multidrug resistant protein emrB [Escherichia coli] dbj BAAL6553.1 (D90892) multidrug resistant protein emrB [Escherichia coli] pir [JCI344 multidrug resistant protein emrA - Escherichia coli gb AAA23724.1 (M86657) multidrug resistance; putative [Escherichia coli] SEQ ID n-1090
SEQ ID n° 9120	PL-1959.1	Contig9 from 3735464 to 3736636	m	72%	dbj BAB20935.2 (D85817) ORF [Staphylococcus aureus] SEQ ID n-1091
SEQ ID n° 9121	PL-1960.1	Contig9 from 3736959 to 3737702	m	57%	pir [A70613 hypothetical protein Rv0636 - Mycobacterium tuberculosis (strain H37RV) emb CAB07125.1 (Z92772) hypothetical protein Rv0636 [Mycobacterium tuberculosis] SEQ ID n-1093
SEQ ID n° 9122	PL-1961.1	Contig9 from 3737759 to 3738574	m	15%	pir [B70448 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Aquifex aeolicus gb AAC07574.1 (AE000752) 3-oxoacyl- [acyl-carrier-protein] synthase II [Aquifex aeolicus] SEQ ID n-1094
SEQ ID n° 9123	PL-1962.1	Contig9 from 3738571 to 3739836	m	55%	pir [B81052 acyl carrier protein NMB1696 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF42044.1 (AE002520) acyl carrier protein [Neisseria meningitidis MC58] SEQ ID n-1095
SEQ ID n° 9124	PL-4767.1	Contig9 from 3739992 to 3740228	m	46%	gb AAG01802.1 AF276772_1 (AF276772) cysteine desulfurase Nifs [Methanosarcina thermophila] #N/A
SEQ ID n° 9125	PL-1963.1	Contig9 from 3740261 to 3741451	m	54%	gb AAG20546.1 (AB005125) nitrogen fixation protein; NifU [Halobacterium sp. 1] SEQ ID n-1096
SEQ ID n° 9126	PL-4768.1	Contig9 from 3741448 to 3741804	m	49%	NRC- #N/A

SEQ ID n° 9127 PL-1964.1	Contig9 from 3741821 to 3742999	m	39%	pir S15161 long-chain-fatty-acid--luciferin- component ligase (EC 6.2.1.19) luxE - Photobacterium phosphoreum emb CAA39107.1 (X55459) fatty acyl-protein synthetase [Photobacterium phosphoreum] pir Z69725 potassium uptake trkA - Bacillus subtilis gb AAB80908.1 (U93876) hypothetical protein YrdP [Bacillus subtilis] emb CAB14605.1 (Z99117) alternate gene name: yrdP [Bacillus subtilis]	SEQ ID n-2097
SEQ ID n° 9128 PL-1965.1	Contig9 from 3743393 to 3744478	p	48%	sp Q51872 LUMQ_PHOLE PROBABLE TRANSCRIPTIONAL REGULATOR LUMQ pir JC4504 porin thermoregulatory protein EnvY homolog - Photobacterium leiognathi gb AAA87846.1 (U35231) lumQ gene product [Photobacterium leiognathi]	SEQ ID n-2098
SEQ ID n° 9129 PL-1966.1	Contig9 from 3744859 to 3745713	m	33%	gb AAG58968.1 AE005608_9 (AE005608) positive regulator for ilvC [Escherichia coli O157:H7]	SEQ ID n-2099
SEQ ID n° 9130 PL-1967.1	Contig9 from 3746294 to 3747175	m	77%	gb AAG58969.1 AE005609_1 (AE005609) ketol-acid reductoisomerase [Escherichia coli O157:H7]	SEQ ID n-2100
SEQ ID n° 9131 PL-1968.1	Contig9 from 3747365 to 3748843	p	90%	gb AAG58972.1 AE005609_4 (AE005609) rep helicase, a single-stranded DNA dependent ATPase [Escherichia coli O157:H7]	SEQ ID n-2101
SEQ ID n° 9132 PL-1969.1	Contig9 from 3749053 to 3751080	p	88%	gb AAG58973.1 AE005609_5 (AE005609) guanosine pentaphosphatase; exopolyposphatase [Escherichia coli O157:H7]	SEQ ID n-2102
SEQ ID n° 9133 PL-1970.1	Contig9 from 3751131 to 3752633	m	80%	sp P24229 RHLEB_ECOLI PUTATIVE ATP-DEPENDENT RNA HELICASE RHLEB pir G65181 rhleB protein - Escherichia coli (strain K-12) gb AAC76785.1 (AE000454) putative ATP-dependent RNA helicase [Escherichia coli K12]	SEQ ID n-2104
SEQ ID n° 9134 PL-1971.1	Contig9 from 3752639 to 3753925	m	88%		SEQ ID n-2105

SEQ ID n° 9135 PL-4771.1	Contig9 from 3754044 to 3754370	p 88%	gb AAAG67270.1 (U16857) Derived from E. coli thioredoxin gene; normal translation termination codon following nucleotide 3050 has been removed [Cloning vector PTRXFUS] sp P03002 RHO_ECOLI TRANSCRIPTION TERMINATION FACTOR RHO p1r TWEER transcription termination factor rho - Escherichia coli gb AA24532.1 (J01673) transcription termination factor [Escherichia coli] gb AAA67583.1 (M87049) transcription termination factor rho [Escherichia coli] gb AAC76788.1 (AE000454) transcription termination factor Rho; polarity suppressor [Escherichia coli K12] gb AGS8979.1 AE005610_3 (AE005610) UDP- GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase; synthesis of enterobacterial common antigen (ECA) [Escherichia coli O157:H7] sp P25905 WZZE_ECOLI LIPOPOLYSACCHARIDE BIOSYNTHESIS PROTEIN WZZE p1r D65182 hypothetical 39.5K protein (rfe 5' region) - Escherichia coli gb AAC76790.1 (AE000454) putative transport protein [Escherichia coli K12] gb AGS8980.1 AE005610_4 (AE005610) putative transport protein [Escherichia coli O157:H7] gb AGS8981.1 AE005610_5 (AE005610) UDP-N-acetyl glucosamine -2-epimerase; synthesis of enterobacterial common antigen (ECA) [Escherichia coli O157:H7] p1r B49350 hypothetical protein 379 (nfrC 3' region) - Escherichia coli gb AGS8982.1 AE005610_6 (AE005610) UDP-N-acetyl- D-mannosaminuronic acid dehydrogenase; synthesis of enterobacterial common antigen (ECA) [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9136 PL-1972.1	Contig9 from 3754847 to 3756106	p 98%		SEQ ID n-21106
SEQ ID n° 9137 PL-1973.1	Contig9 from 3756527 to 3757612	p 83%		SEQ ID n-21107
SEQ ID n° 9138 PL-1974.1	Contig9 from 3757642 to 3758697	p 72%		
SEQ ID n° 9139 PL-1975.1	Contig9 from 3758794 to 3759945	p 85%		SEQ ID n-21108
SEQ ID n° 9140 PL-1976.1	Contig9 from 3759950 to 3761227	p 86%		SEQ ID n-21109
				SEQ ID n-21110

SEQ ID n° 9141	PL-1977.1	Contig9 from 3761224 to 3762294	p 85%	sp P27830 RFFG_ECOLI DTDP-GLUCOSE 4,6- DEHYDRATASE pir G65182 dtdpglucose 4,6- dehydratase (EC 4.2.1.46) - Escherichia coli (strain K-12) pdb IBXK B Chain B, Dtdp-Glucose 4,6-Dehydratase From E. Coli pdb IBXK A Chain A, Dtdp-Glucose 4,6-Dehydratase From E. Coli gb AAC76793.1 (AE000455) dtdp-glucose 4,6- dehydratase [Escherichia coli K12]	SEQ ID n-2111
SEQ ID n° 9142	PL-1978.1	Contig9 from 3762316 to 3763197	p 88%	sp P27831 RFFH_ECOLI GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (DTDP-GLUCOSE SYNTHASE) (DTDP-GLUCOSE PYROPHOSPHORYLASE) pir H65182 glucose-1-phosphate thymidyltransferase (EC 2.7.7.24) - Escherichia coli gb AAC76794.1 (AE000455) glucose-1-phosphate thymidyltransferase [Escherichia coli K12]	SEQ ID n-2112
SEQ ID n° 9143	PL-1979.1	Contig9 from 3763304 to 3763894	p 48%	pir S30684 hypothetical protein o181 - Escherichia coli	SEQ ID n-2113
SEQ ID n° 9144	PL-1980.1	Contig9 from 3763896 to 3765026	p 80%	gb AAF33462.1 (AF2333324) 92% identity with E. coli lipopolysaccharide biosynthesis protein (WECE) (SP:P27833); contains similarity to Pfam family PF01041 (DegT/DnrJ/EryC1/Strs family), score=295.0, E=9.2e-85, N=1 [Salmonella typhimurium LT2]	SEQ ID n-2115
SEQ ID n° 9145	PL-1981.1	Contig9 from 3765028 to 3766278	p 84%	gb AAF33461.1 (AF2333324) 89% identity with E. coli lipopolysaccharide biosynthesis protein (WZXE) (SP:P2783) [Salmonella typhimurium LT2]	SEQ ID n-2116
SEQ ID n° 9146	PL-1982.1	Contig9 from 3766275 to 3767360	p 75%	sp P56258 YIFM_ECOLI HYPOTHETICAL 40.6 KDA PROTEIN IN WZXE-WECF INTERGENIC REGION	SEQ ID n-2117

Contig9 from SEQ ID n° 9147 PL-1983.1	3767357 to 3768736	p	82%	gb AAG58989.1 AE005610_13 (AE005610) TDP- Fuc4NAC:lipidII transferase; synthesis of enterobacterial common antigen (ECA) [Escherichia coli O157:H7] sp P37457 WECG_SALTY PROBABLE UDP-N-ACETYL-D- MANNOSAMINURONIC ACID TRANSFERASE (UDP-MANNACA TRANSFERASE) pir S27727 hypothetical protein - Salmonella typhimurium gb AAA92025.1 (M95047) rffm gene product [Salmonella typhimurium] gb AAF33458.1 (AF233324) S. typhimurium putative UDP-N-acetyl- D-mannosamine transferase (WECG) (SP: P37457) [Salmonella typhimurium LT2] SEQ ID n-3119
Contig9 from SEQ ID n° 9148 PL-1984.1	3768727 to 3769464	p	83%	sp P37456 YIFK_SALTY PROBABLE TRANSPORT PROTEIN YIFK pir S27728 probable transport protein - Salmonella typhimurium gb AAA92026.1 (M95047) transport protein [Salmonella typhimurium] SEQ ID n-3120
Contig9 from SEQ ID n° 9149 PL-1985.1	3769708 to 3771099	p	81%	gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae] pir S75993 hypothetical protein - Synecocystis sp. (strain PCC 6803) dbj BAAL0840.1 (D64006) hypothetical protein [Synecocystis sp.] sp P09128 HEMY_ECOLI HEMY PROTEIN pir S01694 hemY protein - Escherichia coli emb CAA31135.1 (X12614) ORF Y (AA 1 - 398) [Escherichia coli] gb AAA67598.1 (M87049) hemY [Escherichia coli] gb AAC76805.1 (AE000456) a late step of protoheme IX synthesis [Escherichia coli] K12] gb AAG58994.1 AE005611_4 (AE005611) a late step of protoheme IX synthesis [Escherichia coli] O157:H7 SEQ ID n-3122
Contig9 from SEQ ID n° 9150 PL-4776.1	3771506 to 3771607	m	No Hits found	#N/A
Contig9 from SEQ ID n° 9151 PL-1986.1	3772820 to 3774436	p	29%	SEQ ID n-3121
Contig9 from SEQ ID n° 9152 PL-4778.1	3774504 to 3774677	p	50%	#N/A
Contig9 from SEQ ID n° 9153 PL-1987.1	3774743 to 3775981	m	78%	

SEQ ID n° 9154	PL-1988.1	Contig9 from 3775985 to 3777109	m	76%	gb AAG58995.1 AE005611_5 (AE005611) uroporphyrinogen III methylase [Escherichia coli O157:H7]	SEQ ID n-1123
SEQ ID n° 9155	PL-1989.1	Contig9 from 3777130 to 3777870	m	66%	gb AAG58996.1 AE005611_6 (AE005611) uroporphyrinogen III synthase [Escherichia coli O157:H7]	SEQ ID n-1124
SEQ ID n° 9156	PL-1990.1	Contig9 from 3777867 to 3778808	m	86%	sp Q59684 HEM3_PROMI PORPHOBILINOGEN DEAMINASE (PSG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) gb AAC44329.1 (U22969) porphobilinogen deaminase [Proteus mirabilis]	SEQ ID n-1126
SEQ ID n° 9157	PL-1991.1	Contig9 from 3779407 to 3781977	p	85%	sp Q59685 CYAA_PROMI ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) gb AAC44330.1 (U22969) adenylate cyclase [Proteus mirabilis]	SEQ ID n-1127
SEQ ID n° 9158	PL-4779.1	Contig9 from 3782006 to 3782326	m	81%	sp P40128 CYAY_ERWCH CYAY PROTEIN pir [S23700 cyay protein - Erwinia chrysanthemi emb CAA44892.1 (X63207) cyay [Erwinia chrysanthemi]	#N/A
SEQ ID n° 9159	PL-4780.1	Contig9 from 3782405 to 3782590	p	47%	sp P39166 YIFL_ECOLI HYPOTHETICAL 7.2 KD PROTEIN IN CYAY-DAPF INTERGENIC REGION gb AAG59001.1 AE005612_4 (AE005612) Z5325 gene product [Escherichia coli O157:H7] pir [S01913] diaminopimelate epimerase (EC 5.1.1.7) - Escherichia coli (strain K-12) gb AAC76812.1 (AE000457) diaminopimelate epimerase [Escherichia coli K12] gb AAG59002.1 AE005612_5 (AE005612) diaminopimelate epimerase [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9160	PL-1992.1	Contig9 from 3782639 to 3783463	p	86%	gb AAF33444.1 (AF233324) 86% identity with E. coli hypothetical protein (YIGA) (SP:P233305) [Salmonella typhimurium LT2] gb AAC46276.1 (AF028736) site specific recombinase [Serratia marcescens]	SEQ ID n-1128
SEQ ID n° 9161	PL-1993.1	Contig9 from 3783496 to 3784200	p	69%		SEQ ID n-1129
SEQ ID n° 9162	PL-1994.1	Contig9 from 3784197 to 3785108	p	83%		SEQ ID n-1130

SEQ ID n° 9163 PL-1995.1	Contig9 from 3785108 to 3785824	p	68%	gb AAC46277.1 (AF028736) No definition line found [Serratia marcescens]	SEQ ID n-2131
SEQ ID n° 9164 PL-1996.1	Contig9 from 3785891 to 3788053	p	91%	gb AAF33441.1 (AF233324) 98% identity with E. coli DNA helicase (UVRD) (SP:P03018); contains similarity to Pfam family PF00580 (UVRD/REP helicase), score=812.9, E=1.2e-240, N=1 [Salmonella typhimurium LT2] sp P31138 COR_A_SALTY_MAGNESIUM AND COBALT TRANSPORT PROTEIN CORA pir A47157 magnesium transport protein CorA - Salmonella typhimurium gb AA02966.1 (L11043) Mg2+ transport protein [Salmonella typhimurium] gb AAF33440.1 (AF233324) S. typhimurium magnesium transport protein (CORA) (SP:P31138) [Salmonella typhimurium LT2]	SEQ ID n-2132
SEQ ID n° 9165 PL-1997.1	Contig9 from 3788149 to 3789099	p	92%		
SEQ ID n° 9166 PL-4782.1	Contig9 from 3789665 to 3789814	m	No Hits found		SEQ ID n-2133
SEQ ID n° 9167 PL-4783.1	Contig9 from 3789865 to 3790245	m	No Hits found		#N/A
SEQ ID n° 9168 PL-1998.1	Contig9 from 3790253 to 3791143	m	78%	gb AAF33437.1 (AF233324) 90% identity with E. coli rad gene product (RAD) (SP:P27844); contains similarity to Pfam family PF00892 (Integral membrane protein), score=17.4, E=0.05, N=1 [Salmonella typhimurium LT2]	SEQ ID n-2134
SEQ ID n° 9169 PL-3241.1	Contig9 from 3791255 to 3791725	m	79%	sp P27845 YIGI_ECOLI_HYPOTHETICAL 17.1 KD PROTEIN IN RAD-PLDA INTERGENIC REGION	SEQ ID n-2493
SEQ ID n° 9170 PL-1999.1	Contig9 from 3792021 to 3794438	m	51%	pir T44595 alcaligin synthesis protein alcc [validated] - Bordetella bronchiseptica gb AAB40620.1 (U61153) Alcc [Bordetella bronchiseptica]	SEQ ID n-2135

SEQ ID n° 9171	PL-2000.1	Contig9 from 3794438 to 3795739	m	68%	emb CAB87220.1 (AL163641) putative monooxygenase [Streptomyces coelicolor A3(2)]	SEQ ID n-2139
SEQ ID n° 9172	PL-2001.1	Contig9 from 3795770 to 3797314	m	63%	emb CAB87219.1 (AL163641) putative pyridoxal- dependent decarboxylase [Streptomyces coelicolor A3(2)]	SEQ ID n-2140
SEQ ID n° 9173	PL-2002.1	Contig9 from 3797673 to 3798452	m	46%	SP P39405 FHUF_ECOLI FERRIC IRON REDUCTASE PROTEIN FHUF_pir S56594 ferrichrome-iron reductase (EC 1.6.99.-) fhuf [validated] - Escherichia coli gb AAA97266.1 (U14003) ORF_f262b [Escherichia coli] gb AAC77323.1 (AE000507) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-2141
SEQ ID n° 9174	PL-2003.1	Contig9 from 3798627 to 3799439	m	68%	pir T36888 probable iron-siderophore uptake system ATP-binding component - Streptomyces coelicolor emb CAB52849.1 (AL109848) putative iron-siderophore uptake system ATP-binding component [Streptomyces coelicolor A3(2)]	SEQ ID n-2142
SEQ ID n° 9175	PL-2004.1	Contig9 from 3799424 to 3800530	m	50%	pir C82281 ferric vibriobactin ABC transporter, permease protein VC0778 [imported] - Vibrio cholerae (group O1 strain N16961.) gb AAD4882.1 (U52150) cytoplasmic membrane permease [Vibrio cholerae] gb AAF93943.1 (AE004163) ferric vibriobactin ABC transporter, permease protein [Vibrio cholerae]	SEQ ID n-2143
SEQ ID n° 9176	PL-2005.1	Contig9 from 3800469 to 3801482	m	62%	pir T36890 probable iron-siderophore uptake system transmembrane component - Streptomyces coelicolor emb CAB52851.1 (AL109848) putative iron-siderophore uptake system transmembrane component [Streptomyces coelicolor A3(2)]	SEQ ID n-2144
SEQ ID n° 9177	PL-2006.1	Contig9 from 3801479 to 3802495	m	46%	gb AAB97475.1 (U02617) DtxR/iron regulated lipoprotein precursor [Corynebacterium diphtheriae]	SEQ ID n-2145

SEQ ID n° 9178	PL-2007.1	Contig9 from 3802564 to 3804807	m	55%	gb AAD26430.1 AF135154_1 (AF135154) ferric alcaligin siderophore receptor [Bordetella pertussis]	SEQ ID n-2146
SEQ ID n° 9179	PL-2008.1	Contig9 from 3804858 to 3806681	m	64%	pir T44595 alcaligin synthesis protein alcC [validated] - Bordetella bronchiseptica gb AAB40620.1 (U61153) AlCc [Bordetella bronchiseptica]	SEQ ID n-2147
SEQ ID n° 9180	PL-2009.1	Contig9 from 3807130 to 3808956	p	84%	gb AAG59018.1 AE005613_11 (AE005613) ATP- dependent DNA helicase [Escherichia coli O157:H7]	SEQ ID n-2148
SEQ ID n° 9181	PL-2010.1	Contig9 from 3808971 to 3809969	p	66%	emb CAA26932.1 (X03155) lysophospholipase L2 (aa 1-340) [Escherichia coli] prf 1111247A lysophospholipase L2 [Escherichia coli]	SEQ ID n-2150
SEQ ID n° 9182	PL-2011.1	Contig9 from 3809992 to 3810792	p	71%	gb AAG59022.1 AE005614_2 (AE005614) Z5347 gene product [Escherichia coli O157:H7]	SEQ ID n-2151
SEQ ID n° 9183	PL-3242.1	Contig9 from 3810993 to 3811448	p	74%	dbj BAB03895.1 (AP001507) transposase (09) [Bacillus halodurans] dbj BAB03988.1 (AP001507) transposase (09) [Bacillus halodurans] dbj BAB05361.1 (AP001512) transposase (09) [Bacillus halodurans] dbj BAB05614.1 (AP001513) transposase (09) [Bacillus halodurans] dbj BAB06561.1 (AP001516) transposase (09) [Bacillus halodurans] dbj BAB06952.1 (AP001518) transposase (09) [Bacillus halodurans] dbj BAB07185.1 (AP001518) transposase (09) [Bacillus halodurans] dbj BAB07197.1 (AP001518) transposase (09) [Bacillus halodurans]	SEQ ID n-2494

```

sp|P03829|ISA2_SHIDY_INSERTION_ELEMENT_ISO-1SL1
PROTEIN INSA pir||IEBB9 insa protein -
Shigella dysenteriae insertion_sequence IS1-N
gb|AA25031.1|J01737) insa (putative);
putative [unidentified insertion
sequence] gb|AAF28118.1|AF153317_14 (AF153317)
Insa [Shigella dysenteriae]
gb|AAF28138.1|AF153317_35 (AF153317) Insa
[Shigella dysenteriae]

```

#N/A

SEQ ID n~8152

SEQ ID n~2495

#N/A

```

ref|NP_046004.1| ORF H0646 [Halobacterium sp.
NRC-1] ref|NP_046095.1| ORF H1709
[Halobacterium sp. NRC-1] pir||T08276 probable
transposase H0646 - Halobacterium sp. (strain
NRC-1) insertion sequence ISH8
plasmid pNRC100 gb|AAC82843.1| (AF016485) ORF
H0646 [Halobacterium sp. NRC-1] gb|AAC82934.1|
(AF016485) ORF H1709 [Halobacterium sp. NRC-1]
gb|AAG18697.1| (AE004975) Vng0059h
[Halobacterium sp. NRC-1] gb|AAG18910.1|
(AE004993) Vng0337h [Halobacterium sp. NRC-1]
gb|AAG20310.1| (AE005105) Vng2175h
[Halobacterium sp. NRC-1] gb|AAG20766.1|
(AE005145) Vng6079h [Halobacterium sp. NRC-1]
gb|AAG20820.1| (AE005150) Vng6147h
[Halobacterium sp. NRC-1] gb|AAG21042.1|
(AE005169) Vng6447h [Halobacterium sp. NRC-1]

```

SEQ ID n~2153

Contig9 from
SEQ ID n° 9184 PL-4788.1 3811641 to m 68%
3811943

Contig9 from	SEQ ID n°	3812121 to	3813614	No Hits found
Contig9 from	9185 PL-2012.1	3812121 to	3813614	No Hits found

SEQ ID n°	Contig9 from	m	No Hits found
9186 PL-3243.1	3813657 to		
	3814106		

SEQ ID n°	Contig9 from	m	No Hits found
9187 PL-4790.1	3814239 to		
	3814313		

SEQ ID n°	Contig9 from	p
9188 PL-2013.1	3814494 to	318
	3815435	

SEQ ID n° 9189 PL-3244.1	Contig9 from 3815507 to 3815761	p 35%	gb AAG19907.1 (AE005074) Vng1653h [Halobacterium sp. NRC-1] gb AAG20788.1 (AE005147) Vng6106h [Halobacterium sp. NRC-1] gb AAG20832.1 (AE005152) Vng6161h [Halobacterium sp. NRC-1] gb AAG20970.1 (AE005164) Vng6345h [Halobacterium sp. NRC-1]	SEQ ID n-2496
SEQ ID n° 9190 PL-2014.1	Contig9 from 3815813 to 3816547	m No Hits found		SEQ ID n-2154
SEQ ID n° 9191 PL-4794.1	Contig9 from 3817364 to 3817627	m 43%	pir H83457 hypothetical protein PA1508 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04897.1 AE004579_9 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 9192 PL-2016.1	Contig9 from 3817630 to 3818364	m No Hits found		SEQ ID n-2155
SEQ ID n° 9193 PL-2017.1	Contig9 from 3818413 to 3819045	m 33%	pir C83157 hypothetical protein PA3907 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07294.1 AE004808_4 (AE004808) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2156
SEQ ID n° 9194 PL-4795.1	Contig9 from 3819209 to 3819472	m 44%	pir H83457 hypothetical protein PA1508 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04897.1 AE004579_9 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 9195 PL-2018.1	Contig9 from 3819475 to 3820197	m 36%	pir D83157 hypothetical protein PA3908 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07295.1 AE004808_5 (AE004808) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2157

SEQ ID n° 9196	PL-2019.1	Contig9 from 3820221 to 3820829	m	36%	pir C83157 hypothetical protein PA3907 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07294.1 AE004808_4 (AE004808) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-1158
SEQ ID n° 9197	PL-4796.1	Contig9 from 3820831 to 3821175	m	No Hits found	#N/A	
SEQ ID n° 9198	PL-3245.1	Contig9 from 3821178 to 3821669	m	21%	pir A83157 hypothetical protein PA3905 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07292.1 AE004808_2 (AE004808) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2497
SEQ ID n° 9199	PL-2020.1	Contig9 from 3821666 to 3823642	m	53%	pir P82511 vgrG protein VCA0018 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95932.1 (AE004345) vgrG protein [Vibrio cholerae]	SEQ ID n-1160
SEQ ID n° 9200	PL-2021.1	Contig9 from 3823657 to 3825417	m	43%	pir A82499 hypothetical protein VCA0110 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96024.1 (AE004353) hypothetical protein [Vibrio cholerae]	SEQ ID n-1161
SEQ ID n° 9201	PL-4798.1	Contig9 from 3825659 to 3825931	p	34%	pir H83457 hypothetical protein PA1508 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04897.1 AE004579_9 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 9202	PL-2022.1	Contig9 from 3825999 to 3829334	m	79%	emb CAC18672.1 (AJ251781) Bspa protein [Pectobacterium chrysanthemi]	SEQ ID n-1162

[illegible]

SEQ ID n° 9209	PL-4803.1	Contig9 from 3833447 to 3833803	p	65%	sp P42594 YGM_ECOLI HYPOTHETICAL 15.0 KD PROTEIN IN EBGC-UXAA INTERGENIC REGION pir G65096 hypothetical protein YGJM - Escherichia coli (strain K-12) gb AA57883.1 (U18997) ORF_F138 [Escherichia coli] gb AAC76117.1 (AE000390) orf, hypothetical protein [Escherichia coli K12]	#N/A
SEQ ID n° 9210	PL-2025.1	Contig9 from 3834067 to 3835062	m	47%	dbj BAB04109.1 (AP001508) BH0390-unknown conserved protein [Bacillus halodurans]	SEQ ID n-1165
SEQ ID n° 9211	PL-2026.1	Contig9 from 3835081 to 3836271	m	31%	pir T27169 hypothetical protein Y54G11A.4 - Caenorhabditis elegans emb CAA22449.1 (AL034488) predicted using GeneFinder [Caenorhabditis elegans]	SEQ ID n-1166
SEQ ID n° 9212	PL-2027.1	Contig9 from 3836420 to 3837337	p	46%	sp O32255 YVBU_BACSU HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YVBU pir E70030 transcription regulator lysr family homolog yvbu - Bacillus subtilis emb CAB15404.1 (Z99121) similar to transcriptional regulator (Lysr family) [Bacillus subtilis]	SEQ ID n-1167
SEQ ID n° 9213	PL-4806.1	Contig9 from 3837467 to 3837898	m	No Hits found		#N/A
SEQ ID n° 9214	PL-4807.1	Contig9 from 3838086 to 3838280	p	No Hits found		#N/A
SEQ ID n° 9215	PL-2374.2	Contig9 from 3838767 to 3839948	m	81%	gb AAG59362.1 AE005650_1 (AE005650) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-1547

SEQ ID n° 9216	PL-3248.2	Contig9 from 3840096 to 3840560	p 75%	sp P31805 YJEE_ECOLI_HYPOTHETICAL_16.9_KDA PROTEIN IN PSD-AMIB INTERGENIC REGION (URF2) pir S56393 hypothetical 16.9K protein (psd-amib intergenic region) - Escherichia coli gb AA20096.1 (L19346) urf2 [Escherichia coli] gb AAA97064.1 (U14003) urf2 of GenBank Accession Number L19346 [Escherichia coli] gb AAC77125.1 (AE000489) orf, hypothetical protein [Escherichia coli K12] gb AAG59364.1 AE005650_3 (AE005650) orf, hypothetical protein [Escherichia coli O157:H7 EDL933] dbj BAB38567.1 (AP002568) hypothetical protein [Escherichia coli O157:H7] gb AAG59365.1 AE005650_4 (AE005650) N- acetylmuramoyl-1-alanine amidase II; a murein hydrolase [Escherichia coli O157:H7 EDL933] dbj BAB38568.1 (AP002568) N-acetylmuramoyl-1- alanine amidase II [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9217	PL-2373.3	Contig9 from 3840599 to 3841858	p 68%	sp P14161 MUTL_SALTY_DNA_MISMATCH_REPAIR_PROTEIN MUTL_pir A33588 mismatch repair protein mutL - Salmonella typhimurium gb AAA27166.1 (M29687) mismatch repair protein [Salmonella typhimurium] SEQ ID n-1545 gb AAG59367.1 AE005650_6 (AE005650) delta(2)- isopentenylpyrophosphate tRNA-adenosine transferase [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9218	PL-2372.1	Contig9 from 3841868 to 3843763	p 75%		
SEQ ID n° 9219	PL-2371.1	Contig9 from 3843756 to 3844697	p 84%		

sp|P25521|HFQ_ECOLI HOST FACTOR-I PROTEIN (HF-I)
 pir||S56397 host factor I - Escherichia coli
 dbj|BAA00644.1| (D00743) host factor-I protein
 [Escherichia coli] gb|AAC43397.1| (U00005) Host
 Factor-I (HF-I) [Escherichia coli]
 gb|AA097068.1| (U14003) Host Factor-I (HF-I)
 [Escherichia coli] gb|AAC77129.1| (AE000489)
 host factor I for bacteriophage Q beta
 replication, a growth-related protein
 [Escherichia coli K12] gb|AGS59368.1|AE005650_7
 (AE005650) host factor I for bacteriophage Q
 beta replication, a growth-related
 protein [Escherichia coli O157:H7] #N/A
 gb|AAG59369.1|AE005650_8 (AE005650) GTP -
 binding subunit of protease specific for phage
 lambda cII repressor [Escherichia coli O157:H7] SEQ ID n-1543
 sp|P25662|HFLK_ECOLI HFLK PROTEIN pir||B43653
 probable integral membrane proteinase (EC 3.4.-.-
) hflK - Escherichia coli
 gb|AAC43399.1| (U00005) putative integral
 membrane protein required for high
 frequency lysogenization by bacteriophage lambda
 [Escherichia coli] gb|AAA97070.1| (U14003) CG
 Site No. 639; alternate gene name hflA; putative
 integral membrane protease required for high
 frequency lysogenization by
 bacteriophage lambda [Escherichia
 coli] gb|AAC77131.1| (AE000489) protease
 specific for phage lambda cII repressor
 [Escherichia coli K12] gb|AAG59370.1|AE005650_9
 (AE005650) protease specific for phage lambda
 cII repressor [Escherichia coli
 O157:H7]

Contig9 from
 SEQ ID n° 9220 PL-4810.1 3844808 to 81%
 3845116

Contig9 from
 SEQ ID n° 9221 PL-2370.1 3845213 to 90%
 3846493

Contig9 from
 SEQ ID n° 9222 PL-2369.1 3846599 to 81%
 3847819

SEQ ID n-1541

SEQ ID n° 9223	PL-2366.1	Contig9-from 3848983 to 3850281	p	90%	sp P12283 PURA_ECOLI ADENYLOSUCCINATE SYNTHETASE (IMP--ASPARTATE LIGASE) (ADSS) (AMPSASE) pir AJECDS adenylosuccinate synthase (EC 6.3.4.4) purA [validated] - Escherichia coli gb AA97073.1 (U14003) adenylosuccinate synthetase [Escherichia coli] gb AAC77134.1 (AE000490) adenylosuccinate synthetase [Escherichia coli K12] SEQ ID n-2539
SEQ ID n° 9224	PL-4814.1	Contig9 from 3850472 to 3850897	p	81%	pir B31965 hypothetical 16K protein (pura 3' ... region) - Escherichia coli #N/A
SEQ ID n° 9225	PL-2365.1	Contig9 from 3850942 to 3853383	p	82%	pir S56404 virulence-associated protein vacB homolog - Escherichia coli gb AA97075.1 (U14003) vacB [Escherichia coli] gb AAC77136.1 (AE000490) putative enzyme [Escherichia coli K12] SEQ ID n-2538
SEQ ID n° 9226	PL-2364.1	Contig9 from 3853511 to 3854245	p	85%	sp P39290 YJFH_ECOLI HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE YJFH pir S56405 hypothetical 26.6K protein (vacB-aidB intergenic region) - Escherichia coli gb AA97076.1 (U14003) ORF_0243 [Escherichia coli] gb AAC77137.1 (AE000490) orf, hypothetical protein [Escherichia coli K12] gb AGS59376.1 AE005651_5 (AE005651) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2537
SEQ ID n° 9227	PL-4815.1	Contig9 from 3854549 to 3854944	p	86%	sp P02358 RS6_ECOLI 30S RIBOSOMAL PROTEIN S6 #N/A
SEQ ID n° 9228	PL-4817.1	Contig9 from 3854950 to 3855267	p	83%	gb AAG59397.1 AE005652_14 (AE005652) primosomal replication protein N [Escherichia coli O157:H7] #N/A

SEQ ID n° 9229	PL-4818.1	Contig9 from 3855272 to 3855499	p 91%	sp P02374 RS18_ECOLI 30S RIBOSOMAL PROTEIN S18 pir R3EC18 ribosomal protein s18 [validated] - Escherichia coli emb CAA27654.1 (X04022) ribosomal protein s18 (aa 1-75) [Escherichia coli] gb AAA97098.1 (U14003) 30S ribosomal subunit protein S18 [Escherichia coli] gb AAC77159.1 (AE000491) 30S ribosomal subunit protein s18 [Escherichia coli K12] sp P02418 RL9_ECOLI 50S RIBOSOMAL PROTEIN L9 pir S56428 50S ribosomal chain protein L9 - Escherichia coli pir R5EC9 ribosomal protein L9 [validated] - Escherichia coli (strain K-12) emb CAA27655.1 (X04022) ribosome protein L9 (aa 1-149) [Escherichia coli] gb AAA97099.1 (U14003) 50S ribosomal subunit protein L9 [Escherichia coli] gb AAC77160.1 (AE000491) 50S ribosomal subunit protein L9 [Escherichia coli K12] gb AAG59399.1 AE005652_16 (AE005652) 50S ribosomal subunit protein L9 [Escherichia coli O157:H7] SEQ ID n-2501	#N/A
SEQ ID n° 9231	PL-2363.1	Contig9 from 3856282 to 3857166	p 59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] gb AAG28533.1 AF198621_4 (AF198621) cysteine synthase [Bacillus stearothermophilus] dbj BAB06906.1 (AP001518) argininosuccinate synthase (citrulline-aspartate ligase) [Bacillus halodurans] pir S76729 hypothetical protein - Synecocystis sp. (strain PCC 6803) dbj BAA18641.1 (D90916) hypothetical protein [Synecocystis sp.] SEQ ID n-2536	SEQ ID n-2536
SEQ ID n° 9232	PL-2362.1	Contig9 from 3857953 to 3858981	p 50%		SEQ ID n-2535
SEQ ID n° 9233	PL-2361.1	Contig9 from 3858971 to 3860161	p 57%		SEQ ID n-2534
SEQ ID n° 9234	PL-2360.1	Contig9 from 3860158 to 3860961	p 56%		SEQ ID n-2533

Contig9 from SEQ ID n° 9235 PL-2359.1	3860985 to 3862682	p	58%	sp P74178 YB78_SYN33_HYPOTHETICAL_69.1 RD PROTEIN SL11178 pir S75808 modulation protein Synecocystis sp. (strain PCC 6803) dbj BA18267.1 (D90913) modulation protein [Synecocystis sp.] emb CAB92558.1 (AL356812) putative integral membrane protein. [Streptomyces coelicolor A3(2)]	SEQ ID n-1531 SEQ ID n-1530
Contig9 from SEQ ID n° 9236 PL-2358.1	3862895 to 3864121	p	37%		
Contig9 from SEQ ID n° 9237 PL-2357.1	3864132 to 3865442	p	No Hits found	pir D83407 probable transcription regulator PAL898 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAF01471.1 AF190630_1 (AF190630) PhzR [Pseudomonas aeruginosa] gb AAG05287.1 AB004616_1 (AB004616) probable transcriptional regulator [Pseudomonas aeruginosa] pir S56432 peptidylprolyl isomerase (EC 5.2.1.8) - Escherichia coli gb AA97103.1 (U14003) ORF_0259a [Escherichia coli] gb AAC77164.1 (AB000492) FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli K12]	SEQ ID n-1529 SEQ ID n-1528
Contig9 from SEQ ID n° 9238 PL-2356.1	3865479 to 3866195	m	42%		
Contig9 from SEQ ID n° 9239 PL-2355.1	3866448 to 3867086	p	85%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] gb AAG59412.1 AE005654_1 (AE005654) affects pool of 3'-phosphoadenosine-5'-phosphosulfate in pathway of sulfite synthesis [Escherichia coli O157:H7]	SEQ ID n-1527 SEQ ID n-1526
Contig9 from SEQ ID n° 9240 PL-2354.1	3867529 to 3868554	m	21%		
Contig9 from SEQ ID n° 9241 PL-2353.1	3869408 to 3870151	p	79%		

SEQ ID n° 9242 PL-2352.1	Contig9 from 3870232 to m 63% 3870786	pir F82061 conserved hypothetical protein VC2550 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95691.1 (AE004324) conserved hypothetical protein [Vibrio cholerae] SEQ ID n-1524
SEQ ID n° 9243 PL-4823.1	Contig9 from 3871077 to p 79% 3871283	pir S56442 hypothetical protein o81 Escherichia coli #N/A
SEQ ID n° 9244 PL-2351.1	Contig9 from 3871395 to m 84% 3872726	sp P39319 YFEL_ECOLI HYPOTHETICAL 49.8 KD PROTEIN IN CYSQ-MSRA INTERGENIC REGION pir S56443 hypothetical 49.8K protein (cysq- msra intergenic region) - Escherichia coli gb AA97114.1 (U14003) ORF f447 [Escherichia coli] gb AAC77175.1 (AE000493) putative transport protein [Escherichia coli K12] gb AAG59416.1 AE005654_5 (AE005654) putative transport protein [Escherichia coli O157:H7] SEQ ID n-1523
SEQ ID n° 9245 PL-2350.1	Contig9 from 3872881 to m 71% 3873528	sp P27110 MSRA_ECOLI PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PROTEIN-METHIONINE-S-OXIDE REDUCTASE) (PEPTIDE MET(O) REDUCTASE) pir S56444 protein-methionine-S-oxide reductase (EC 1.8.4.6) - Escherichia coli gb AA24399.1 (M89992) peptide methionine sulfoxide reductase [Escherichia coli] gb AA97115.1 (U14003) peptide methionine sulfoxide reductase [Escherichia coli] gb AAC77176.1 (AE000493) peptide methionine sulfoxide reductase [Escherichia coli K12] SEQ ID n-1522

Contig9 from SEQ ID n° 9246 PL-2349.1 3873643 to 3875385	P 74%	<p>sp P39320 YTFM_ECOLI HYPOTHETICAL 64.8 KD PROTEIN IN MSRA-CHPBI INTERGENIC REGION</p> <p>PRECUSOR (O577) pir [S56445 hypothetical 64.8K protein (msra-chpbi intergenic region)] - Escherichia coli gb AAA97116.1 (U14003) ORF_0577 [Escherichia coli] gb AAC77177.1 (AE000493) orf, hypothetical protein [Escherichia coli K12]</p> <p>sp P39321 YTFN_ECOLI HYPOTHETICAL 136.8 KD PROTEIN IN MSRA-CHPB INTERGENIC REGION</p> <p>pir [H65233 ytfn protein - Escherichia coli (strain K-12)] gb AAC77178.1 (AE000493) orf, hypothetical protein [Escherichia coli K12]</p> <p>sp P39323 YTFP_ECOLI HYPOTHETICAL 12.9 KDA PROTEIN IN MSRA-CHPBI INTERGENIC REGION</p> <p>pir [S56448 hypothetical 12.9K protein (msra- chpbi intergenic region)] - Escherichia coli gb AAA97119.1 (U14003) ORF_0113 [Escherichia coli] gb AAC77179.1 (AE000493) orf, hypothetical protein [Escherichia coli K12] gb AAG59420.1 AE005654_9 (AE005654) orf, hypothetical protein [Escherichia coli O157:H7]</p> <p>sp P17288 IPYR_ECOLI INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE)</p> <p>pir [PWEC inorganic pyrophosphatase (EC 3.6.1.1) - Escherichia coli gb AAB88583.1 (M23550) inorganic pyrophosphatase [Escherichia coli] gb AAA97123.1 (U14003) ppa [Escherichia coli] gb AAC77183.1 (AE000494) inorganic pyrophosphatase [Escherichia coli K12] gb AAG59424.1 AE005655_3 (AE005655) inorganic pyrophosphatase [Escherichia coli O157:H7]</p>	SEQ ID n-3520
Contig9 from SEQ ID n° 9247 PL-2348.1 3875382 to 3879155	P 73%		SEQ ID n-3519
Contig9 from SEQ ID n° 9248 PL-4825.1 3879158 to 3879505	P 71%		#N/A
Contig9 from SEQ ID n° 9249 PL-2347.1 3879605 to 3880135	M 76%		SEQ ID n-3518

SEQ ID n° 9250	PL-2346.1	Contig9 from 3880753 to 3881757	m	86%	sp P09200 F16P_ECOLI FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1- PHOSPHOHYDROLASE) (FBPASE) pir PAC fructose- biphosphatase (EC 3.1.3.11) - Escherichia coli emb CAA31062.1 (X12545) fructose-1,6- biphosphatase (AA 1-332) [Escherichia coli] gb AAA97129.1 (U14003) fructose-1,6- biphosphatase [Escherichia coli] gb AAC77189.1 (AE000494) fructose- biphosphatase [Escherichia coli K12] SEQ ID n~1517
SEQ ID n° 9251	PL-2345.1	Contig9 from 3881923 to 3883293	p	82%	gb AAG59430.1 AE005655_9 (AE005655) putative ligase [Escherichia coli O157:H7] sp P15282 ARGR_ECOLI ARGININE REPRESSOR pir A3388 arginine repressor protein - Escherichia coli emb CAA32148.1 (X13968) xerA gene product (AA 1 - 156) [Escherichia coli] gb AA23486.1 (M17532) arginine regulatory protein [Escherichia coli] gb AA58039.1 (U18997) CG Site No. 1011; alternate name Rarg [Escherichia coli] gb AAC76269.1 (AE000403) repressor of arg regulon; cer-mediated site specific recombination [Escherichia coli K12] gb AAG58365.1 AE005551_8 (AE005551) repressor of arg regulon; cer-mediated site specific recombination [Escherichia coli O157:H7] SEQ ID n~1516
SEQ ID n° 9252	PL-3253.1	Contig9 from 3883338 to 3883808	m	87%	gb AAG21998.1 AF282309_1 (AF282309) malate dehydrogenase [Yersinia pestis] gb AAG21999.1 AF282310_1 (AF282310) malate dehydrogenase [Yersinia pseudotuberculosis] SEQ ID n~1515

SEQ ID n° 9254 PL-3254.1	Contig9 from 3885430 to 3885696	m 34%	sp P18837 SFSB_ECOLI SUGAR FERMENTATION STIMULATION PROTEIN B (NER-LIKE PROTEIN) pir BVECNP nlp protein - Escherichia coli emb CAA48736.1 (X68873) Ner-like protein, homologous to Ner protein of bacteriophages Mu and D108 [Escherichia coli] gb AA57989.1 (U18997) Ner-like protein [Escherichia coli] gb AAC76220.1 (AE000399) regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu [Escherichia coli K12] gb AAG58322.1 AE005547_8 (AE005547) regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu [Escherichia coli O157:H7] SEQ ID n-2504	
SEQ ID n° 9255 PL-4828.1	Contig9 from 3885921 to 3886229	p 48%	sp P07040 RPC1_BPD10 REPRESSOR PROTEIN CI pir S07370 probable repressor protein - phage D108 emb CAA27474.1 (X03847) put. repressor protein (aa 1-174) [Bacteriophage D108] sp P07040 RPC1_BPD10 REPRESSOR PROTEIN CI pir S07370 probable repressor protein - phage D108 emb CAA27474.1 (X03847) put. repressor protein (aa 1-174) [Bacteriophage D108] sp P19641 ISPB_ECOLI OCTAPRENYL-DIPHOSPHATE SYNTHASE (OCTAPRENYL PYROPHOSPHATE SYNTHETASE) (OPP SYNTHETASE) pir E65109 octaprenyl-diphosphate synthase (EC 2.5.1.-) - Escherichia coli gb AA57988.1 (U18997) ORF_0323 [Escherichia coli] gb AAC76219.1 (AE000399) octaprenyl diphosphate synthase [Escherichia coli K12]	#N/A
SEQ ID n° 9256 PL-4829.1	Contig9 from 3886285 to 3886686	p 24%		#N/A
SEQ ID n° 9257 PL-2343.1	Contig9 from 3886708 to 3887679	m 85%		SEQ ID n-2514

SEQ ID n° 9258 PL-4831.1	Contig9 from 3887931 to 3888239	p 84%	sp P02422 RL21_ECOLI 50S RIBOSOMAL PROTEIN L21 pir R5EC21 ribosomal protein L21 [validated] - Escherichia coli dbj BAA02525.1 (D13267) ribosomal protein L21 [Escherichia coli] gb AAA57987.1 (U18997) 50S ribosomal subunit protein L21 [Escherichia coli] gb AAC76217.1 (AE000399) 50S ribosomal subunit protein L21 [Escherichia coli K12] gb AAG58320.1 AE005547_6 (AE005547) 50S ribosomal subunit protein L21 [Escherichia coli #N/A
SEQ ID n° 9259 PL-4833.1	Contig9 from 3888259 to 3888516	p 92%	sp P02427 RL27_ECOLI 50S RIBOSOMAL PROTEIN L27 pir R5EC27 ribosomal protein L27 [validated] - Escherichia coli dbj BAA02526.1 (D13267) ribosomal protein L27 [Escherichia coli] gb AAA57986.1 (U18997) 50S ribosomal subunit protein L27 [Escherichia coli] gb AAC76217.1 (AE000399) 50S ribosomal subunit protein L27 [Escherichia coli K12] gb AAG58319.1 AE005547_5 (AE005547) 50S ribosomal subunit protein L27 [Escherichia coli O157:H7] #N/A
SEQ ID n° 9260 PL-2342.1	Contig9 from 3888769 to 3889944	p 81%	gb AAG58317.1 AE005547_3 (AE005547) putative GTP binding factor [Escherichia coli O157:H7] SEQ ID n-2513

sp|P24228|PBP4_ECOLI PENICILLIN-BINDING PROTEIN
4 PRECURSOR (PBP-4) [INCLUDES: D-
ALANYL-D-ALANINE CARBOXYPEPTIDASE (DD-PEPTIDASE)
(DD-CARBOXYPEPTIDASE); D-ALANYL-D-ALANINE-
ENDOPEPTIDASE (DD-ENDOPEPTIDASE)]
pir||A54535 serine-type D-Ala-D-Ala
carboxypeptidase (EC 3.4.16.4) precursor -
Escherichia coli emb|CAA42070.1| (X59460)
penicillin-binding protein 4 (PBP4)
[Escherichia coli] emb|CAA42643.1| (X50038) D-
alanyl-D-alanine carboxypeptidase [Escherichia
coli] gb|AA57983.1| (U18997) D-alanyl-D-
alanine carboxypeptidase, fraction B
[Escherichia coli] gb|AAA97505.1| (U01376)
ampicillin-binding protein [Escherichia coli]
gb|AAC76214.1| (AE000399) D-alanyl-D-alanine
carboxypeptidase, fraction B;
penicillin-binding protein 4 [Escherichia coli
K12]

SEQ ID n-1512

Contig9 from
SEQ ID n° 9261 PL-2341.1 3890012 to m 75%
3891538

sp|P21346|GREA_ECOLI TRANSCRIPTION ELONGATION
FACTOR GREA (TRANSCRIPT CLEAVAGE FACTOR
GREA) pir||JQ0752 suppressor protein grea -
Escherichia coli pdb|1GRJ| Grea Transcript
Cleavage Factor From Escherichia Coli
emb|CAA38521.1| (X54718) Grea protein
[Escherichia coli] gb|AAA97506.1| (U01376)
transcription elongation factor [Escherichia
coli]

SEQ ID n-2505

Contig9 from
SEQ ID n° 9262 PL-3256.1 3891721 to p 94%
3892197

SEQ ID n° 9263	PL-4835.1	Contig9 from 3892330 to 3892623	m	82%	sp P42550 YHBY_ECOLI_HYPOTHETICAL_10.8_KD PROTEIN IN FTSJ-GREA INTERGENIC REGION (O97) pir F65108 hypothetical 10.8 kD protein in ftsj- grea intergenic region - Escherichia coli (strain K-12) gb AA57981.1 (U18997) ORF_097 [Escherichia coli] gb AAC76212.1 (AE000398) orf, hypothetical protein [Escherichia coli K12] gb AAG58314.1 AE005546_8 (AE005546) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9264	PL-4836.1	Contig9 from 3892661 to 3892795	m	No Hits found	sp P28692 RRMJ_ECOLI_RIBOSOMAL_RNA_LARGE_SUBUNIT METHYLTRANSFERASE J (RRNA O-)-METHYLTRANSFERASE) (23S RRNA M2U2552 pir S35108 23S rRNA methyltransferase (EC 2.1.1.1-) [validated] - Escherichia coli gb AA23812.1 (M83138) ftsJ [Escherichia coli] gb AA57980.1 (U18997) ftsJ [Escherichia coli] gb AAA97507.1 (U01376) regulatory protein [Escherichia coli] gb AAC76211.1 (AE000398) cell division protein [Escherichia coli K12] gb AAG58313.1 AE005546_7 (AE005546) cell division protein [Escherichia coli O157:H7] SEQ ID n-1511	#N/A
SEQ ID n° 9266	PL-2339.1	Contig9 from 3893442 to 3895403	p	92%	gb AAA97508.1 (U01376) ATP-binding protein [Escherichia coli] gb AA57978.1 (U18997) dihydropteroate synthase [Escherichia coli] gb AAC76209.1 (AE000398) 7,8-dihydropteroate synthase [Escherichia coli K12] gb AAG58311.1 AE005546_5 (AE005546) 7,8- dihydropteroate synthase [Escherichia coli O157:H7]	SEQ ID n-1509
SEQ ID n° 9267	PL-2338.1	Contig9 from 3895486 to 3896331	p	82%		SEQ ID n-1508

SEQ ID n° 9268	PL-2337.1	Contig9 from 3896328 to 3897665	p 87%	gb AAG58310.1 AE005546_4 (AE005546) similar to phosphoglucosyltransferases and phosphomannomutases [Escherichia coli O157:H7] sp P33582 SECG_ECOLI PROTEIN-EXPORT MEMBRANE PROTEIN SECG (PREPROTEIN TRANSLOCASE BAND 1 SUBUNIT) (P12) pir S40402 protein-export protein secG - Escherichia coli dbj BAA03930.1 (D16463) p12 [Escherichia coli] gb AAA57976.1 (U18997) p12 [Escherichia coli] gb AAA97511.1 (U01376) membrane protein [Escherichia coli] gb AAC76207.1 (AE000398) protein export - membrane protein [Escherichia coli K12]	SEQ ID n-2507
SEQ ID n° 9269	PL-4839.1	Contig9 from 3897842 to 3898180	p 81%	pir WMECN5 nus operon 15K protein - Escherichia coli gb AAA57973.1 (U18997) gtc start; differences from database entry [Escherichia coli] gb AAC76204.1 (AE000397) orf, hypothetical protein [Escherichia coli K12] gb AAG58306.1 AE005545_8 (AE005545) orf, hypothetical protein [Escherichia coli O157:H7] sp P03003 NUSA_ECOLI N UTILIZATION SUBSTANCE PROTEIN A (NUSA PROTEIN) (L FACTOR) pir FJEC transcription termination-antitermination factor nusa - Escherichia coli gb AAA57972.1 (U18997) L factor [Escherichia coli] gb AAC76203.1 (AE000397) transcription pausing; L factor [Escherichia coli K12] gb AAG58305.1 AE005545_7 (AE005545) transcription pausing; L factor [Escherichia coli O157:H7] sp Q9ZFP3 IF2_SALTY TRANSLATION INITIATION FACTOR IF-2 emb CAA05549.1 (AJ002552) initiation factor IF2-alpha [Salmonella typhimurium]	SEQ ID n-2506
SEQ ID n° 9270	PL-4840.1	Contig9 from 3898280 to 3898468	p No Hits found		#N/A
SEQ ID n° 9271	PL-3257.1	Contig9 from 3898660 to 3899124	p 89%		#N/A
SEQ ID n° 9272	PL-2336.1	Contig9 from 3899146 to 3900654	p 91%		
SEQ ID n° 9273	PL-2334.1	Contig9 from 3900679 to 3903408	p 89%		

Contig9 from SEQ ID n° 9274 PL-3259.1 3903474 to 3903884	p 79%	sp O34272 RBFA_YEREN RIBOSOME-BINDING FACTOR A emb CAA71698.1 (Y10692) yhbB [Yersinia enterocolitica] SEQ ID n-2508
Contig9 from SEQ ID n° 9275 PL-2332.1 3903884 to 3904831	p 78%	sp P09171 TRUB_ECOLI TRNA PSEUDOURIDINE SYNTHASE B (TRNA PSEUDOURIDINE 5S SYNTHASE) (PS155 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) (P35 PROTEIN) pir Q9EC35 trna-pseudouridine synthase (EC 5.4.99.-) trUB [validated] - Escherichia coli emb CAA32021.1 (X13775) P35 gene product (AA 1-314) [Escherichia coli] emb CAA31635.1 (X13270) P35 gene product (AA 1- 314) [Escherichia coli] gb AAC76200.1 (AE000397) trna pseudouridine 5S synthase [Escherichia coli K12] gb AAG58302.1 AE005545_4 (AE005545) trna pseudouridine 5S synthase [Escherichia coli O157:H7] SEQ ID n-2502
Contig9 from SEQ ID n° 9276 PL-4844.1 3904954 to 3905223	p 88%	sp P41120 RS15_PHOLU 30S RIBOSOMAL PROTEIN S15 pir S38882 ribosomal protein S15 - Xenorhabdus luminescens emb CAA53670.1 (X76069) ribosomal protein S15 [Photorhabdus luminescens] sp P41121 PNP_PHOLU POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE) (CAP87K) pir S38883 polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) - Xenorhabdus luminescens emb CAA53671.1 (X76069) polynucleotide phosphorylase [Photorhabdus luminescens] SEQ ID n-2501

SEQ ID n° 9278 PL-2330.1	Contig9 from 3907846 to 3908730	p	87%	<p>sp P39833 NLPI_ECOLI_LIPOPROTEIN_NLPI_PRECURSOR pir G65106 hypothetical 33.6 kD protein in dead pnp intergenic region - Escherichia coli (strain K-12) gb AA57966.1 (U18997) ORF_f294 [Escherichia coli] gb AAC76197.1 (AE000397) putative control proteins [Escherichia coli K12] gb AGS8299.1 AE005545_1 (AE005545) putative control proteins [Escherichia coli O157:H7]</p>	SEQ ID n-1500
SEQ ID n° 9279 PL-2329.1	Contig9 from 390887 to 3910821	p	86%	<p>gb AGS8298.1 AE005544_12 (AE005544) inducible ATP-independent RNA helicase [Escherichia coli O157:H7]</p>	SEQ ID n-1498
SEQ ID n° 9280 PL-2328.1	Contig9 from 3910960 to 3912762	m	83%	<p>sp P94532 CSTA_BACSU CARBON STARVATION PROTEIN A HOMOLOG pir A69609 carbon starvation protein csta [similarity] - Bacillus subtilis emb CAA99596.1 (Z75208) carbon starvation induced protein [Bacillus subtilis] emb CAB14831.1 (Z99118) carbon starvation- induced protein [Bacillus subtilis] sp P33356 YEHT_ECOLI_HYPOTHETICAL_27.9_KD PROTEIN_IN_MOLR-BGLX_INTERGENIC_REGION pir D64980 yeht protein - Escherichia coli (strain K-12) gb AA60488.1 (U00007) yeht [Escherichia coli] gb AAC75186.1 (AE000301) orf, hypothetical protein [Escherichia coli K12] dbj BAB19554.1 (AP000400) hypothetical protein [Escherichia coli O157:H7]</p>	SEQ ID n-1497
SEQ ID n° 9281 PL-2327.1	Contig9 from 3912933 to 3913655	m	86%	<p>gb AGS7193.1 AE005439_12 (AE005439) orf, hypothetical protein [Escherichia coli O157:H7] prf 2014253V yeht gene [Escherichia coli]</p>	SEQ ID n-1496

SEQ ID n° 9282	PL-2326.1	Contig9 from 3913652 to 3914683	m	80%	sp P33357 YEHU_ECOLI_HYPOTHETICAL_62.1_KD PROTEIN IN MOLR-BGLX INTERGENIC REGION PRECURSOR pir E64980_hypothetical_62.1_KD protein in molr-bglx intergenic region - Escherichia coli (strain K-12) gb AAC75187.1 (AE000301) putative 2-component sensor protein [Escherichia coli K12] SEQ ID n-1495
SEQ ID n° 9283	PL-4846.1	Contig9 from 3914803 to 3915249	p	75%	gb AAG53985.1 AF327444_1 (AF327444) putative transposase A [Erwinia herbicola] #N/A
SEQ ID n° 9284	PL-3260.1	Contig9 from 3915246 to 3915641	p	77%	gb AAG53986.1 AF327444_2 (AF327444) putative transposase B [Erwinia herbicola] SEQ ID n-2510
SEQ ID n° 9285	PL-2325.1	Contig9 from 3915625 to 3916272	m	78%	dbj BAB19555.1 (AP000400) hypothetical protein [Escherichia coli O157:H7] gb AAG57194.1 AE005439_13 (AE005439) putative 2- component sensor protein [Escherichia coli O157:H7] SEQ ID n-1494
SEQ ID n° 9286	PL-2324.1	Contig9 from 3916510 to 3917481	p	76%	pir G83220_hypothetical_protein_PA3402 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06790.1 AE004761_6 (AE004761) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-1493
SEQ ID n° 9287	PL-2323.1	Contig9 from 3917489 to 3918634	p	66%	pir F83220_hypothetical_protein_PA3401 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06789.1 AE004761_5 (AE004761) hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-1492
SEQ ID n° 9288	PL-2322.3	Contig9 from 3918634 to 3919782	p	64%	pir E83220_hypothetical_protein_PA3400 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06788.1 AE004761_4 (AE004761) hypothetical protein [Pseudomonas aeruginosa] #N/A

Contig9 from SEQ ID n° 9289 PL-4850.2 3920067 to 3920354	P	64%	ref NP_046944.1 gp48 [Bacteriophage N15] pir T13135 protein gp48 - phage N15 gb AAC19087.1 (AF064539) gp48 [Bacteriophage N15]	#N/A
Contig9 from SEQ ID n° 9290 PL-2321.1 3920465 to 3921007	m	No Hits found	sp P39823 PSS_BACSU CDP-DIACYLGLYCEROL--SERINE O- PHOSPHATIDYLTRANSFERASE (PHOSPHATIDYLSERINE SYNTHASE) pir A55537 CDPdiacylglycerol--serine O- phosphatidyltransferase (EC 2.7.8.8) ppsa [validated] - Bacillus subtilis dbj BAA07225.1 (D38022) phosphatidylserine synthase [Bacillus subtilis] emb CAB12021.1 (Z99105) phosphatidylserine synthase [Bacillus subtilis] dbj BAA33124.1 (AB006424)	SEQ ID n-3490
Contig9 from SEQ ID n° 9291 PL-2320.1 3920997 to 3921620	m	28%	PHOSPHATIDYLSERINE SYNTHASE [Bacillus subtilis] pir B82579 peptide synthase XF2276 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85075.1 AE004039_10 (AE004039) peptide synthase [Xylella fastidiosa] pir C65084 hypothetical protein b2981 - Escherichia coli (strain K-12) gb AAAG9148.1 (U28377) ORF_f390 [Escherichia coli] gb AAC76017.1 (AE000381) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-3489
Contig9 from SEQ ID n° 9292 PL-2319.1 3921617 to 3923203	m	42%	ref NP_069544.1 phosphoenolpyruvate synthase (ppsa) [Archaeoglobus fulgidus] sp Q29548 PPSA_ARCFU PROBABLE	SEQ ID n-3487
Contig9 from SEQ ID n° 9293 PL-2318.1 3923200 to 3924255	m	17%	PHOSPHOENOLPYRUVATE SYNTHASE (PYRUVATE, WATER DIKINASE) pyruvate, water dikinase (EC 2.7.9.2) - Archaeoglobus fulgidus gb AAE90532.1 (AE001056) phosphoenolpyruvate synthase (ppsa) [Archaeoglobus fulgidus]	SEQ ID n-3486
Contig9 from SEQ ID n° 9294 PL-2317.1 3924248 to 3927013	m	18%		SEQ ID n-3485

SEQ ID n° 9295 PL-2316.1	Contig9 from 3927158 to 3929659	m	26%	sp Q58116 HMDH_METUJ 3-HYDROXY-3-METHYLGLOUTARYL- COENZYME A REDUCTASE (HMG-COA REDUCTASE) pir A64388 3-hydroxy-3-methylglutaryl coenzyme A reductase (EC 1.1.1.1.-) - Methanococcus jannaschii gb AAB98699.1 (U67517) 3-hydroxy-3-methylglutaryl coenzyme A reductase [Methanococcus jannaschii] SEQ ID n-1484	SEQ ID n-1483	#N/A
SEQ ID n° 9296 PL-2315.1	Contig9 from 3929680 to 3930570	m	No Hits found	sp P45474 YHBT_ECOLI HYPOTHETICAL 19.7 KD PROTEIN IN SOHA-MTR INTERGENIC REGION (F174) pir A65106 hypothetical 19.7 KD protein in soha- mtr intergenic region - Escherichia coli (strain K-12) gb AAA57960.1 (U18997) ORF_f174 [Escherichia coli] gb AAC76191.1 (AE000396) orf, hypothetical protein [Escherichia coli K12] gb AAG58293.1 AE005544_7 (AE005544) orf, hypothetical protein [Escherichia coli O157:H7]		#N/A
SEQ ID n° 9297 PL-4853.1	Contig9 from 3930710 to 3930943	m	No Hits found	sp P45473 YHBS_ECOLI HYPOTHETICAL 18.5 KDA PROTEIN IN SOHA-MTR INTERGENIC REGION pir H65105 hypothetical protein b3156 - Escherichia coli (strain K-12) gb AAA57959.1 (U18997) ORF_f167; end overlaps end of o100 by 14 bases; start overlaps f174, other starts possible [Escherichia coli] gb AAC76190.1 (AE000396) orf, hypothetical protein [Escherichia coli K12] gb AAG58292.1 AE005544_6 (AE005544) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2511		
SEQ ID n° 9298 PL-4854.1	Contig9 from 3931245 to 3931487	p	58%			
SEQ ID n° 9299 PL-3261.1	Contig9 from 3931537 to 3932040	p	70%			

SEQ ID n° 9300 PL-4855.1	Contig9 from 3932009 to 3932323	m 60%	sp P45472 YHBQ_ECOLI_HYPOTHETICAL_11.3_KD PROTEIN IN SOHA-MTR INTERGENIC REGION (O100) pir G65105 hypothetical 11.3 kD protein in soha- mtr intergenic region - Escherichia coli (strain K-12) gb AA57958.1 (U18997) ORF_o100 [Escherichia coli] gb AAC76189.1 (AE000396) orf, hypothetical protein [Escherichia coli K12]	#N/A
SEQ ID n° 9301 PL-4856.1	Contig9 from 3932598 to 3932849	p 60%	gb AAG55174.1 AE005261_4 (AE005261) orf, hypothetical protein-[Escherichia coli O157:H7]	#N/A
SEQ ID n° 9302 PL-3262.1	Contig9 from 3932973 to 3933404	p 60%	sp P45471 YHBP_ECOLI_HYPOTHETICAL_16.8_KD PROTEIN IN SOHA-MTR INTERGENIC REGION (F147) pir F65105 hypothetical protein yhbp - Escherichia coli (strain K-12) gb AA57957.1 (U18997) ORF_f147; end overlaps end of o186 by 20 bases [Escherichia coli] gb AAC76188.1 (AE000396) orf, hypothetical protein [Escherichia coli K12] sp P39329 NRDG_ECOLI_ANAEROBIC_RIBONUCLEOSIDE- TRIPHOSPHATE_REDUCTASE_ACTIVATING_PROTEIN (CLASS_III_ANAEROBIC_RIBONUCLEOTIDE_REDUCTASE SMALL COMPONENT) pir A55692 anaerobic ribonucleotide reductase activase (EC 1.97.1.1) - Escherichia coli gb AA97134.1 (U14003) ORF_f154 [Escherichia coli] emb CAA86937.1 (Z46865) activase for anaerobic ribonucleoside triphosphate reductase [Escherichia coli] gb AAC77194.1 (AE000495) anaerobic ribonucleotide reductase activating protein [Escherichia coli K12] gb AAG59434.1 AE005656_2 (AE005656) anaerobic ribonucleotide reductase activating protein [Escherichia coli O157:H7]	SEQ ID n-2512
SEQ ID n° 9303 PL-3263.1	Contig9 from 3933407 to 3933871	m 80%		SEQ ID n-2513

SEQ ID n° 9304 PL-2314.1	Contig9 from 3933891 to 3936029	m	87%	gb AAG59435.1 AE005656_3 (AE005656) anaerobic ribonucleoside-triphosphate reductase [Escherichia coli O157:H7] pir S56469 hypothetical 13.5K protein (mgTA- pyrI intergenic region) - Escherichia coli gb AA97140.1 (U14003) ORF_f141 [Escherichia coli] gb AAC7200.1 (AE000495) orf, hypothetical protein [Escherichia coli K12] sp P08421 PYRI_SALTY ASPARTATE CARBAMOYLTRANSFERASE REGULATORY CHAIN pir DTEBCT aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain - Salmonella typhimurium emb CA29130.1 (X05641) pyrI (AA 1-153) [Salmonella typhimurium] SEQ ID n-2482
SEQ ID n° 9305 PL-4857.1	Contig9 from 3936280 to 3936666	m	84%	#N/A
SEQ ID n° 9306 PL-3264.1	Contig9 from 3936884 to 3937348	m	79%	SEQ ID n-2514
SEQ ID n° 9307 PL-4859.1	Contig9 from 3937332 to 3937511	m	No Hits found	#N/A
SEQ ID n° 9308 PL-1953.1	Contig9 from 3938404 to 3939924	p	No Hits found	SEQ ID n-1085
SEQ ID n° 9309 PL-1952.1	Contig9 from 3940341 to 3941135	p	49%	pir A82295 conserved hypothetical protein VC0673 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93838.1 (AE004153) conserved hypothetical protein [Vibrio cholerae] pdb 1F3I A Chain A, Crystal Structure Of Tn5 Transposase Complexed With End Dna SEQ ID n-1084
SEQ ID n° 9310 PL-1951.1	Contig9 from 3941327 to 3942709	m	57%	SEQ ID n-1083
SEQ ID n° 9311 PL-4863.1	Contig9 from 3942720 to 3943031	m	No Hits found	#N/A
SEQ ID n° 9312 PL-1950.1	Contig9 from 3943859 to 3944782	m	91%	gb AAF01338.1 AF190426_2 (AF190426) aspartate transcarbamylase catalytic subunit [Erwinia herbicola] SEQ ID n-1082

SEQ ID n° 9313	PL-1949.1	Contig9 from 3945089 to 3946105	m	84%	gb AAG59453.1 AE005657_13 (AE005657) ornithine carbamoyltransferase 1 [Escherichia coli O157:H7]	SEQ ID n-2080
SEQ ID n° 9314	PL-3265.1	Contig9 from 3946270 to 3946677	p	67%	sp P37163 YJGD_ECOLI_HYPOTHETICAL 15.6 KD PROTEIN IN ARG1-VALS INTERGENIC REGION (O138) pir S56480_hypothetical 15.6K protein (argi- vals intergenic region) - Escherichia coli gb AAA97151.1 (U14003) ORF_0138 [Escherichia coli] gb AAC77212.1 (AE000496) orf, hypothetical protein [Escherichia coli K12] gb AAG59454.1 AE005657_14 (AE005657) orf, hypothetical protein [Escherichia coli O157:H7] gb AAC38630.1 (AF047028) insecticidal toxin complex protein TccC [Photothabdus luminescens]	SEQ ID n-2515
SEQ ID n° 9315	PL-1948.1	Contig9 from 3946792 to 3949602	m	56%	dbj BAB03889.1 (AF001507) amino acid ABC transporter (amino acid-binding protein) [Bacillus halodurans]	SEQ ID n-2079
SEQ ID n° 9316	PL-1947.1	Contig9 from 3949959 to 3950732	m	61%	gb AAG24255.1 (AY009114) YckI [Bacillus subtilis]	SEQ ID n-2078
SEQ ID n° 9317	PL-1946.1	Contig9 from 3950820 to 3951584	m	70%	dbj BAB03890.1 (AF001507) amino acid ABC transporter (permease) [Bacillus halodurans]	SEQ ID n-2077
SEQ ID n° 9318	PL-1945.2	Contig9 from 3951562 to 3952263	m	68%	dbj BAB03889.1 (AF001507) amino acid ABC transporter (amino acid-binding protein) [Bacillus halodurans]	SEQ ID n-2076
SEQ ID n° 9319	PL-2262.2	Contig9 from 3952659 to 3953432	m	62%	gb AAG59457.1 AE005657_17 (AE005657) valine tRNA synthetase [Escherichia coli O157:H7]	SEQ ID n-2425
SEQ ID n° 9320	PL-2263.1	Contig9 from 3953869 to 3956766	m	88%	gb AAG59458.1 AE005657_18 (AE005657) DNA polymerase III, chi subunit [Escherichia coli O157:H7]	SEQ ID n-2426
SEQ ID n° 9321	PL-3267.1	Contig9 from 3956780 to 3957229	m	67%		SEQ ID n-2516

SEQ ID n° 9322	PL-2264.1	Contig9 from 3957293 to 3958813	m	92%	<p>sp P11648 AMPA_ECOLI_CYTOSOL_AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (AMINOPEPTIDASE A/I) pir APECA leucyl aminopeptidase (EC 3.4.11.1) A - Escherichia coli emb CAA33225.1 (X15130) aminopeptidase A/I (AA 1 - 503) [Escherichia coli] gb AAA97157.1 (U14003) aminopeptidase A/1 [Escherichia coli] emb CAA50164.1 (X86443) aminopeptidase A [Escherichia coli] gb AAC77217.1 (AE000496) aminopeptidase A/I [Escherichia coli K12] gb AAG59459.1 (AE005658_1 (AE005658) aminopeptidase A/I [Escherichia coli O157:H7]</p>	SEQ ID n-1427
SEQ ID n° 9323	PL-2265.1	Contig9 from 3959099 to 3960199	p	77%	<p>sp P39340 YJGP_ECOLI_HYPOTHETICAL_40.4_KD PROTEIN IN PEPA-GNTV INTERGENIC REGION (O366) pir S56487 hypothetical 40.4K protein (pepa- gntv intergenic region) - Escherichia coli gb AAA97158.1 (U14003) ORF_0366 [Escherichia coli] gb AAC77218.1 (AE000497) orf, hypothetical protein [Escherichia coli K12] gb AAG59460.1 (AE005658_2 (AE005658) orf, hypothetical protein [Escherichia coli O157:H7]</p>	SEQ ID n-1428
SEQ ID n° 9324	PL-2266.1	Contig9 from 3960199 to 3961278	p	83%	<p>sp P39341 YJGQ_ECOLI_HYPOTHETICAL_39.8_KD PROTEIN IN PEPA-GNTV INTERGENIC REGION (O361) pir S56488 hypothetical 39.8K protein (pepa- gntv intergenic region) - Escherichia coli gb AAA97159.1 (U14003) ORF_0361 [Escherichia coli] gb AAC77219.1 (AE000497) orf, hypothetical protein [Escherichia coli K12] gb AAG59461.1 (AE005658_3 (AE005658) orf, hypothetical protein [Escherichia coli O157:H7] pir H64765 yaiH protein - Escherichia coli gb AAC73479.1 (AE000144) putative enzyme [Escherichia coli K12]</p>	SEQ ID n-1429
SEQ ID n° 9325	PL-2267.1	Contig9 from 3961391 to 3962653	m	60%	<p>gb AAG54722.1 (AE005216_10 (AE005216) putative enzyme [Escherichia coli O157:H7]</p>	SEQ ID n-1430

SEQ ID n° 9326	PL-4867.1	Contig9 from 3963089 to 3963184	m	No Hits found	#N/A
SEQ ID n° 9327	PL-2268.1	Contig9 from 3963402 to 3964658	p	73%	sp P39347 INTB_ECOLI_PROPHAGE_P4_INTEGRASE (INT(P4)) pir S56496 prophage P4 integrase - Escherichia coli gb AA97167.1 (U14003) ORF_0396 [Escherichia coli] gb AAC77227.1 (AB000498) prophage P4 integrase [Escherichia coli K12] SEQ ID n-2431
SEQ ID n° 9328	PL-2269.1	Contig9 from 3964709 to 3965656	p	No Hits found	SEQ ID n-2432
SEQ ID n° 9329	PL-4870.1	Contig9 from 3965759 to 3966022	m	65%	gb AAF06963.1 AF157599_2 (AF157599) ECO0109IREP [Escherichia coli] #N/A
SEQ ID n° 9330	PL-4871.1	Contig9 from 3966139 to 3966426	p	53%	gb AAF22961.1 AF157489_1 (AF157489) Pln [Phototrichobacterium luminescens] #N/A
SEQ ID n° 9331	PL-4872.1	Contig9 from 3966491 to 3966664	p	No Hits found	#N/A
SEQ ID n° 9332	PL-4873.1	Contig9 from 3966693 to 3966953	m	65%	gb AAF06963.1 AF157599_2 (AF157599) ECO0109IREP [Escherichia coli] #N/A
SEQ ID n° 9333	PL-2270.1	Contig9 from 3967488 to 3968630	m	22%	pir A36134 RepA protein - Escherichia coli plasmid TF-FC2 gb AA27381.1 (M73777) replication protein A [Plasmid pTF-FC2] ref NP_052245.1 Orf3 [Francisella tularensis] gb AAC12937.1 (AF055345) Orf3 [Francisella tularensis] SEQ ID n-2434
SEQ ID n° 9334	PL-2271.1	Contig9 from 3968784 to 3969650	m	40%	SEQ ID n-2435
SEQ ID n° 9335	PL-4877.1	Contig9 from 3970142 to 3970270	p	No Hits found	#N/A
SEQ ID n° 9336	PL-4878.1	Contig9 from 3970239 to 3970550	p	No Hits found	#N/A

SEQ ID n° 9337	PL-4879.1	Contig9 from 3970653 to 3971012	p	78%	gb AAG58859.1 AE005598_3 (AE005598) orf; hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9338	PL-4881.1	Contig9 from 3970996 to 3971319	p	81%	gb AAG58860.1 AE005598_4 (AE005598) orf; hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9339	PL-4882.1	Contig9 from 3971322 to 3971504	p	No Hits found		#N/A
SEQ ID n° 9340	PL-2272.1	Contig9 from 3971497 to 3972873	p	No Hits found		SEQ ID n-1436
SEQ ID n° 9341	PL-4883.1	Contig9 from 3972863 to 3973174	p	No Hits found		#N/A
SEQ ID n° 9342	PL-2273.1	Contig9 from 3973224 to 3973979	p	No Hits found		SEQ ID n-1437
SEQ ID n° 9343	PL-2274.1	Contig9 from 3973976 to 3974968	p	No Hits found		SEQ ID n-1438
SEQ ID n° 9344	PL-2275.1	Contig9 from 3975465 to 3976730	p	81%	gb AAF06962.1 AF157599_1 (AF157599) P4 integrase- like protein [Escherichia coli]	SEQ ID n-1439
SEQ ID n° 9345	PL-3268.1	Contig9 from 3977144 to 3977575	p	51%	ref NP_050966.1 P5 [Bacteriophage APSE-1] sp Q9T1U3 REGQ_BPAPS PROBABLE ANTITERMINATION PROTEIN Q (P5) gb AAF03999.1 AF157835_56 (AF157835) P5 [Bacteriophage APSE-1]	SEQ ID n-14517
SEQ ID n° 9346	PL-2276.1	Contig9 from 3977669 to 3979894	m	56%	gb AAAG64865.1 (U23723) orf732 [Escherichia coli]	SEQ ID n-1440
SEQ ID n° 9347	PL-2277.1	Contig9 from 3979917 to 3981038	m	45%	gb AAAG64864.1 (U23723) orf300 [Escherichia coli]	SEQ ID n-1441

Contig9 from SEQ ID n° 9348 PL-4886.1	p	29%	ref NP_058387.1 orf; hypothetical protein [Salmonella typhi] gb AAF70012.1 AF250878_173 (AF250878) orf; hypothetical protein [Salmonella typhi] #N/A
Contig9 from SEQ ID n° 9349 PL-2279.1	m	26%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] ... SEQ ID n-2443
Contig9 from SEQ ID n° 9350 PL-4888.1	m	57%	ref NP_042044.1 psu gene product (AA 1-190) [Bacteriophage P4] sp P05460 VPSU_BPP4 POLARITY SUPPRESSION PROTEIN (AMBER MUTATION-SUPPRESSING PROTEIN) emb CAA35906.1 (X51522) psu gene product (AA 1-190) [Bacteriophage P4] #N/A
Contig9 from SEQ ID n° 9351 PL-2280.1	m	53%	gb AAG58541.1 AE005567_2 (AE005567) putative DNA processing protein [Escherichia coli O157:H7] SEQ ID n-2445
Contig9 from SEQ ID n° 9352 PL-2281.1	m	56%	pir T35189 probable ATP-dependent DNA helicase Streptomyces coelicolor emb CAA18513.1 (AL022374) SC5B8.05, probable ATP-dependent DNA helicase, len: 7 19 aa; similar in N- terminal half to many e.g. RECO_ECOLIF1 5043 atp-dependent dna helicase recq (607 aa), fasta score s; opt: 546 z-score: 615.9 E(): 4.1e-27, 35.9% identity in 362 aa ov> SEQ ID n-2446
Contig9 from SEQ ID n° 9353 PL-2282.1	m	5%	gb AAK00458.1 (AF200692) unknown [Shigella flexneri 2a] SEQ ID n-2447
Contig9 from SEQ ID n° 9354 PL-2283.1	m	82%	sp P15031 FECE_ECOLI IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE pir QRECM3 membrane-bound iron(III) dicitrate transport protein - Escherichia coli gb AA23765.1 (M26397) fecE [Escherichia coli] gb AA97183.1 (U14003) fecE [Escherichia coli] gb AAC77243.1 (AE000499) ATP-binding component of citrate-dependent iron(III) transport protein [Escherichia coli K12] SEQ ID n-2448

SEQ ID n° 9355	PL-2284.1	Contig9 from 3992330 to 3993286	m	60%	<p>sp P15029 FECD_ECOLI IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD pir S56513 citrate-dependent iron transport protein fecD - Escherichia coli pir QRECD2 iron(III) dicitrate transport protein 2, cytosolic - Escherichia coli gb AAA97184.1 (U14003) CG Site No. 18394 [Escherichia coli] gb AAC77244.1 (AE000499) citrate-dependent iron transport, membrane-bound protein [Escherichia coli K12] SEQ ID n-1449</p> <p>sp P15030 FECC_ECOLI IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECC pir S56514 fecC protein - Escherichia coli pir QRECD1 iron(III) dicitrate transport protein 1, cytosolic - Escherichia coli gb AAA97185.1 (U14003) fecC [Escherichia coli] gb AAC77245.1 (AE000499) citrate-dependent iron(III) transport protein, cytosolic [Escherichia coli K12] SEQ ID n-1450</p>
SEQ ID n° 9356	PL-2285.1	Contig9 from 3993283 to 3994281	m	83%	<p>sp P15028 FECB_ECOLI IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR sp P13036 FECA_ECOLI IRON(III) DICITRATE TRANSPORT PROTEIN FECA PRECURSOR pir QRECEFA iron(III) dicitrate transport system outer membrane receptor precursor - Escherichia coli (strain K-12) gb AAC77247.1 (AE000499) outer membrane receptor; citrate- dependent iron transport, outer membrane receptor [Escherichia coli K12] SEQ ID n-1452</p>
SEQ ID n° 9357	PL-2286.1	Contig9 from 3994278 to 3995186	m	82%	
SEQ ID n° 9358	PL-2287.1	Contig9 from 3995246 to 3997606	m	89%	

SEQ ID n° 9359 PL-2288.1	Contig9 from 3997691 to 3998656	m 71%	sp P23485 FECR_ECOLI FECR PROTEIN pir B37804 fecR protein - Escherichia coli gb AAA23767.1 (M63115) fecR [Escherichia coli] gb AA97188.1 (U14003) fecR [Escherichia coli] gb AAC77248.1 (AE000500) regulator for fec operon, periplasmic [Escherichia coli K12]	SEQ ID n-1453
SEQ ID n° 9360 PL-3274.1	Contig9 from 3998658 to 3999179	m -84%	sp P23484 FECI_ECOLI PROBABLE RNA POLYMERASE SIGMA FACTOR FECI pir JVO111 transcription activator fecI - Escherichia coli gb AAA23766.1 (M63115) fecI [Escherichia coli] gb AA97189.1 (U14003) fecI [Escherichia coli] gb AAC77249.1 (AE000500) probable RNA polymerase sigma factor [Escherichia coli K12]	SEQ ID n-2521
SEQ ID n° 9361 PL-4896.1	Contig9 from 4001628 to 4001792	p No Hits found	ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	#N/A SEQ ID n-1454
SEQ ID n° 9362 PL-2289.1	Contig9 from 4002228 to 4003241	p 72%	gb AAG55972.1 AE005330_4 (AE005330) putative holin protein of prophage CP-933X [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9363 PL-4899.1	Contig9 from 4004161 to 4004436	p No Hits found	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	#N/A
SEQ ID n° 9364 PL-4902.1	Contig9 from 4005243 to 4005569	p 66%		
SEQ ID n° 9365 PL-2290.1	Contig9 from 4006115 to 4007140	p 21%		
SEQ ID n° 9366 PL-3275.1	Contig9 from 4007482 to 4007916	p No Hits found		

SEQ ID n° 9367	PL-2291.1	Contig9 from 4007955 to 4009208	p	53%	gb AAC63217.1 (AF039135) juvenile hormone esterase-related protein [Leptinotarsa decemlineata]	SEQ ID n-1457
SEQ ID n° 9368	PL-4907.1	Contig9 from 4009549 to 4009713	m	No Hits found		#N/A
SEQ ID n° 9369	PL-3276.1	Contig9 from 4009726 to 4010271	p	41%	gb AAG60892.1 AF322013_11 (AF322013) ID459 [Bradyrhizobium japonicum]	SEQ ID n-2523
SEQ ID n° 9370	PL-4909.1	Contig9 from 4010183 to 4010407	p	29%	gb AAC82519.1 (AF027768) Reta [Serratia marcescens]	#N/A
SEQ ID n° 9371	PL-4910.1	Contig9 from 4010500 to 4010706	p	No Hits found		#N/A
SEQ ID n° 9372	PL-2292.1	Contig9 from 4010636 to 4012198	p	15%	pir C83234 hypothetical protein PA3290 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06678.1 AE004751_4 (AE004751) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-1458
SEQ ID n° 9373	PL-4916.1	Contig9 from 4012623 to 4012745	m	83%	pir G83403 conserved hypothetical protein PA1938 [imported] - Pseudomonas aeruginosa (strain PAO1)	#N/A
SEQ ID n° 9374	PL-4917.1	Contig9 from 4013810 to 4013010	m	60%	gb AAG05326.1 AE004620_5 (AE004620) conserved hypothetical protein [Pseudomonas aeruginosa] pir G83403 conserved hypothetical protein PA1938 [imported] - Pseudomonas aeruginosa (strain PAO1)	#N/A
SEQ ID n° 9375	PL-4919.1	Contig9 from 4013177 to 4013401	m	No Hits found	gb AAG05326.1 AE004620_5 (AE004620) conserved hypothetical protein [Pseudomonas aeruginosa]	#N/A

SEQ ID n°	Contig9 from	m	No Hits found	#N/A
9376 PL-4920.1	4013895 to 4014044			
9377 PL-2293.1	4014172 to 4014924	p	66%	<p>pir [E83174 hypothetical protein PA3775 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AA07162.1 AE004796_7 (AE004796) hypothetical protein [Pseudomonas aeruginosa]</p> <p>pir [G82983 probable MFS transporter PA5311 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AA08696.1 AE004943_12 (AE004943) probable MFS transporter [Pseudomonas aeruginosa]</p> <p>SEQ ID n-1459</p>
9378 PL-2294.1	4015033 to 4016229	p	53%	
9379 PL-2295.1	4016587 to 4017957	p	87%	<p>gb AAG58013.1 AE005518_7 (AE005518) Z4223 gene product [Escherichia coli O157:H7]</p> <p>sp P32703 YJCE_ECOLI_PUTATIVE NA(+)/H(+)</p> <p>EXCHANGER YJCE pir [H65214 hypothetical 60.5 kD protein in soxR-acs intergenic region - Escherichia coli (strain K-12) gb AAC43159.1 (U00006) similar to eukaryotic Na+/H+ exchangers [Escherichia coli] gb AAC77035.1 (AE000480) orf, hypothetical protein [Escherichia coli K12]</p> <p>gb AAA67624.1 (M87049) trans-activator of metB and meth [Escherichia coli]</p> <p>SEQ ID n-1461</p>
9380 PL-2296.1	4018230 to 4019879	p	84%	<p>SEQ ID n-1460</p>
9381 PL-2297.1	4020106 to 4021041	m	83%	<p>SEQ ID n-1462</p> <p>SEQ ID n-1463</p>

SEQ ID n° 9382-PL-2298.1	Contig9 from 4021150 to 4023426	p	87%	sp P25665 METE_ECOLI 5- METHYLtetrahydropteroyltriGLUTAMATE-- HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE) pir [A42863 5- methy]tetrahydropteroyltriGLUTAMATE-- homocysteine S-methyltransferase (EC 2.1.1.14) - Escherichia coli (strain K-12) gb AAC76832.1 (AE000458) tetrahydropteroyltriGLUTAMATE methyltransferase [Escherichia coli K12]	SEQ ID n-2464
				pir [T36711 probable dioxxygenase - Streptomyces coelicolor emb CAB45209.1 (AL079308) putative dioxxygenase [Streptomyces coelicolor A3(2)] sp P28618 PCP_BACSU PYRROLIDONE-CARBOXYLATE PEPTIDASE (S-OXOPROLYL-PEPTIDASE) (PYROGLUTAMYL-PEPTIDASE I) (PGP-I) (PYRASE) pir [S23432 pyroglutamyl-peptidase I (EC 3.4.19.3) pcp - Bacillus subtilis emb CAA46833.1 (X66034) TRANSFERRED ENTRY: 3.4.19.3 [Bacillus subtilis] dbj BA06485.1 (D30808) pyrrolidone carboxy-peptidase [Bacillus subtilis] emb CAB12059.1 (Z99105) pyrrolidone- carboxylate peptidase [Bacillus subtilis]	
SEQ ID n° 9383-PL-2299.1	Contig9 from 4023669 to 4024502	p	19%	emb CAB94934.1 (AJ278525) uridine phosphorylase [Yersinia pseudotuberculosis]	SEQ ID n-2469
				dbj RAA81645.1 (AB028630) protein-tyrosine phosphatase [Clostridium perfringens]	
SEQ ID n° 9384-PL-2300.1	Contig9 from 4024747 to 4025403	m	61%	gb AAG54369.1 AE005183_6 (AE005183) orf2, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2471
SEQ ID n° 9385-PL-2301.1	Contig9 from 4026254 to 4027009	p	89%		SEQ ID n-2470
SEQ ID n° 9386-PL-2302.1	Contig9 from 4027104 to 4027886	p	52%		SEQ ID n-2470
SEQ ID n° 9387-PL-2303.1	Contig9 from 4028025 to 4028615	p	41%		SEQ ID n-2471

Contig9 from SEQ ID n° 9388 PL-2304.1 4028721 to 4030076	p 77%	gb AAF33423.1 (AF233324) 88% identity to E. coli hypothetical protein (YIGN) (SP:P27850) [Salmonella typhimurium LT2] SEQ ID n-2472 gb AAG59029.1 AE005614_9 (AE005614) 2-octaprenyl- 6-methoxy-1,4-benzoquinone --> 2- octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone [Escherichia coli O157:H7] SEQ ID n-1473
Contig9 from SEQ ID n° 9389 PL-2305.1 4030149 to 4030904	p 83%	sp P27852 YIGP_ECOLI HYPOTHETICAL 22.2 KD PROTEIN IN UBIE-RFAH INTERGENIC REGION pir C65188 hypothetical 22.3 kD protein in udp- rfaH intergenic region - Escherichia coli (strain K-12) gb AAC76837.1 (AE000459) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-1474 sp O07443 AARF PROST UBIQUINONE BIOSYNTHESIS PROTEIN AARF (AMINOGLYCOSIDE ACETYLTRANSFERASE REGULATOR) pir T51162 aminoglycoside acetyltransferase regulator [imported] - Providencia stuartii gb AB96577.1 (AF002165) aminoglycoside acetyltransferase regulator [Providencia stuartii] SEQ ID n-2475
Contig9 from SEQ ID n° 9391 PL-2307.1 4031543 to 4033180	p 90%	sp P57045 TATA_SALTY SEC-INDEPENDENT PROTEIN TRANSLOCASE PROTEIN TATA gb AAF33419.1 (AF233324) 83% identity with amino acids 10-79 of E. coli hypothetical protein (YIGT) (SP:P27856) [Salmonella typhimurium LT2] #N/A
Contig9 from SEQ ID n° 9392 PL-4925.1 4033407 to 4033667	p 78%	sp O69415 TATB_ECOLI SEC-INDEPENDENT PROTEIN TRANSLOCASE PROTEIN TATB emb CAA06725.1 (AJ005830) TatB protein [Escherichia coli] gb AAC19241.1 (AF067848) MttA2 [Escherichia coli] #N/A
Contig9 from SEQ ID n° 9393 PL-4926.1 4033671 to 4034114	p 72%	

gb AAF33418.1 (AF233324) 90% identity to B. coli SEC-independent protein translocase protein (TATC); contains similarity to Pfam family PF00902 (MttB family), score=147.4, E=2.6e-40, N=1 [Salmonella typhimurium LT2] Seq ID n-1476	Contig9 from 4034136 to 4034918	p 87%	pir G82363 delta-aminolevulinic acid dehydratase VC0105 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93283.1 (AE004101) delta-aminolevulinic acid dehydratase [Vibrio cholerae] gb AAF33417.1 (AF233324) 88% identity to B. coli transcriptional activator RFAH (SW:P26614) [Salmonella typhimurium LT2] Seq ID n-2525	Seq ID n-1477
gb AAF33412.1 (AF233324) 92% identity to B. coli hypothetical protein (YIGC) (SW:P26615) [Salmonella typhimurium LT2] sp P43129 FRE_PHOLU_NAD(P)H-FLAVIN REDUCTASE (NAD(P)H:FLAVIN OXIDOREDUCTASE) dbj BAA04597.1 (D17745) NAD(P)H-flavin reductase, Fre [Photobacterium luminescens] Seq ID n-1479	Contig9 from 4036091 to 4036579	m 79%	gb AAG59039.1 AE005615_7 (AE005615) thiolase I; 3-ketoacyl-CoA thiolase; acetyl-CoA transferase [Escherichia coli O157:H7] Seq ID n-1481	Seq ID n-1480
gb AAG59039.1 AE005615_7 (AE005615) thiolase I; 3-ketoacyl-CoA thiolase; acetyl-CoA transferase [Escherichia coli O157:H7] Seq ID n-1481	Contig9 from 4039474 to 4040640	m 82%		

SEQ ID n°	Accession	Gene	Protein	Function	SEQ ID n-2394
sp P21177 FADB_ECOLI FATTY OXIDATION COMPLEX					
		ALPHA SUBUNIT [INCLUDES: ENOYL-COA			
		HYDRATASE ; DELTA(3)-CIS-DELTA(2)-TRANS-ENOYL-			
		COA			
		ISOMERASE ; 3-HYDROXYACYL-COA			
		DEHYDROGENASE ;			
		3-HYDROXYBUTYRYL-COA			
		EPIMERASE] pir A39592 fatty acid beta			
		oxidation complex alpha chain - Escherichia coli			
		gb AAAG2777.1 (M74164) 79-kDa multifunctional			
		protein [Escherichia coli] gb AAAG7643.1			
		(M87049) large (alpha) subunit of the fatty acid-			
		oxidizing			
		multienzyme complex			
		[Escherichia coli] gb AAC76849.1 (AE000460) 4-			
		enzyme protein: 3-hydroxyacyl-CoA dehydrogenase;			
		3-hydroxybutyryl-CoA epimerase;			
		delta(3)-cis-delta(2)-trans-enoil-CoA isomerase;			
		enoil-CoA hydratase [Escherichia coli K12]			
		sp P21165 PBPQ_ECOLI XAA-PRO DIPEPTIDASE (X-PRO			
		DIPEPTIDASE) (PROLINE DIPEPTIDASE)			
		(PROLIDASE) (IMIDODIPEPTIDASE) pir H65189 X-			
		pro dipeptidase (EC 3.4.13.9) - Escherichia coli			
		(strain K-12) gb AAC76850.1 (AE000460) proline			
		dipeptidase [Escherichia coli K12]			
		gb AAG59042.1 AE005615_10 (AE005615) orf,			
		hypothetical protein [Escherichia coli O157:H7]			
		sp P21166 TRKH_ECOLI TRK SYSTEM POTASSIUM UPTAKE			
		PROTEIN TRKH pir A56151 trkH protein			
		(corrected) - Escherichia coli			
		gb AAG59043.1 AE005615_11 (AE005615) potassium			
		uptake protein, requires TrkE [Escherichia			
		coli O157:H7]			
		gb AAAG7647.1 (M87049) o181 [Escherichia coli]			

988

SEQ ID n° 9405	PL-2853.1	Contig9 from 4053768 to 4054697	P	86%	gb AAG59205.1 AE005633_2 (AE005633) homoserine transsuccinylase [Escherichia coli O157:H7] SEQ ID n-2067
SEQ ID n° 9406	PL-2854.1	Contig9 from 4054997 to 4056595	P	87%	sp P08997 MSY_ECOLI MALATE SYNTHASE A (MSA) pir SYECMA malate synthase (EC 4.1.3.2) A - Escherichia coli emb CAA30973.1 (X12431) malate synthase [Escherichia coli] gb AAC43108.1 (U00006) malate synthase A [Escherichia coli] gb AAC76984.1 (AE000474) malate synthase A [Escherichia coli K12] sp P05313 ACEA_ECOLI ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) pir WZECIC isocitrate lyase (EC 4.1.3.1) - Escherichia coli emb CAA30974.1 (X12431) isocitrate lyase [Escherichia coli] gb AAC43109.1 (U00006) isocitrate lyase [Escherichia coli] gb AAC76985.1 (AE000474) isocitrate lyase [Escherichia coli K12] SEQ ID n-2068
SEQ ID n° 9407	PL-2855.1	Contig9 from 4056692 to 4057999	P	90%	gb AAC43891.1 (U43356) isocitrate dehydrogenase kinase/phosphatase [Salmonella enterica] gb AAC43893.1 (U43357) isocitrate dehydrogenase kinase/phosphatase [Salmonella enterica] SEQ ID n-2069
SEQ ID n° 9408	PL-2856.1	Contig9 from 4058051 to 4059808	P	81%	pir RPECIR acetate operon repressor - Escherichia coli gb AA50561.1 (M63914) repressor of the aceBAK operon [Escherichia coli] gb AAC43112.1 (U00006) CG Site No. 614 [Escherichia coli] gb AAC76988.1 (AE000475) repressor of aceBA operon [Escherichia coli K12] gb AAG59210.1 AE005633_7 (AE005633) repressor of aceBA operon [Escherichia coli O157:H7] SEQ ID n-2070
SEQ ID n° 9409	PL-2857.1	Contig9 from 4060230 to 4060796	P	No Hits found	SEQ ID n-2071
SEQ ID n° 9410	PL-2858.1	Contig9 from 4061088 to 4061918	M	82%	SEQ ID n-2072

SEQ ID n° 9411	PL-2859.1	Contig9 from 4062683 to 4064182	p 34%	gb AAF57570.1 (AE003796) CG10073 gene product [Drosophila melanogaster]	SEQ ID n-2073
SEQ ID n° 9412	PL-2860.1	Contig9 from 4064984 to 4065820	p 34%	pir H83490 hypothetical protein PA1239 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04628.1 AE004553_5 (AE004553) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2075
SEQ ID n° 9413	PL-4963.1	Contig9 from 4065813 to 4066196	p 46%	emb CAB99168.1 (AL390188) putative integral membrane protein [Streptomyces coelicolor A3(2)]	#N/A
SEQ ID n° 9414	PL-2861.1	Contig9 from 4066244 to 4067140	p No Hits found		SEQ ID n-2076
SEQ ID n° 9415	PL-2862.1	Contig9 from 4067189 to 4068235	p 31%	gb AAC44790.1 (U76606) isobutylamine N- hydroxylase [Streptomyces viridifaciens] sp O66442 ARGD_AQUAE ACETYLORNITHINE AMINOTRANSFERASE (ACOFAT) pir G70301 N- acetylornithine aminotransferase - Aquifex aeolicus gb AAC06390.1 (AE000669) N- acetylornithine aminotransferase [Aquifex aeolicus]	SEQ ID n-2077
SEQ ID n° 9416	PL-2863.1	Contig9 from 4068328 to 4070895	p 18%	emb CAB99167.1 (AL390188) hypothetical protein 2SCG18.34c [Streptomyces coelicolor A3(2)]	SEQ ID n-2078
SEQ ID n° 9417	PL-2864.1	Contig9 from 4070879 to 4071916	p 45%	gb AAD01942.1 (AF032440) D-alanine-D-alanyl carrier protein ligase; DltA [Staphylococcus xylosus]	SEQ ID n-2079
SEQ ID n° 9418	PL-2865.1	Contig9 from 4072124 to 4073587	m 53%	sp P39580 DLTB_BACSU DLTB PROTEIN pir S39659 dlTB protein - Bacillus subtilis emb CAA51560.1 (X73124) ipa-4r [Bacillus subtilis] emb CAB15877.1 (Z99123) alternate gene name: ipa-4r [Bacillus subtilis]	SEQ ID n-2080
SEQ ID n° 9419	PL-2866.1	Contig9 from 4073584 to 4074708	m 48%		SEQ ID n-2081

SEQ ID n° 9420	PL-2867.1	Contig9 from 4074852 to 4076054	m	43%	emb CAB51922.1 (A012255) extramembranal protein [Listeria monocytogenes]	SEQ ID n-2082
SEQ ID n° 9421	PL-4964.1	Contig9 from 4076051 to 4076362	m	43%	sp P39579 DLTC_BACSU D-ALANYL CARRIER PROTEIN (DCP) pir S39658 D-alanine carrier protein dlc - Bacillus subtilis emb CAA51559.1 - (X73124) lpa-3r [Bacillus subtilis] gb AAB34706.1 D-alanyl carrier protein, Dcp=dlc product [Bacillus subtilis], Peptide, 78 aa emb CAB15878.1 (Z99123) D- alanyl carrier protein (Dcp) [Bacillus subtilis] - #N/A gb AAG59223.1 AE005635_3 (AE005635) aspartokinase III, lysine sensitive [Escherichia coli O157:H7]	SEQ ID n-2083
SEQ ID n° 9422	PL-2868.1	Contig9 from 4077253 to 4078632	m	80%	sp P11243 G6PI_CLAUN GLUCOSE-6-PHOSPHATE ISOMERASE, CHLOROPLAST (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) SEQ ID n-2084 gb AAG59238.1 AE005637_2 (AE005637) chorismate lyase [Escherichia coli O157:H7]	SEQ ID n-2528
SEQ ID n° 9423	PL-2869.1	Contig9 from 4078931 to 4080577	p	87%	sp O52366 UBIA_PROST 4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (4-HB POLYPRENYLTRANSFERASE) gb AAB88868.1 (AF036909) 4-hydroxybenzoate octaprenyltransferase [Providencia stuartii]	SEQ ID n-2086
SEQ ID n° 9424	PL-3280.1	Contig9 from 4080879 to 4081397	p	57%	pir XUECAG glycerol-3-phosphate O- acyltransferase (EC 2.3.1.15) - Escherichia coli gb AAC77011.1 (AE000477) glycerol-3- phosphate acyltransferase [Escherichia coli K12]	SEQ ID n-2087
SEQ ID n° 9425	PL-2870.1	Contig9 from 4081420 to 4082286	p	84%		
SEQ ID n° 9426	PL-2871.1	Contig9 from 4082330 to 4084786	m	84%		

SEQ ID n° 9427	PL-4966.1	Contig9 from 4084916 to 4085287	p	79%	sp P00556 KDGL_ECOLI_DIACYLGLYCEROL_KINASE (DAGK) (DIGLYCERIDE_KINASE) (DGK) pir KIECDG probable diacylglycerol kinase (EC 2.7.1.107) - Escherichia coli gb AAC43136.1 (U000006) diacylglycerol kinase [Escherichia coli] gb AA24394.1 (K00127) diglyceride kinase [Escherichia coli] gb AAC77012.1 (AB000477) diacylglycerol kinase [Escherichia coli K12] gb AAG59241.1 AE005637_5 (AE005637) diacylglycerol kinase [Escherichia coli O157:H7] sp Q07267 LEXA_PROBE_LEXA_REPRESSOR pir S33693 lexA protein - Providencia rettgeri emb CAA50300.1 (X70965) LexA repressor [Providencia rettgeri]	#N/A
SEQ ID n° 9428	PL-2872.1	Contig9 from 4085407 to 4086012	p	90%	pir B65212 hypothetical 21.7 kD protein in dinF. qor intergenic region - Escherichia coli (strain_K-12) -gb AAC77016.1 (AE000478) putative regulator [Escherichia coli K12]	SEQ ID n-2088
SEQ ID n° 9429	PL-3281.1	Contig9 from 4086172 to 4086684	m	73%	sp P76228 YXJ1_ECOLI_HYPOTHETICAL_40.3_KDA PROTEIN IN GDHA-TOPB INTERGENIC REGION pir I39549 Lactate oxidase - Aerococcus viridans dbj BAA09172.1 (D50611) lactate oxidase [Aerococcus viridans] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7] ref NP_050998.1 P37 [Bacteriophage APSE-1] sp Q9TIR1 TFA_BPAPS PROBABLE TAIL FIBER ASSEMBLY PROTEIN (P37) gb AAF03980.1 AF157835_37 (AF157835) P37 [Bacteriophage APSE-1]	SEQ ID n-2529
SEQ ID n° 9430	PL-2873.1	Contig9 from 4086904 to 4088046	p	39%	sp P76228 YXJ1_ECOLI_HYPOTHETICAL_40.3_KDA PROTEIN IN GDHA-TOPB INTERGENIC REGION pir I39549 Lactate oxidase - Aerococcus viridans dbj BAA09172.1 (D50611) lactate oxidase [Aerococcus viridans] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7] ref NP_050998.1 P37 [Bacteriophage APSE-1] sp Q9TIR1 TFA_BPAPS PROBABLE TAIL FIBER ASSEMBLY PROTEIN (P37) gb AAF03980.1 AF157835_37 (AF157835) P37 [Bacteriophage APSE-1]	SEQ ID n-2089
SEQ ID n° 9431	PL-2874.1	Contig9 from 4088374 to 4089462	m	55%	sp P76228 YXJ1_ECOLI_HYPOTHETICAL_40.3_KDA PROTEIN IN GDHA-TOPB INTERGENIC REGION pir I39549 Lactate oxidase - Aerococcus viridans dbj BAA09172.1 (D50611) lactate oxidase [Aerococcus viridans] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7] ref NP_050998.1 P37 [Bacteriophage APSE-1] sp Q9TIR1 TFA_BPAPS PROBABLE TAIL FIBER ASSEMBLY PROTEIN (P37) gb AAF03980.1 AF157835_37 (AF157835) P37 [Bacteriophage APSE-1]	SEQ ID n-2090
SEQ ID n° 9432	PL-2875.1	Contig9 from 4090064 to 4090900	p	17%	sp P76228 YXJ1_ECOLI_HYPOTHETICAL_40.3_KDA PROTEIN IN GDHA-TOPB INTERGENIC REGION pir I39549 Lactate oxidase - Aerococcus viridans dbj BAA09172.1 (D50611) lactate oxidase [Aerococcus viridans] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7] ref NP_050998.1 P37 [Bacteriophage APSE-1] sp Q9TIR1 TFA_BPAPS PROBABLE TAIL FIBER ASSEMBLY PROTEIN (P37) gb AAF03980.1 AF157835_37 (AF157835) P37 [Bacteriophage APSE-1]	SEQ ID n-2091
SEQ ID n° 9433	PL-3282.1	Contig9 from 4090879 to 4091328	p	62%	sp P76228 YXJ1_ECOLI_HYPOTHETICAL_40.3_KDA PROTEIN IN GDHA-TOPB INTERGENIC REGION pir I39549 Lactate oxidase - Aerococcus viridans dbj BAA09172.1 (D50611) lactate oxidase [Aerococcus viridans] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7] ref NP_050998.1 P37 [Bacteriophage APSE-1] sp Q9TIR1 TFA_BPAPS PROBABLE TAIL FIBER ASSEMBLY PROTEIN (P37) gb AAF03980.1 AF157835_37 (AF157835) P37 [Bacteriophage APSE-1]	SEQ ID n-2530
SEQ ID n° 9434	PL-2876.1	Contig9 from 4091483 to 4092073	p	No Hits found	sp P76228 YXJ1_ECOLI_HYPOTHETICAL_40.3_KDA PROTEIN IN GDHA-TOPB INTERGENIC REGION pir I39549 Lactate oxidase - Aerococcus viridans dbj BAA09172.1 (D50611) lactate oxidase [Aerococcus viridans] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7] ref NP_050998.1 P37 [Bacteriophage APSE-1] sp Q9TIR1 TFA_BPAPS PROBABLE TAIL FIBER ASSEMBLY PROTEIN (P37) gb AAF03980.1 AF157835_37 (AF157835) P37 [Bacteriophage APSE-1]	SEQ ID n-2092

sp P37668 YIAG_ECOLI HYPOTHETICAL 11.0 KD		PROTEIN IN BISC-CSPA INTERGENIC REGION (O96)		pir S47776 hypothetical 11K protein (bisc-cspa		intergenic region) - Escherichia coli	
SEQ ID n° 9435	PL-4968.1	Contig9 from	p	46%	gb AAB18532.1 (U00039) No definition line found	#N/A	
		4092276 to			[Escherichia coli] gb AAC76579.1 (AE000433)		
		4092572			ori, hypothetical protein [Escherichia coli K12]		
					gb AAG58704.1 (AE005582_7 (AE005582) orf,		
					hypothetical protein [Escherichia coli O157:H7]		
		Contig9 from	p	69%	ref NP_046945.1 gp49 [Bacteriophage N15]	#N/A	
		4092897 to			pir T13136 protein gp49 - phage N15		
		4093016			gb AAC19088.1 (AF064539) gp49 [Bacteriophage	#N/A	
					N15]		
		Contig9 from	p	78%	ref NP_046944.1 gp48 [Bacteriophage N15]	#N/A	
		4093013 to			pir T13135 protein gp48 - phage N15		
		4093297			gb AAC19087.1 (AF064539) gp48 [Bacteriophage		
					N15]		
		Contig9 from	p	81%	pir H65212 hypothetical 38.4 kD protein in dinF		
		4093714 to			qor intergenic region - Escherichia		
		4094751			coli (strain K-12) gb AAC77019.1 (AE000478)		
					orf, hypothetical protein [Escherichia coli K12] SEQ ID n-2093		
		Contig9 from	p	41%	ref NP_071813.1 unknown [Methanothermobacter	#N/A	
		4095332 to			wolfeii prophage psiM100]		
		4095778			gb AAG39952.1 (AF301375_12 (AF301375) unknown		
					[Methanothermobacter wolfeii prophage psiM100]		
		Contig9 from	p	21%	dbj BAB06239.1 (AP001515) transposase related	SEQ ID n-2094	
		4095828 to			protein (20) [Bacillus halodurans]		
		4096853			ref NP_071814.1 unknown [Methanothermobacter		
					wolfeii prophage psiM100]		
		Contig9 from	p	60%	gb AAG39953.1 (AF301375_13 (AF301375) unknown	#N/A	
		4097470 to			[Methanothermobacter wolfeii prophage psiM100]		
		4097847			gb AAG59249.1 (AE005638_3 (AE005638) quinone		
			m	83%	oxidoreductase [Escherichia coli O157:H7]	SEQ ID n-2097	
		Contig9 from					
		4098058 to					
		4099041					

Contig9 from SEQ ID n° 9443 PL-2881.1 4099212 to 4100621	p 89%	sp P10338 DNAB_SALTY REPLICATIVE DNA HELICASE SEQ ID n-2098
Contig9 from SEQ ID n° 9444 PL-2882.1 4100661 to 4101740	p 78%	sp P29743 ALR1_ECOLI ALANINE RACEMASE, BIOSYNTHETIC pir PC1296 alanine racemase (EC 5.1.1.1), biosynthetic - Escherichia coli (strain K-12) gb AAC77023.1 (AE000478) alanine racemase 1 [Escherichia coli K12] sp P04693 TYRB_ECOLI AROMATIC-AMINO-ACID AMINOTRANSFERASE (AROAT) (ARAT) pir XNECY aromatic-amino-acid transaminase (EC 2.6.1.57) tyrB [validated] - Escherichia coli pdb 3TAT A Chain A, Tyrosine Aminotransferase From E. Coli pdb 3TAT B Chain B, Tyrosine Aminotransferase From E. Coli pdb 3TAT C Chain C, Tyrosine Aminotransferase From E. Coli pdb 3TAT D Chain D, Tyrosine Aminotransferase From E. Coli pdb 3TAT E Chain E, Tyrosine Aminotransferase From E. Coli pdb 3TAT F Chain F, Tyrosine Aminotransferase From E. Coli gb AA24703.1 (M12047) tyrosine aminotransferase [Escherichia coli] gb AAC43148.1 (U00006) tyrosine aminotransferase [Escherichia coli] emb CAA27278.1 (X03628) aromatic aminotransferase (tyrB) [Escherichia coli] gb AAC77024.1 (AE000478) tyrosine aminotransferase, tyrosine repressible [Escherichia coli K12] ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis] SEQ ID n-2100
Contig9 from SEQ ID n° 9445 PL-2883.1 4101790 to 4102989	p 81%	
Contig9 from SEQ ID n° 9446 PL-2884.1 4103382 to 4104395	p 72%	
		SEQ ID n-2101

SEQ ID n° 9447	PL-4976.1	Contig9 from 4104444 to 4104698	p 80%	pir S49177 colicin E4 immunity protein - Escherichia coli plasmid Cole4_emb CAA45168.1 (X63621) immunity protein [Escherichia coli]	#N/A
SEQ ID n° 9448	PL-3284.1	Contig9 from 4104770 to 4105189	m 59%	gb AAG56337.1 AE005362_7 (AE005362) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2532
SEQ ID n° 9449	PL-7102.1	Contig9 from 4105229 to 4105405	m No Hits found		#N/A
SEQ ID n° 9450	PL-2885.1	Contig9 from 4106094 to 4107179	p 58%	gb AAG57304.1 AE005449_2 (AE005449) putative kinase [Escherichia coli O157:H7]	SEQ ID n-2102
SEQ ID n° 9451	PL-2886.1	Contig9 from 4107182 to 4108120	p 79%	gb AAG57303.1 AE005449_1 (AE005449) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2103
SEQ ID n° 9452	PL-2887.1	Contig9 from 4108181 to 4111015	m 94%	sp P37434 UVR_A_SALTY EXCINUCLEASE ABC SUBUNIT A gb AAA27250.1 (M93014) DNA repair enzyme [Salmonella typhimurium]	SEQ ID n-2104
SEQ ID n° 9453	PL-2888.1	Contig9 from 4111374 to 4111910	p 74%	sp P25762 SSB_SERMA SINGLE-STRAND BINDING PROTEIN (SSB) (HELIIX-DESTABILIZING PROTEIN) pir JN0632 single-stranded DNA-binding protein Serratia marcescens_emb CAA46208.1 (X65080) single-stranded DNA-binding protein [Serratia marcescens]	SEQ ID n-2105
SEQ ID n° 9454	PL-4980.1	Contig9 from 4112274 to 4112462	p 50%	ref NP_049098.1 GroupII intron-associated maturase [Sphingomonas aromaticivorans] pir T31170 maturase-related protein (group II intron) - Sphingomonas aromaticivorans_plasmid pNL1_gb AAD03894.1 (AF079317) GroupII intron-associated maturase [Sphingomonas aromaticivorans]	#N/A
SEQ ID n° 9455	PL-2889.1	Contig9 from 4112824 to 4113906	p 42%	emb CAB46587.1 (AJ132945) hypothetical protein [Versinia enterocolitica]	SEQ ID n-2106

SEQ ID n° 9456	PL-3890.1	4113941 to 4114873	Contig9 from	-p	No Hits found			SEQ ID n-2108
SEQ ID n° 9457	PL-3285.1	4115212 to 4115772	Contig9 from	p	No Hits found			SEQ ID n-2533
SEQ ID n° 9458	PL-416.2	4115773 to 4118931	Contig9 from	p	40%	emb CAA71698.1 (Y10687) purine NTPase [Sulfolobus acidocaldarius]		SEQ ID n-3222
SEQ ID n° 9459	PL-415.1	4119695 to 4120621	Contig9 from	m	69%	sp P21683 CRTB_PANAN PHYTOENE SYNTHASE pir E37802 crtB protein - Erwinia uredovora dbj BAAL4128.1 (D90087) crtB [Pantoea ananas] sp P21685 CRTI_PANAN PHYTOENE DEHYDROGENASE (PHYTOENE DESATURASE) pir D37802 phytoene dehydrogenase (EC 1.3.-.-) crtI - Erwinia uredovora dbj BAAL4127.1 (D90087) crtI [Pantoea ananas]		SEQ ID n-3221
SEQ ID n° 9460	PL-414.1	4120618 to 4122099	Contig9 from	m	82%	pir SE2585 dycopene cyclase - Erwinia herbicola gb AAA21262.1 (M90698) dycopene cyclase [Erwinia herbicola]		SEQ ID n-3220
SEQ ID n° 9461	PL-413.1	4122092 to 4123267	Contig9 from	m	63%	sp Q01335 YCR6_ERWHE HYPOTHETICAL 37.2 KD PROTEIN IN CRTE-CRTX INTERGENIC REGION (ORF6) pir S52979 hypothetical protein 6 - Erwinia herbicola gb AAA64978.1 (M87280) gene not found in Erwinia uredovora crt gene cluster; ORF6 [Erwinia herbicola]		SEQ ID n-3219
SEQ ID n° 9462	PL-412.1	4123381 to 4124097	Contig9 from	m	69%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]		SEQ ID n-3218
SEQ ID n° 9463	PL-411.1	4124089 to 4124973	Contig9 from	p	59%	sp Q01335 YCR6_ERWHE HYPOTHETICAL 37.2 KD PROTEIN IN CRTE-CRTX INTERGENIC REGION (ORF6) pir S52979 hypothetical protein 6 - Erwinia herbicola gb AAA64978.1 (M87280) gene not found in Erwinia uredovora crt gene cluster; ORF6 [Erwinia herbicola]		SEQ ID n-3217
SEQ ID n° 9464	PL-3286.1	4124986 to 4125408	Contig9 from	m	61%			SEQ ID n-2534

SEQ ID n° 9465	PL-410.1	Contig9 from 4125431 to 4126333	m	55%	sp P21684 CRTE_PANAN GERANYLGERANYL PYROPHOSPHATE SYNTHETASE (GGPP SYNTHETASE) (FARNESYLTRANSFERASE) pir A37802 CRTT protein - Erwinia uredovora dbj BAAL1424.1 (D90087) crtB [Pantoea ananas] SEQ ID n-9216
SEQ ID n° 9466	PL-409.1	Contig9 from 4126568 to 4128040	m	46%	pir S76169 hypothetical protein - Synechocystis sp. (strain PCC 6803) dbj BAAL18428.1 (D90914) lignostilbene-alpha,beta-dioxygenase [Synechocystis sp.] SEQ ID n-9214
SEQ ID n° 9467	PL-4984.1	Contig9 from 4128133 to 4128327	m	No Hits found	#N/A
SEQ ID n° 9468	PL-4985.1	Contig9 from 4128400 to 4128729	m	No Hits found	#N/A
SEQ ID n° 9469	PL-408.1	Contig9 from 4130489	m	70%	pir S75249 esterase sl10992 - Synechocystis sp. (strain-PCC 6803) dbj BAAL17163.1 (D90904) esterase [Synechocystis sp.] SEQ ID n-9213
SEQ ID n° 9470	PL-407.1	Contig9 from 4130612 to 4131721	m	91%	gb AAD46162.1 AFI30307.1 (AFI30307) glutathione-dependent formaldehyde dehydrogenase [Acinetobacter baumannii] SEQ ID n-9212
SEQ ID n° 9471	PL-4986.1	Contig9 from 4132050 to 4132208	m	No Hits found	#N/A
SEQ ID n° 9472	PL-4987.1	Contig9 from 4132229 to 4132534	m	No Hits found	#N/A
SEQ ID n° 9473	PL-4988.1	Contig9 from 4132636 to 4132893	p	No Hits found	#N/A
SEQ ID n° 9474	PL-406.1	Contig9 from 4133326 to 4134534	p	38%	pir B82317 hypothetical protein VC0492 [Imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93665.1 (AE004135) hypothetical protein [Vibrio cholerae] SEQ ID n-9205

SEQ ID n° 9475	PL-3287.1	Contig9 from 4134537 to 4135019	p	No Hits found	ref NP_059777.1 yme [Agrobacterium tumefaciens] gb AAB91579.2 (AF242891) yme [Agrobacterium tumefaciens]	SEQ ID n-2535
SEQ ID n° 9476	PL-405.1	Contig9 from 4135022 to 4137007	p	48%		SEQ ID n-9195
SEQ ID n° 9477	PL-404.1	Contig9 from 4137205 to 4138077	p	69%	gb AGS9478.1 AB005659_13 (AB005659) Z5892 gene product [Escherichia coli O157:H7]	SEQ ID n-9188
SEQ ID n° 9478	PL-403.2	Contig9 from 4138907 to 4140532	p	54%	pir T13261 hypothetical protein 536 - Lactococcus lactis phage BK5-T gb AAA98584.1 (L44593) ORF536; putative [Lactococcus phage BK5. T]	SEQ ID n-9179
SEQ ID n° 9479	PL-4990.1	Contig9 from 4140747 to 4140899	m	67%	gb AAF22961.1 AF157489_1 (AF157489) Pln [Photorhabdus luminescens]	#N/A
SEQ ID n° 9480	PL-402.1	Contig9 from 4141304 to 4144420	m	88%	sp P10486 TIR1_ECOLI TYPE I RESTRICTION ENZYME ECOR124II R PROTEIN (R.ECOR124II) pir S02168 type I site-specific deoxyribonuclease (EC 3.1.21.3) EcoR124/3 chain hsdR - Escherichia coli plasmid R124/3 emb CAA31543.1 (X13145) hsdR protein (AA 1-1033) [Escherichia coli]	SEQ ID n-9171
SEQ ID n° 9481	PL-401.1	Contig9 from 4144446 to 4145600	m	70%	pir H81152 anticodon nuclease NMB0832 [Imported] - Neisseria meningitidis (group B strain MD58) gb AAF41243.1 (AB002436) anticodon nuclease [Neisseria meningitidis MC58] pir I41084 type I site-specific deoxyribonuclease (EC 3.1.21.3) ECODXXI chain hsds - Escherichia coli emb CAA52162.1 (X73984) hsdS [Escherichia coli]	SEQ ID n-9160
SEQ ID n° 9482	PL-400.1	Contig9 from 4145602 to 4146699	m	58%		SEQ ID n-9156

SEQ ID n° 9483	PL-399.1	Contig9 from 4146696 to 4148252	m	91%	sp P10484 TIM1_ECOLI TYPE I RESTRICTION ENZYME ECOR124II_M PROTEIN (M.ECOR124II) pir S02166 type I site-specific deoxyribonuclease (EC 3.1.21.3) EcoR124/3 chain hsdM - Escherichia coli plasmid R124/3 emb CAA31541.1 (X13145) hsdM protein (AA 1-520) [Escherichia coli] SEQ ID n-3146
SEQ ID n° 9484	PL-4992.1	Contig9 from 4148577 to 4148876	m	58%	gb AAG54584.1 AE005203_13 (AE005203) integrase protein for prophage CP-933I [Escherichia coli O157:H7] #N/A
SEQ ID n° 9485	PL-398.1	Contig9 from 4149168 to 4150043	p	82%	gb AAG54886.1 AE005234_2 (AE005234) 5,10- methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase [Escherichia coli O157:H7] SEQ ID n-3138
SEQ ID n° 9486	PL-4993.1	Contig9 from 4150043 to 4150255	p	66%	gb AAG54885.1 AE005234_1 (AE005234) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 9487	PL-397.1	Contig9 from 4151096 to 4151980	m	59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis] SEQ ID n-9128
SEQ ID n° 9488	PL-4994.1	Contig9 from 4152349 to 4152765	p	38%	sp P39291 YJFI_ECOLI HYPOTHETICAL 14.9 KD PROTEIN IN VACB-AIDB INTERGENIC REGION (O133A) pir S56406 hypothetical 14.9K protein b4181 - Escherichia coli gb AAA97077.1 (U14003) orf_o133a [Escherichia coli] gb AAC77138.1 (AE000490) orf, hypothetical protein [Escherichia coli K12] gb AAG59377.1 AE005651_5 (AE005651) orf, hypothetical protein pir C83179 conserved hypothetical protein PA3731 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07118.1 AE004792_3 (AE004792) conserved hypothetical protein [Pseudomonas aeruginosa] SEQ ID n-3118

SEQ ID n° 9490	PL-395.1	Contig9 from 4153535 to 4154197	p 37%	sp P39293 YJFK_ECOLI_HYPOTHETICAL_25.0_KD PROTEIN IN VACB-AIDB INTERGENIC REGION (O219) pir S56408 hypothetical 25.0K protein (vacB- aidB intergenic region) - Escherichia coli gb AAA97079.1 (U14003) ORF_O219 [Escherichia coli] gb AAC77140.1 (AE000490) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-3107	
SEQ ID n° 9491	PL-4995.1	Contig9 from 4154198 to 4154635	p 55%	sp P39294 YJFL_ECOLI_HYPOTHETICAL_14.2_KD PROTEIN IN VACB-AIDB INTERGENIC REGION (O132) pir S56409 hypothetical 14.2K protein (vacB- aidB intergenic region) - Escherichia coli gb AAA97080.1 (U14003) ORF_O132 [Escherichia coli] gb AAC77141.1 (AE000490) orf, hypothetical protein [Escherichia coli K12] gb AAG59380.1 AE005651_9 (AE005651) yjfl gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9492	PL-393.1	Contig9 from 4154648 to 4155535	p 26%	gb AAG58176.1 AE005533_9 (AE005533) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-9092
SEQ ID n° 9493	PL-392.1	Contig9 from 4155655 to 4156821	p 70%	sp P24196 YGIC_ECOLI_HYPOTHETICAL_45.0_KD PROTEIN IN TOLC-RIBB INTERGENIC REGION (ORFA) (O386) pir S22361 hypothetical protein A - Escherichia coli gb AAA71876.1 (M77129) ORFA [Escherichia coli] gb AAA69206.1 (U28377) ORF_O386; alternate name ygiC; orfA of M77129 [Escherichia coli] gb AAC76074.1 (AE000385) putative synthetase/amidase [Escherichia coli K12] gb AAG58177.1 AE005533_10 (AE005533) putative synthetase/amidase [Escherichia coli O157:H7] pir D83072 conserved hypothetical protein PA4584 [imported] - Pseudomonas aeruginosa (strain PAO1)	SEQ ID n-9084
SEQ ID n° 9494	PL-391.1	Contig9 from 4157046 to 4157876	m 52%	gb AAG07972.1 AE004872_3 (AE004872) conserved hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-9075

Contig9 from SEQ ID n° 9495 PL-390.1 4157882 to 4159108	m	81%	pir C83072 conserved hypothetical protein PA4583 [imported] - Pseudomonas aeruginosa (strain PAO1)	SEQ ID n-3068
Contig9 from SEQ ID n° 9496 PL-389.1 4160365 to 4162143	m	72%	gb AAG07971.1 AE004872.2 (AE004872) conserved hypothetical protein [Pseudomonas aeruginosa] pir S71006 biotin carboxylase protein A1 Saccharopolyspora erythraea emb CAA63308.1 (X92556) biotin carboxylase and biotin carboxyl carrier protein [Saccharopolyspora erythraea]	SEQ ID n-3058
Contig9 from SEQ ID n° 9497 PL-388.1 4162152 to 4163765	m	43%	gb AAC46262.1 (AF006000) unknown [Bordetella pertussis]	SEQ ID n-3049
Contig9 from SEQ ID n° 9498 PL-387.1 4163783 to 4164559	m	62%	emb CAB56671.1 (AL121596) hypothetical protein SCF51A.19 [Streptomyces coelicolor A3(2)]	SEQ ID n-3041
Contig9 from SEQ ID n° 9499 PL-386.1 4164646 to 4165308	m	66%	sp P42673 PCP_PSEPL PYRROLIDONE-CARBOXYLATE PEPTIDASE (5-OXOPROLYL-PEPTIDASE) (PYROGLUTAMYL-PEPTIDASE I) (PGP-I) (PYRASE) pir A55583 pyroglutamyl-peptidase I (EC 3.4.19.3) - Pseudomonas fluorescens emb CAA53519.1 (X75919) TRANSFERRED ENTRY: 3.4.19.3 [Pseudomonas fluorescens]	SEQ ID n-3031
Contig9 from SEQ ID n° 9500 PL-385.1 4165318 to 4166334	m	60%	pir A81402 probable integral membrane protein Cj0553 [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB75189.1 (AL139075) putative integral membrane protein [Campylobacter jejuni]	SEQ ID n-3022
Contig9 from SEQ ID n° 9501 PL-384.1 4166334 to 4167062	m	60%	emb CAB56670.1 (AL121596) possible integral membrane protein [Streptomyces coelicolor A3(2)]	SEQ ID n-3012
Contig9 from SEQ ID n° 9502 PL-383.1 4167524 to 4168294	p	47%	emb CAB61681.1 (AL133213) putative GntR-family transcriptional regulator. [Streptomyces coelicolor A3(2)]	SEQ ID n-3004

SEQ ID n° 9503	PL-5000.1	4168646 to 4168882	Contig9 from	p	62%	gb AAG59474.1 AE005659_9 (AE005659) Z5888 gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9504	PL-382.1	4169118 to 4169759	Contig9 from	m	51%	emb CAB56727.1 (AL121600) hypothetical protein SCF76.07 [Streptomyces coelicolor A3(2)]	SEQ ID n-2996
SEQ ID n° 9505	PL-381.1	4169874 to 4170863	Contig9 from	p	52%	pir T3527I probable transcription regulator - Streptomyces coelicolor emb CAB40696.1 (AL049587) putative transcriptional regulator [Streptomyces coelicolor A3(2)]	SEQ ID n-2987
SEQ ID n° 9506	PL-5004.1	4170809 to 4171033	Contig9 from	m	52%	emb CAC05852.1 (AL391753) ORF173, CcdB,	#N/A
SEQ ID n° 9507	PL-5005.1	4171034 to 4171252	Contig9 from	m	57%	emb CAC05851.1 (AL391753) ORF173a,	#N/A
SEQ ID n° 9508	PL-5006.1	4171419 to 4171628	Contig9 from	m	84%	gb AAE22961.1 AF157489_1 (AF157489) Pln [Photorhabdus luminescens]	#N/A
SEQ ID n° 9509	PL-5007.1	4172014	Contig9 from	p	49%	gb AAG59474.1 AE005659_9 (AE005659) Z5888 gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9510	PL-380.1	4172148 to 4172759	Contig9 from	p	No Hits found		SEQ ID n-2977
SEQ ID n° 9511	PL-379.1	4172929 to 4174125	Contig9 from	m	No Hits found		SEQ ID n-2968
SEQ ID n° 9512	PL-378.1	4174505 to 4175494	Contig9 from	p	71%	gb AAD37770.1 AF146532_10 (AF146532) glycosyltransferase [Klebsiella pneumoniae]	SEQ ID n-2958
SEQ ID n° 9513	PL-377.1	4175548 to 4176498	Contig9 from	m	80%	gb AAK03851.1 (AE006214) IunH [Pasteurella multocida]	SEQ ID n-2947

SEQ ID n° 9521	PL-5012.1	Contig9 from 4183280 to 4183711	p	No Hits found	pir F83310 conserved hypothetical protein PA2684 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06072.1 AE004696_6 (AE004696) conserved hypothetical protein [Pseudomonas aeruginosa]	#N/A	SEQ ID n-2903
SEQ ID n° 9522	PL-372.1	Contig9 from 4183736 to 4188010	p	32%			
SEQ ID n° 9523	PL-5014.1	Contig9 from 4188023 to 4188328	p	No Hits found		#N/A	
SEQ ID n° 9524	PL-3291.1	Contig9 from 4188424 to 4188948	p	23%	gb AAG54899.1 AE005235_6 (AE005235) Z0702 gene product [Escherichia coli O157:H7]		SEQ ID n-2539
SEQ ID n° 9525	PL-371.1	Contig9 from 4188964 to 4189575	p	No Hits found			SEQ ID n-2895
SEQ ID n° 9526	PL-370.1	Contig9 from 4189678 to 4190562	p	59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]		SEQ ID n-2887
SEQ ID n° 9527	PL-7100.1	Contig9 from 4190602 to 4190766	p	No Hits found		#N/A	
SEQ ID n° 9528	PL-369.1	Contig9 from 4191012 to 4191671	m	61%	sp P54794 MOAR_KLEAE MONOAMINE REGULON TRANSCRIPTIONAL REGULATOR pir A36937 monoamine regulon positive regulator Moar - Klebsiella pneumoniae dbj BAO3667.1 (D15072) regulator protein [Klebsiella aerogenes]		SEQ ID n-2876
SEQ ID n° 9529	PL-368.1	Contig9 from 4192245 to 4193738	p	79%	pir G83136 probable amino acid permease PA4072 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07459.1 AE004823_5 (AE004823) probable amino acid permease [Pseudomonas aeruginosa]		SEQ ID n-2866

1004

SEQ ID n° 9530	PL-367.1	Contig9 from 4193809 to 4194309	p	34%	pir P83136 hypothetical protein PA071 [imported] ---Pseudomonas aeruginosa (strain PA01) gb AAG07458.1 AE004823_4 (AE004823) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2856
SEQ ID n° 9531	PL-5017.1	Contig9 from 4194397 to 4194792	p	No Hits found		#N/A
SEQ ID n° 9532	PL-366.1	Contig9 from 4194785 to 4195747	p	No Hits found		SEQ ID n-2846
SEQ ID n° 9533	PL-365.1	Contig9 from 4196090 to 4197538	m	32%	emb CAB71551.1 (AJ270937) aromatic amino acid decarboxylase [Sorangium cellulosum]	SEQ ID n-2838
SEQ ID n° 9534	PL-364.1	Contig9 from 4197563 to 4198864	m	48%	gb AAG27518.1 AF230494_1 (AF230494) L-ornithine N5-hydroxylase [Pseudomonas sp. B10] sp P21175 BRAC_PSEAE LEUCINE-, ISOLEUCINE-, VALINE-, THREONINE-, AND ALANINE-BINDING PROTEIN PRECURSOR (LIVAT-BP) (LEU/ILE/VAL/THR/ALA-BINDING PROTEIN) pir A36125 ABC-type transport system branched- chain amino acid-binding protein brAC precursor [validated] - Pseudomonas aeruginosa (strain PAO) pir H83509 branched-chain amino acid transport protein BrAC PA1074 [imported] - Pseudomonas aeruginosa (strain PAO1) dbj BA14254.1 (D90223) BrAC [periplasmic protein] [Pseudomonas aeruginosa] gb AAG04463.1 AE004539_5 (AE004539) branched- chain amino acid transport protein BrAC [Pseudomonas aeruginosa]	SEQ ID n-2829
SEQ ID n° 9535	PL-363.1	Contig9 from 4198867 to 4199832	m	33%		SEQ ID n-2824

1005

Contig9 from 4199843 to 4200970	Seq ID n° 9536 PL-362.1	38%	pir G75122 sarcosine oxidase, chain beta (soxb) PAB1843 - Pyrococcus abyssi (strain Ozeay) emb CAB49696.1 (AJ248285) sarcosine oxidase, subunit beta (soxb) [Pyrococcus abyssi]	SEQ ID n-2816
Contig9 from 4200973 to 4202466	Seq ID n° 9537 PL-361.1	40%	pir T35923 probable tRNA synthetase - Streptomyces coelicolor emb CAA22745.1 (AL035206) putative tRNA synthetase [Streptomyces coelicolor A3(2)]	SEQ ID n-2806
Contig9 from 4202469 to 4202837	Seq ID n° 9538 PL-5019.1	38%	pir T35922 hypothetical protein SC9B5.02 - Streptomyces coelicolor emb CAA22744.1 (AL035206) hypothetical protein SC9B5.02 [Streptomyces coelicolor A3(2)]	#N/A
Contig9 from 4202834 to 4204201	Seq ID n° 9539 PL-360.1	56%	dbj BAB06343.1 (AP001516) diaminobutyrate-- pyruvate transaminase [Bacillus halodurans]	SEQ ID n-2798
Contig9 from 4204203 to 4205528	Seq ID n° 9540 PL-359.1	52%	sp Q51548 PVDA_PSHAE L-ORNITHINE-5-MENOOXYGENASE (L-ORNITHINE N5-OXYGENASE) pir D83346 L- ornithine N5-oxygenase PA2386 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05774.1 AE004665_1 (AE004665) L-ornithine N5-oxygenase [Pseudomonas aeruginosa] pir E83496 hypothetical protein PA1186 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04575.1 AE004549_2 (AE004549) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2789
Contig9 from 4205581 to 4206540	Seq ID n° 9541 PL-358.1	66%	pir E83498 probable transcription regulator PA1184 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04573.1 AE004548_7 (AE004548) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-2780
Contig9 from 4206941 to 4207879	Seq ID n° 9542 PL-357.1	63%		SEQ ID n-2771

1006

SEQ ID n° 9543	PL-356.1	Contig9 from 4208378 to 4209001	p	80%	pir D83496 probable glutathione S-transferase PA1185-[imported] - Pseudomonas aeruginosa (strain PAO1)	SEQ ID n-2760
SEQ ID n° 9544	PL-355.1	Contig9 from 4209216 to 4210661	p	52%	gb AAG04574.1 AB004549_1 (AB004549) probable glutathione S-transferase [Pseudomonas aeruginosa]	SEQ ID n-2750
SEQ ID n° 9545	PL-354.1	Contig9 from 4210956 to 4212584	p	22%	gb AAF66546.1 AF140605_2 (AF140605) phenol 2- hydroxylase component A [Bacillus thermoglucosidasius]	SEQ ID n-2741
SEQ ID n° 9546	PL-353.1	Contig9 from 4212689 to 4214131	p	78%	pir B83340 hypothetical protein PA2451 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05839.1 AB004672_7 (AE004672) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2734
SEQ ID n° 9547	PL-352.1	Contig9 from 4214475 to 4215695	p	46%	gb AAG54729.1 AB005217_7 (AB005217) alkaline phosphatase [Escherichia coli O157:H7]	SEQ ID n-2729
SEQ ID n° 9548	PL-5022.1	Contig9 from 4215740 to 4215937	p	No Hits found	pir D71676 bicyclomycin resistance protein (bcr2) RP698 - Rickettsia prowazekii emb CAA15134.1 (AJ235272) BICYCLOMYCIN RESISTANCE PROTEIN (bcr2) [Rickettsia prowazekii]	#N/A
SEQ ID n° 9549	PL-3293.1	Contig9 from 4216051 to 4216266	m	No Hits found		SEQ ID n-2540
SEQ ID n° 9550	PL-5023.1	Contig9 from 4216214 to 4216426	p	No Hits found		#N/A
SEQ ID n° 9551	PL-5024.1	Contig9 from 4216613 to 4216738	m	No Hits found		#N/A

sp|P39406|RSMC_ECOLI_RIBOSOMAL_RNA_SMALL_SUBUNIT
METHYLTRANSFERASE C (RRNA) (GUANINE-N2

) -METHYLTRANSFERASE (16S RRNA M2G1207

METHYLTRANSFERASE) pir||S56595 hypothetical
37.6K protein (dnaT-hold intergenic region) -

Escherichia coli gb|AA97267.1| (U14003)

ORF f3435 [Escherichia coli] gb|AAC77324.1|

(AE000507) putative enzyme [Escherichia coli
K12]

SEQ ID n-2722

sp|P28632|HOLD_ECOLI_DNA_POLYMERASE_III, PSI
SUBUNIT pir||A48647 DNA-directed DNA polymerase
(EC 2.7.7.7) III psi chain -

Escherichia coli gb|AAA03076.1| (L05387) DNA

polymerase III psi subunit [Escherichia coli]

gb|AAA24435.1| (L04575) DNA polymerase III psi

subunit [Escherichia coli] gb|AAA97268.1|

(U14003) DNA polymerase III psi subunit

[Escherichia coli] gb|AAC77325.1| (AE000507)

DNA polymerase III, psi subunit [Escherichia
coli K12]

SEQ ID n-2541

sp|P09453|RIMI_ECOLI_RIBOSOMAL-PROTEIN-ALANINE
ACETYLTRANSFERASE (ACETYLATING ENZYME FOR

N-TERMINAL OF RIBOSOMAL PROTEIN S18)

pir||D65252 ribosomal-protein-alanine N-

acetyltransferase (EC 2.3.1.128) rimi -

Escherichia coli (strain K-12) gb|AAC77326.1|

(AE000507) acyltransferase for 30S ribosomal

subunit protein S18; acetylation of N-

terminal alanine [Escherichia coli K12]

gb|AAG59553.1|AE005668_8 (AE005668)

acyltransferase for 30S ribosomal subunit

protein S18; acetylation of N-

terminal alanine [Escherichia coli

O157:H7]

SEQ ID n-2542

Contig9 from
SEQ ID n° 9552 PL-351.1 4216896 to m 66%
4217912

Contig9 from
SEQ ID n° 9553 PL-3294.1 4218043 to p 48%
4218456

Contig9 from
SEQ ID n° 9554 PL-3295.1 4218425 to p 59%
4218871

1008

SEQ ID n° 9555	PL-350.1	Contig9 from 4219028 to 4220617	p	92%	sp Q56121 RF3_SALTY PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3) dbj BAA09090.1 (D50496) peptide release factor 3/RF3 [Salmonella typhimurium] gb AAG59555.1 AE005668_11 (AE005668)	SEQ ID n-2715
SEQ ID n° 9556	PL-5025.1	Contig9 from 4221004 to 4221381	p	62%	hyperosmotically inducible periplasmic protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9557	PL-349.1	Contig9 from 4221577 to 4222584	p	69%	gb AAG59558.1 AE005669_2 (AE005669) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2705
SEQ ID n° 9558	PL-5026.1	Contig9 from 4222600 to 4222746	m	77%	emb CAB41498.1 (AJ238399) hypothetical transposase [Escherichia coli]	#N/A
SEQ ID n° 9559	PL-5028.1	Contig9 from 4222791 to 4222922	m	No Hits found		#N/A
SEQ ID n° 9560	PL-348.1	Contig9 from 4222962 to 4223618	m	No Hits found		
SEQ ID n° 9561	PL-347.1	Contig9 from 4224065 to 4225087	m	95%	gb AAF97408.1 (AY004320) photopexin B [Photorhabdus luminescens]	SEQ ID n-2687
SEQ ID n° 9562	PL-346.1	Contig9 from 4225181 to 4226875	m	96%	gb AAF97407.1 (AY004319) photopexin A [Photorhabdus luminescens]	SEQ ID n-2676
SEQ ID n° 9563	PL-345.1	Contig9 from 4227200 to 4228081	p	No Hits found		SEQ ID n-2665
SEQ ID n° 9564	PL-3296.1	Contig9 from 4228582 to 4229001	m	No Hits found		SEQ ID n-2543
SEQ ID n° 9565	PL-344.1	Contig9 from 4229589 to 4230377	p	No Hits found		SEQ ID n-2656
SEQ ID n° 9566	PL-343.1	Contig9 from 4230696 to 4231658	m	31%	gb AAF97407.1 (AY004319) photopexin A [Photorhabdus luminescens]	SEQ ID n-2648

Contig9 from 4240182 to 4241393	gb AAF63418.1 (AF146029) putative multidrug- resistance protein [Aeromonas-- hydrophila]	p 43%	SEQ ID n-2614
Contig9 from 4241673 to 4242113	pir C82498 conserved hypothetical protein VCA0108 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96022.1 (AE004353) conserved hypothetical protein [Vibrio cholerae]	p No Hits found	#N/A
Contig9 from 4243020 to 4244552	pir D83634 hypothetical protein PA0079 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03469.1 AE004447_2 (AE004447) hypothetical protein [Pseudomonas aeruginosa]	p 57%	SEQ ID n-2603
Contig9 from 4244569 to 4245930	pir F82499 hypothetical protein VCA0115 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96029.1 (AE004353) hypothetical protein [Vibrio cholerae]	p 41%	SEQ ID n-2596
Contig9 from 4245973 to 4246617	pir B82819 outer membrane protein XF0343 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF83153.1 AE003886_12 (AE003886) outer membrane protein [Xylella fastidiosa]	p 36%	SEQ ID n-2586
Contig9 from 4246634 to 4248310	pir E83349 probable ClpA/B-type proteinase PA2371 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05759.1 AE004663_5 (AE004663) probable ClpA/B-type protease [Pseudomonas aeruginosa]	p 11%	SEQ ID n-2578
Contig9 from 4248559 to 4251240	pir C83458 conserved hypothetical protein PA1511 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04900.1 AE004579_12 (AE004579) conserved hypothetical protein [Pseudomonas aeruginosa]	p 60%	SEQ ID n-2569
Contig9 from 4251237 to 4253615		p 41%	SEQ ID n-2559

SEQ ID n° 9583	PL-331.1	Contig9 from 4253626 to 4254666	p	No Hits found		SEQ ID n-2554
SEQ ID n° 9584	PL-330.1	Contig9 from 4254666 to 4257266	p	No Hits found		SEQ ID n-2546
SEQ ID n° 9585	PL-329.1	Contig9 from 4257263 to 4258273	p	No Hits found		SEQ ID n-2538
SEQ ID n° 9586	PL-328.1	Contig9 from 4258351 to 4259340	p	No Hits found		SEQ ID n-2527
SEQ ID n° 9587	PL-327.1	Contig9 from 4259526 to 4260194	p	No Hits found		SEQ ID n-2519
SEQ ID n° 9588	PL-5042.1	Contig9 from 4260222 to 4260497	p	38%	pir H83457 hypothetical protein PA1508 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04897.1 AE004579_9 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 9589	PL-326.1	Contig9 from 4260500 to 4261675	p	No Hits found		SEQ ID n-2509
SEQ ID n° 9590	PL-325.1	Contig9 from 4261668 to 4265027	p	26%	pir G83637 hypothetical protein PA0077 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03467.1 AE004446_15 (AE004446) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2500
SEQ ID n° 9591	PL-5044.1	Contig9 from 4265440 to 4265628	p	No Hits found		#N/A
SEQ ID n° 9592	PL-5045.1	Contig9 from 4265629 to 4265799	p	No Hits found		#N/A

SEQ ID n~2547

SEQ ID n~2473

SEQ ID n~2462

SEQ ID n~2451

#N/A

SEQ ID n~2439

SEQ ID n~2428

#N/A

SEQ ID n°	Contig9 from	P	No Hits found
593	4265772 to 4266263		
PL-3301.1			
594	4268970		
PL-322.1			
595	4268967 to 4269575		
PL-321.1			
596	4269576 to 4270958		
PL-320.1			
597	4271128 to 4271451		
PL-5049.1			
598	4271528 to 4272529		
PL-319.1			
599	4272740 to 4273483		
PL-318.1			
9600	4273521 to 4273646		
PL-5050.1			

1013

Contig9 from: SEQ ID n° 9601 PL-317.1 4273649 to 4275247	p	38%	pir B83439 hypothetical protein PA1656 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05045.1 AE004593.7 (AE004593) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2417
Contig9 from: SEQ ID n° 9602 PL-315.1 4275326 to 4277092	p	48%	pir A82499 hypothetical protein VCA0110 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96024.1 (AE004353) hypothetical protein [Vibrio cholerae]	SEQ ID n-2395
Contig9 from: SEQ ID n° 9603 PL-314.1 4277092 to 4278132	p	40%	gb AAG54528.1 AE005198.9 (AE005198)_Z0259 gene product [Escherichia coli O157:H7]	SEQ ID n-2384
Contig9 from: SEQ ID n° 9604 PL-3302.1 4278113 to 4278649	p	27%	pir B83437 hypothetical protein PA1666 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05055.1 AE004594.7 (AE004594) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2548
Contig9 from: SEQ ID n° 9605 PL-5051.1 4278653 to 4279087	p	31%	pir B83439 hypothetical protein PA1659 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05048.1 AE004593.10 (AE004593) hypothetical protein [Pseudomonas aeruginosa]	#N/A
Contig9 from: SEQ ID n° 9606 PL-313.1 4279139 to 4280518	p	48%	gb AAG54518.1 AE005197.7 (AE005197) Z0249 gene product [Escherichia coli O157:H7]	SEQ ID n-2373
Contig9 from: SEQ ID n° 9607 PL-3304.1 4280704 to 4281198	p	22%	sp P33562 T2BB_BACSU TYPE II RESTRICTION ENZYME BSUBI (ENDONUCLEASE BSUBI) (R.BSUBI) pir S35516 type II site-specific deoxyribonuclease (EC 3.1.21.4) BsuBI - Bacillus subtilis gb AA18170.1 (Z01541) restriction endonuclease [Bacillus subtilis]	SEQ ID n-2549
Contig9 from: SEQ ID n° 9608 PL-5052.1 4281718 to 4282131	p	29%	gb AAG57124.1 AE005432.5 (AE005432) Z3230 gene product [Escherichia coli O157:H7]	#N/A

1014

SEQ ID n° 9609	PL-5053.1	Contig9 from 4282222 to 4282539	P	38%	gb AAG57125.1 AE005432_6 (AE005432) Z3231 gene product [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9610	PL-312.2	Contig9 from 4283514 to 4284290	P	62%	pir S35196 hypothetical protein 3 - Saccharopolyspora hirsuta gb AA26487.1 (M98258) polyketide reductase [Saccharopolyspora hirsuta]	SEQ ID n-2362
SEQ ID n° 9611	PL-311.1	Contig9 from 4284293 to 4285006	P	33%	gb AAD10395.1 (U46488) NrpG [Proteus mirabilis]	SEQ ID n-2351
SEQ ID n° 9612	PL-310.1	Contig9 from 4284999 to 4285814	P	57%	gb AAF01818.1 AF187532_14 (AF187532) putative polyketide cyclase [Streptomyces nogalater] sp Q02578 KAS1_STRCN PUTATIVE POLYKETIDE BETA- KETOACYL SYNTHASE 1 pir JCI210 polyketide beta- ketoacyl synthase (EC 2.3.1.-) chain 1 - Streptomyces cyaneus gb AA26726.1 (M33704) cura protein [Streptomyces curacoi] emb CAA44380.1 (X62518) beta-ketoacyl synthase [Streptomyces cyaneus] prf 1807129B cura gene [Streptomyces cyaneus] pir H82776 3-oxoacyl-[ACP] synthase II XF0673 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF83483.1 AE003911_5 (AE003911) 3-oxoacyl-[ACP] synthase II [Xylella fastidiosa]	SEQ ID n-2340
SEQ ID n° 9613	PL-309.1	Contig9 from 4286466 to 4287752	P	59%	pir H82776 3-oxoacyl-[ACP] synthase II XF0673 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF83483.1 AE003911_5 (AE003911) 3-oxoacyl-[ACP] synthase II [Xylella fastidiosa]	SEQ ID n-2328
SEQ ID n° 9614	PL-308.1	Contig9 from 4287745 to 4288860	P	34%	dbj BAB05725.1 (AP001514) long-chain acyl-CoA synthetase (ligase) [Bacillus halodurans]	SEQ ID n-2317
SEQ ID n° 9615	PL-5054.1	Contig9 from 4288895 to 4289143	P	No Hits found		#N/A
SEQ ID n° 9616	PL-307.1	Contig9 from 4289167 to 4290714	P	44%	gb AAF00205.1 AF164960_1 (AF164960) cyclase [Streptomyces fradiae]	SEQ ID n-2306
SEQ ID n° 9617	PL-306.1	Contig9 from 4290714 to 4292156	P	27%		SEQ ID n-2295

SEQ ID n° 9618	PL-305.1	Contig9 from 4292176 to 4293330	p 23%	pir T30216 hypothetical protein z - Streptomyces hygroscopicus emb CAA60450.1 (X86780) orfZ [Streptomyces hygroscopicus] pir E75566 probable repressor protein - Deinococcus radiodurans (strain R1) gb AA09645.1 AE001868_7 (AE001868) repressor protein, putative [Deinococcus radiodurans]	SEQ ID n-2284
SEQ ID n° 9619	PL-304.1	Contig9 from 4294283 to 4294984	p 27%		SEQ ID n-2273
SEQ ID n° 9620	PL-5055.1	Contig9 from 4295628 to 4295972	m No Hits found	#N/A	
SEQ ID n° 9621	PL-303.1	Contig9 from 4297001 to 4298104	p 20%	sp P53554 BIOI_BACSU BIOTIN BIOSYNTHESIS; CYTOCHROME P450-LIKE ENZYME pir G69594 cytochrome P450 bioI - Bacillus subtilis gb AAB17462.1 (U51868) cytochrome P450-like enzyme [Bacillus subtilis] gb AAC00266.1 (AF008220) cytochrome P450 enzyme [Bacillus subtilis] emb CAB14997.1 -(Z99119) cytochrome P450-like enzyme [Bacillus subtilis] gb AAC38630.1 (AF047028) insecticidal toxin complex protein Tccc [Photorhabdus luminescens]	SEQ ID n-2262
SEQ ID n° 9622	PL-302.1	Contig9 from 4298421 to 4301318	m 59%	pir S28478 rfbN protein - Vibrio cholerae emb CAA42144.1 (X59554) rfbN [Vibrio cholerae] prf 2203284D rfbN gene [Vibrio cholerae] pir A42951 fatty-acyl-CoA reductase (EC 1.2.1.-) luxC - Xenorhabdus luminescens gb AAD05355.1 (M90092) fatty acid reductase [Xenorhabdus luminescens]	SEQ ID n-2251
SEQ ID n° 9623	PL-301.1	Contig9 from 4303031 to 4304161	p 38%		SEQ ID n-2241
SEQ ID n° 9624	PL-300.1	Contig9 from 4304163 to 4306568	p 17%		SEQ ID n-2230
SEQ ID n° 9625	PL-299.1	Contig9 from 4306598 to 4307869	p 43%	dbj BAA75335.1 (AB011837) ORF12 [Bacillus halodurans]	SEQ ID n-2217
SEQ ID n° 9626	PL-298.1	Contig9 from 4307866 to 4308789	p 19%	gb AAC44553.1 (U34346) unknown [Paracoccus denitrificans]	SEQ ID n-2206

Contig9 from SEQ ID n° 9627 PL-296.1 4310851	p 27%	pir A56394 pyocin S3 - Pseudomonas aeruginosa (strain P12) emb CAA54958.1 (X77996) killer protein of pyocin S3 [Pseudomonas aeruginosa] SEQ ID n-2184
Contig9 from SEQ ID n° 9628 PL-3306.1 4311306	p 43%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] SEQ ID n-2550
Contig9 from SEQ ID n° 9629 PL-3307.1 4311882	p 35%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] SEQ ID n-2551
Contig9 from SEQ ID n° 9630 PL-3308.1 4312458	p 32%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] SEQ ID n-2552
Contig9 from SEQ ID n° 9631 PL-3309.1 4313027	p 45%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] SEQ ID n-2553
Contig9 from SEQ ID n° 9632 PL-3310.1 4313604	p 54%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] SEQ ID n-2555
Contig9 from SEQ ID n° 9633 PL-3311.1 4314163	p 31%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] SEQ ID n-2556
Contig9 from SEQ ID n° 9634 PL-3312.1 4314739	p 34%	pir B56394 pyocin S3 immunity protein - Pseudomonas aeruginosa (strain P12) emb CAA54959.1 (X77996) immunity protein of pyocin S3 [Pseudomonas aeruginosa] SEQ ID n-2557
Contig9 from SEQ ID n° 9635 PL-295.1 4318067	p 93%	gb AAC38628.1 (AF047028) insecticidal toxin complex protein TccA [Photobacterium luminescens] SEQ ID n-2173

SEQ ID n° 9636	PL-294.1	Contig9 from 4319162 to 4322856	p	96%	gb AAC38629.1 (AF047028) insecticidal toxin complex protein TccB [Photorhabdus luminescens]	SEQ ID n-2162
SEQ ID n° 9637	PL-293.1	Contig9 from 4322990 to 4326121	p	96%	gb AAC38630.1 (AF047028) insecticidal toxin complex protein TccC [Photorhabdus luminescens]	SEQ ID n-2152
SEQ ID n° 9638	PL-5065.1	Contig9 from 4326202 to 4326357	m	69%	gb AAC38631.1 (AF047028) insecticidal toxin complex protein TccZ [Photorhabdus luminescens]	#N/A
SEQ ID n° 9639	PL-5066.1	Contig9 from 4326445 to 4326747	p	No Hits found		#N/A
SEQ ID n° 9640	PL-5067.1	Contig9 from 4326741 to 4327076	p	73%	gb AAG55308.1 (AE005273_1 (AE005273) unknown in ISEC8 [Escherichia coli O157:H7])	#N/A
SEQ ID n° 9641	PL-292.1	Contig9 from 4327140 to 4328645	p	53%	gb AAG55717.1 (AE005309_7 (AE005309) unknown in ISEC8 [Escherichia coli O157:H7]) ref NP_053113.1 orf51 [Escherichia coli] dbj BAAB4886.1 (AB024946) orf51 [Escherichia coli]	SEQ ID n-2141
SEQ ID n° 9642	PL-5069.1	Contig9 from 4328684 to 4328950	m	79%	gb AAC38631.1 (AF047028) insecticidal toxin complex protein TccZ [Photorhabdus luminescens]	#N/A
SEQ ID n° 9643	PL-291.2	Contig9 from 4329677 to 4330780	p	58%	sp P37535 YAAN_BACSU HYPOTHETICAL 43.8 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION pir S66056 yaan protein - Bacillus subtilis dbj BAAB05262.1 (D26185) unknown [Bacillus subtilis] emb CAB11802.1 (Z99104) similar to toxic cation resistance [Bacillus subtilis]	#N/A
SEQ ID n° 9644	PL-290.1	Contig9 from 4330841 to 4331890	p	No Hits found		SEQ ID n-2119
SEQ ID n° 9645	PL-3319.1	Contig9 from 4332262 to 4332690	m	62%	pir F75337 transposase - Deinococcus radiodurans (strain R1) gb AAFL11477.1 (AE002031_6 (AE002031) transposase [Deinococcus radiodurans])	SEQ ID n-2558

SEQ ID n° 9646 PL-289.1	Contig9 from 4333081 to 4334163	p 36%	gb AA012476.1 AC037197_1 (AC037197) Putative histidine decarboxylase [Oryza sativa]	SEQ ID n-2107
SEQ ID n° 9647 PL-3320.1	Contig9 from 4334232 to 4334660	p 62%	pir F75337 transposase - Deinococcus radiodurans (strain R1) gb AA011477.1 AE002031_6 (AE002031) transposase [Deinococcus radiodurans]	SEQ ID n-2560
SEQ ID n° 9648 PL-3321.1	Contig9 from 4334762 to 4335220	p 39%	emb CAA70530.1 (Y09356) pyridoxal-dependent histidine decarboxylase [Pseudomonas fluorescens]	SEQ ID n-2561
SEQ ID n° 9649 PL-288.1	Contig9 from 4335562 to 4336176	m 60%	pir T36373 hypothetical protein SCE94.13 - Streptomyces coelicolor emb CA040862.1 (AL049628) hypothetical protein [Streptomyces coelicolor A3(2)]	SEQ ID n-2096
SEQ ID n° 9650 PL-3322.1	Contig9 from 4336438 to 4336902	p 71%	pir T36372 probable asnC-family transcription regulator - Streptomyces coelicolor emb CA010328.1 (AJ131213) putative transcriptional regulator [Streptomyces coelicolor A3(2)] emb CA040861.1 (AL049628) putative asnC-family transcriptional regulator [Streptomyces coelicolor A3(2)]	SEQ ID n-2562
SEQ ID n° 9651 PL-5072.1	Contig9 from 4337118 to 4337408	m No Hits found		#N/A
SEQ ID n° 9652 PL-287.1	Contig9 from 4337926 to 4339593	p No Hits found		SEQ ID n-2085
SEQ ID n° 9653 PL-286.1	Contig9 from 4340154 to 4341179	m 21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-2074
SEQ ID n° 9654 PL-285.1	Contig9 from 4341677 to 4345360	p 45%	dbj BAB18040.1 (AB033991) BtrA [Bacillus circulans]	SEQ ID n-2064
SEQ ID n° 9655 PL-5077.1	Contig9 from 4345379 to 4345732	p No Hits found		#N/A

SEQ ID n° 9656	PL-5079.1	Contig9 from 4345737 to 4345853	P	No Hits found	#N/A
SEQ ID n° 9657	PL-5080.1	Contig9 from 4345883 to 4346320	P	No Hits found	#N/A
SEQ ID n° 9658	PL-284.1	Contig9 from 4346329 to 4348182	P	42%	pir S75352 ABC-type transport protein slr2019 - Synechocystis sp. (strain PCC 6803) dbj BAAL7266.1 (D90904) ABC transporter [Synechocystis sp.] SEQ ID n-2053
SEQ ID n° 9659	PL-283.1	Contig9 from 4348184 to 4348900	P	39%	dbj BAA25511.1 (AB011157) KIAA0585 protein [Homo sapiens] SEQ ID n-2042
SEQ ID n° 9660	PL-282.1	Contig9 from 4348897 to 4350156	P	25%	pir D82414 agmatinase VCA0814 [Imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96712.1 (AE004409) agmatinase [Vibrio cholerae] SEQ ID n-2032
SEQ ID n° 9661	PL-281.1	Contig9 from 4350900 to 4360028	P	7%	emb CAC19891.1 (AJ011301) toxin B [Clostridium difficile] SEQ ID n-2021
SEQ ID n° 9662	PL-5089.1	Contig9 from 4360068 to 4360391	P	No Hits found	#N/A
SEQ ID n° 9663	PL-278.1	Contig9 from 4360973 to 4361566	m	72%	pir S56363 divalent cation tolerance protein cutA3, inner membrane - Escherichia coli gb AA97034.1 (U14003) yJdC [Escherichia coli] emb CAA85376.1 (Z36905) 199 residue polypeptide [Escherichia coli] gb AAC77095.1 (AE000486) orf, hypothetical protein [Escherichia coli K12] gb AA059334.1 AE005647_3 (AE005647) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-1987

Contig9 from	4361563 to	m	72%	4363290	Seq ID n° 9664	PL-277.1	pir S56364 inner membrane copper tolerance protein cycZ - Escherichia coli...gb AA97035.1 (U14003) cycZ [Escherichia coli] gb AAC77096.1 (AE000486) thiol:disulfide interchange protein; copper tolerance [Escherichia coli K12]	SEQ ID n-1976
Contig9 from	4363475 to	m	90%	4364776	Seq ID n° 9665	PL-276.1	sp P04539 DCUA_ECOLI ANAEROBIC C4-DICARBOXYLATE TRANSPORTER DCUA pir S56366 dicarboxylate membrane-transporter protein A - Escherichia coli pir Q0EC94 dicarboxylate membrane-transporter protein A - Escherichia coli emb CAA56259.1 (X79887) dicarboxylate membrane-transporter protein [Escherichia coli] gb AA97037.1 (U14003) genA [Escherichia coli] gb AAB30213.1 GenA=integral inner-membrane protein involved in anaerobic C4-dicarboxylic acid-transport [Escherichia coli, K12, Peptide, 433 aa] gb AAC77098.1 (AE000486) anaerobic dicarboxylate transport [Escherichia coli K12] gb AGS9337.1 AE005647_6 (AE005647) anaerobic dicarboxylate transport [Escherichia coli O157:H7]	SEQ ID n-1965
Contig9 from	4364917 to	m	91%	4366341	Seq ID n° 9666	PL-275.1	sp P33109 ASPA_SERMA ASPARTATE AMMONIA-LYASE (ASPARTASE) pir JS0764 aspartate ammonia-lyase (EC 4.3.1.1) - Serratia marcescens dbj BAA02518.1 (D13252) aspartase [Serratia marcescens]	SEQ ID n-1954
Contig9 from	4366719 to	p	69%	4367207	Seq ID n° 9667	PL-3324.1	sp P37147 FXSA_ECOLI FXSA PROTEIN (SUPPRESSOR OF F EXCLUSION OF PHAGE T7) gb AAB36686.1 (U78484) FXSA [Escherichia coli]	SEQ ID n-2563

[illegible]

1024

SEQ ID n°	9682	PL-267.1	Contig9 from 4382115 to 4383092	P	83%	pir S56383 lysine--tRNA ligase (EC 6.1.1.6) genx - Escherichia coli gb AAA97054.1 (U14003) lysyl-tRNA synthetase analog [Escherichia coli] gb AAC77115.1 (AE000488) putative lysyl-tRNA synthetase [Escherichia coli K12] gb AAG59356.1 AE005649_1 (AE005649) putative lysyl-tRNA synthetase [Escherichia coli O157:H7]	SEQ ID n-1865
SEQ ID n°	9683	PL-266.1	Contig9 from 4383142 to 4384218	M	84%	gb AAG57370.1 AE005456_7 (AE005456) glycerophosphodiester phosphodiesterase, periplasmic [Escherichia coli O157:H7]	SEQ ID n-1855
SEQ ID n°	9684	PL-265.1	Contig9 from 4384398 to 4385750	M	91%	gb AAG57371.1 AE005456_8 (AE005456) sn-glycerol- 3-phosphate permease [Escherichia coli O157:H7]	SEQ ID n-1846
SEQ ID n°	9685	PL-3327.1	Contig9 from 4386254 to 4386685	P	55%	ref NP_052313.1 ORF C8 [Ralstonia solanacearum] ---dbj BAA32221.1 (AB015669) ORF C8 [Ralstonia solanacearum] pir B82736 hemolysin-type calcium binding protein XF1011 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF83821.1 AE003938_12 (AE003938) hemolysin- type calcium binding protein [Xylella fastidiosa]	SEQ ID n-2566
SEQ ID n°	9686	PL-264.1	Contig9 from 4387112 to 4388269	P	30%	gb AAF78381.1 AC069551_14 (AC069551) T10022.22 [Arabidopsis thaliana]	SEQ ID n-1836
SEQ ID n°	9687	PL-3328.1	Contig9 from 4388847	P	29%	sp P45511 GLDA_CITFR GLYCEROL DEHYDROGENASE (GLDH) gb AAB48844.1 (U09771) glycerol dehydrogenase [Citrobacter freundii]	SEQ ID n-2567
SEQ ID n°	9688	PL-263.1	Contig9 from 4389038 to 4390138	M	72%	gb AAG57917.1 AE005508_8 (AE005508) L- fuculokinase [Escherichia coli O157:H7]	SEQ ID n-1825
SEQ ID n°	9689	PL-5108.1	Contig9 from 4390335 to 4390577	P	39%		#N/A

SEQ ID n° 9690	PL-5109.1	Contig9 from 4390711 to 4390959	p 60%	sp P11553 FUCK_ECOLI_L-FUCULOKINASE_pir KIBCFK fucokinase (EC 2.7.1.52) - Escherichia coli emb CAA33128.1 (X15025) fuck ORF (AA 1-482) [Escherichia coli] gb AAB40453.1 (U29581) L- fuculose kinase [Escherichia coli] gb AAC75845.1 (AE000364) L-fuculokinase [Escherichia coli K12]	#N/A
SEQ ID n° 9691	PL-5110.1	Contig9 from 4391089 to 4391268	m No Hits found		#N/A
SEQ ID n° 9692	PL-3329.1	Contig9 from 4391316 to 4391768	p 80%	gb AAG57919.1 AE005508_10 (AE005508) positive regulator of the fuc operon [Escherichia coli O157:H7]	SEQ ID n-2558
SEQ ID n° 9693	PL-262.1	Contig9 from 4391765 to 4392649	m 59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]	SEQ ID n-2814
SEQ ID n° 9694	PL-261.1	Contig9 from 4392946 to 4393620	m 71%	gb AAG58580.1 AE005570_7 (AE005570) orf, hypothetical protein [Escherichia coli O157:H7] sp P37618 YHP_ECOLI_HYPOTHETICAL_9.1_KDA PROTEIN IN FTSY-NIKA INTERGENIC REGION pir S47689 hypothetical 9.1K protein (ftsY-nika intergenic region) - Escherichia coli gb AAB18445.1 (U00039) No definition line found [Escherichia coli] gb AAC76495.1 (AE000423) orf, hypothetical protein [Escherichia coli K12] gb AAG58579.1 AE005570_6 (AE005570) orf, hypothetical protein [Escherichia coli O157:H7] emb CAA04762.1 (AJ001437) putative P-type cation-translocating membrane ATPase [Proteus mirabilis]	SEQ ID n-2803
SEQ ID n° 9695	PL-5111.1	Contig9 from 4393805 to 4394059	p 80%		#N/A
SEQ ID n° 9696	PL-260.1	Contig9 from 4394209 to 4396494	m 76%		SEQ ID n-3792

Contig9 from 4396639 to m 4397265	SEQ ID n° 9697 PL-259.1	69%	m	sp P37616 YHHN_ECOLI_HYPOTHETICAL_23-8_KD PROTEIN IN FTSY-NIKA INTERGENIC REGION (O208) pir [S47687 hypothetical protein o208 .. Escherichia coli gb AAB18443.1 (U00039) No definition line found [Escherichia coli] gb AAC76493.1 (AE000422) putative enzyme [Escherichia coli K12]	SEQ ID n-1782			#N/A
Contig9 from 4397536 to m 4397817	SEQ ID n° 9698 PL-5113.1	64%	m	pir [S47685 hypothetical protein o130 .. Escherichia coli gb AAB18441.1 (U00039) overlaps previous ORF, probably uses downstream start [Escherichia coli]				
Contig9 from 4397841 to p 4398425	SEQ ID n° 9699 PL-258.1	74%	m	gb AAG58574.1 AE005570_1 (AE005570) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-1771			
Contig9 from 4398585 to p 4399859	SEQ ID n° 9700 PL-257.1	85%	p	gb AAG58573.1 AE005569_13 (AE005569) cell division membrane protein [Escherichia coli O157:H7]	SEQ ID n-1761			
Contig9 from 4399866 to p 4400531	SEQ ID n° 9701 PL-256.1	89%	p	sp P10115 FTSE_ECOLI_CELL_DIVISION_ATP-BINDING PROTEIN FTSE pir CECFE cell division ATP- binding protein ftse - Escherichia coli emb CAA27985.1 (X04398) ORF 2 (AA 1-222); 25 kD (put. ftseB) [Escherichia coli] gb AAB18438.1 (U00039) CG Site No. 736 [Escherichia coli] gb AAC76488.1 (AE000422) ATP-binding component of a membrane-associated complex involved in cell division [Escherichia coli K12] gb AAG58572.1 AE005569_12 (AE005569) ATP-binding component of a membrane-associated complex involved in cell division [Escherichia coli O157:H7]	SEQ ID n-1751			
Contig9 from 4400524 to p 4401498	SEQ ID n° 9702 PL-255.1	77%	p	gb AAG58571.1 AE005569_11 (AE005569) cell division membrane protein [Escherichia coli O157:H7]	SEQ ID n-1740			
Contig9 from 4401628 to m 4401876	SEQ ID n° 9703 PL-5115.1	No Hits found	m					#N/A

SEQ ID n° 9704	PL-254.1	Contig9 from 4401935 to 4402792	p	94%	sp P50508 RP32.ENTCL RNA POLYMERASE SIGMA-32 FACTOR_pir S60165-transcription initiation factor sigma_32 - Enterobacter cloacae. dbj BAA09440.1 (D50829) sigma-32 homolog [Enterobacter cloacae] SEQ ID n-1729
SEQ ID n° 9705	PL-253.1	Contig9 from 4402889 to 4404028	p	71%	sp P42100 GRK BACSU GLYCERATE KINASE pir A70071 conserved hypothetical protein yxaa Bacillus subtilis dbj BAA21580.1 (AB005554) homologs are found in E. coli and H. influenzae; see SWISS_PROT ACC#: P42100 [Bacillus subtilis] emb CAB16041.1 (Z99124) similar to hypothetical proteins [Bacillus subtilis] SEQ ID n-1718
SEQ ID n° 9706	PL-5116.1	Contig9 from 4404016 to 4404414	m	56%	gb AAG58566.1 AE005569_6 (AE005569) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 9707	PL-252.1	Contig9 from 4404794 to 4405906	p	82%	pir BLECL leucine-specific binding protein precursor - Escherichia coli gb AAB18433.1 (U00039) CG Site No. 550 [Escherichia coli] gb AAC76483.1 (AE000421) high-affinity leucine- specific transport system; periplasmic binding protein [Escherichia coli K12] SEQ ID n-1707
SEQ ID n° 9708	PL-251.1	Contig9 from 4405968 to 4406894	p	87%	pir S47676 livH protein - Escherichia coli pir QRECLH leucine transport protein livH - Escherichia coli gb AAB18432.1 (U00039) CG Site No. 552 [Escherichia coli] gb AAC76482.1 (AE000421) high-affinity branched-chain amino acid transport system; membrane component [Escherichia coli K12] gb AAG58564.1 AE005569_4 (AE005569) high- affinity branched-chain amino acid transport system; membrane component [Escherichia coli O157:H7] SEQ ID n-1696
SEQ ID n° 9709	PL-250.1	Contig9 from 4406891 to 4408168	p	80%	gb AAG58563.1 AE005569_3 (AE005569) high- affinity branched-chain amino acid transport [Escherichia coli O157:H7] SEQ ID n-1685

1028

SP P30293 LIVG_SALTY HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BENDING			
PROTEIN LIVG (LIV-I, PROTEIN G) pir JH0670_high			
SEQ ID n° 9710	PL-249.1	p 82%	affinity branched-chain amino acid transport Liv
I system LivF protein - Salmonella			
Contig9 from			
4408165 to			
4408938			
typhimurium dbj BAA02131.1 (D12589) LivF			
protein [Salmonella typhimurium]			
SEQ ID n° 9711	PL-248.1	p 84%	gb AAG58561.1 AE005569_1 (AE005569) ATP-binding component of leucine transport [Escherichia coli O157:H7]
SEQ ID n-2673			
Contig9 from			
4408941 to			
4409642			
Contig9 from			
4410745 to			
4411146			
Contig9 from			
4411176 to			
4412435			
SEQ ID n° 9712	PL-5118.1	p No Hits found	gb AAC63079.1 (AF035423) putative juvenile hormone esterase [Leptinotarsa decemlineata]
SEQ ID n-2662			
Contig9 from			
4412695 to			
4413474			
SEQ ID n° 9714	PL-246.1	m 62%	pir C82481 transcription-regulator AraC/XylS family VCA0266 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96177.1 (AE004366) transcriptional regulator, AraC/XylS family [Vibrio cholerae]
SEQ ID n-2651			
Contig9 from			
4413578 to			
4414741			
SEQ ID n° 9715	PL-245.1	p 64%	pir D82481 multidrug resistance protein D VCA0267 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96178.1 (AE004366) multidrug resistance protein D [Vibrio cholerae]
SEQ ID n-2629			

#N/A

SEQ ID n-2651

SEQ ID n-2640

SEQ ID n-2629

SEQ ID n° 9719	PL-242.1	Contig9 from 4417721 to 4419172	m	85%	pir D65118 pantothenate permease [validated] - Escherichia coli -gb AA58061.1 (U18997) pantothenate permease [Escherichia coli] gb AAC76290.1 (AE00404) sodium/pantothenate symporter [Escherichia coli K12] gb AAG58386.1 AE005553 8 (AE005553) sodium/pantothenate symporter [Escherichia coli O157:H7]	SEQ ID n~1597
SEQ ID n° 9720	PL-5121.1	Contig9 from 4419156 to 4419398	m	75%	gb AAG58385.1 AE005553_7 (AE005553) orf, hypothetical protein-[Escherichia coli O157:H7] pir F81419 probable efflux protein CJ0035C [imported] - Campylobacter jejuni (strain NCTC 11168) emb CAB72528.1 (AL139074) putative efflux protein [Campylobacter jejuni]	#N/A
SEQ ID n° 9721	PL-241.1	Contig9 from 4420093 to 4421280	p	47%	gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae] pir B70567 probable mhpE protein - Mycobacterium tuberculosis (strain H37RV) emb CAB08693.1 (Z95390) mhpE [Mycobacterium tuberculosis]	SEQ ID n~1575
SEQ ID n° 9722	PL-5122.1	Contig9 from 4421319 to 4421492	p	No Hits found		SEQ ID n~1563
SEQ ID n° 9723	PL-240.1	Contig9 from 4421600 to 4423216	p	29%		SEQ ID n~1553
SEQ ID n° 9724	PL-239.1	Contig9 from 4423222 to 4424031	p	36%		SEQ ID n~1542
SEQ ID n° 9725	PL-238.1	Contig9 from 4424028 to 4424771	p	No Hits found		SEQ ID n~1532
SEQ ID n° 9726	PL-237.1	Contig9 from 4424768 to 4426933	p	36%	sp Q48806 DLPA_LEGPN DLPA PROTEIN pir S61390 dlpA protein - Legionella pneumophila gb AAA79904.1 (U07940) DlpA [Legionella pneumophila]	
SEQ ID n° 9727	PL-236.1	Contig9 from 4426855 to 4427610	p	55%	sp Q48806 DLPA_LEGPN DLPA PROTEIN pir S61390 dlpA protein - Legionella pneumophila gb AAA79904.1 (U07940) DlpA [Legionella pneumophila]	

Contig9 from	4427607 to	p	35%	<p>pir C69122 hypothetical protein MTH1911 - Methanobacterium thermoautotrophicum (strain Delta H) gb AAB8371.1 (AE000942) unknown [Methanothermobacter thermoautotrophicus] SEQ ID n-1521 ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis] SEQ ID n-1510</p>
Contig9 from	4429534 to	p	36%	<p>sp P24182 ACCC_ECOLI BIOTIN CARBOXYLASE (A SUBUNIT OF ACETYL-COA CARBOXYLASE (ACC) pir JS0632 acetyl-CoA carboxylase (EC 6.4.1.2) biotin carboxylase chain [validated] - Escherichia coli pdb 1DV1 A Chain A, Structure Of Biotin Carboxylase (Apo) pdb 1DV1 B Chain B, Structure Of Biotin Carboxylase-(Apo) pdb 1BNC A Chain A, Mol_id: 1; Molecule: Biotin Carboxylase; Chain: A, B; Ec: 6.3.4.14 pdb 1BNC B Chain B, Mol_id: 1; Molecule: Biotin Carboxylase; Chain: A, B; Ec: 6.3.4.14 gb AA23409.1 (M80458) biotin carboxylase [Escherichia coli] gb AA23746.1 (M83198) biotin carboxylase [Escherichia coli] gb AA58059.1 (U18997) biotin carboxylase [Escherichia coli] gb AAC76288.1 (AE000404) acetyl CoA carboxylase, biotin carboxylase subunit [Escherichia coli K12] SEQ ID n-1498</p>
Contig9 from	4431061 to	m	94%	<p>SEQ ID n° 9728 PL-235.1</p>
Contig9 from	4432410			<p>SEQ ID n° 9729 PL-234.1</p>
Contig9 from	4432410			<p>SEQ ID n° 9730 PL-232.1</p>

SEQ ID n° 9731	PL-3331.1	Contig9 from 4432423 to 4432893	m	71%	sp P02905 BCCP_ECOLI BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (BCCP) pir BKEC9 acetyl-CoA carboxylase (EC 5.4.1.2) biotin carboxyl carrier protein [validated] - Escherichia coli emb CAA32933.1 (X14825) Acetyl-CoA carboxylase (AA 1 - 156) [Escherichia coli] gb AA23408.1 (M80458) biotin carboxyl carrier protein [Escherichia coli] gb AA23744.1 (M32214) biotin carboxyl carrier protein (fabE) [Escherichia coli] gb AA23745.1 (M83198) biotin carboxyl carrier protein [Escherichia coli] gb AA58058.1 (U18997) biotin carboxyl carrier protein [Escherichia coli] gb AAC76287.1 (AE000404) acetylCoA carboxylase, BCCP subunit; carrier of biotin [Escherichia coli K12] gb AA58383.1 AE005553_5 (AE005553) acetylCoA carboxylase, BCCP subunit; carrier of biotin [Escherichia coli O157:H7] gb AAD10235.1 (AF011408) type II 3- dehydroquinase [Aeromonas salmonicida subsp. salmonicida] sp P26646 YHDH_ECOLI PROTEIN YHDH pir J50688 hypothetical 35K protein (fabE 5' region) - Escherichia coli gb AA23407.1 (M80458) 35 kDa protein [Escherichia coli] gb AA58056.1 (U18997) ORF_0324; orf of ECOACOAC [Escherichia coli] gb AAC76285.1 (AE000404) putative dehydrogenase [Escherichia coli K12] pir BVECEB rod shape-determining protein envB - Escherichia coli gb AA58054.1 (U18997) frameshifts changes start relative to ECOMREB [Escherichia coli] gb AAC76283.1 (AE000404) regulator of ftsI, penicillin binding protein 3, septation function [Escherichia coli K12]
SEQ ID n° 9732	PL-3332.1	Contig9 from 4432923 to 4433375	m	74%	SEQ ID n-3570 SEQ ID n-2571
SEQ ID n° 9733	PL-231.1	Contig9 from 4433585 to 4434562	m	71%	
SEQ ID n° 9734	PL-230.1	Contig9 from 4435064 to 4436167	p	92%	SEQ ID n-2478 SEQ ID n-2467

SEQ ID n° 9735	PL-229.1	Contig9 from 4436279 to 4437313	p 75%	gb AAG58377.1 AE005552_7 (AE005552) rod shape- determining protein [Escherichia coli O157:H7] SEQ ID n-2455
SEQ ID n° 9736	PL-3333.1	Contig9 from 4437313 to 4437801	p 82%	sp P16927 MRD_ECOLI ROD SHAPE-DETERMINING PROTEIN MRD pir JV0060 rod shape-determining protein mred - Escherichia coli gb AAA24156.1 (M31792) Mred protein (gtg start codon) [Escherichia coli] gb AAAS8052.1 (U18997) mred [Escherichia coli] gb AAC76281.1 (AE000404) rod shape-determining protein [Escherichia coli K12] gb AAG58376.1 AE005552_6 (AE005552) rod shape-determining protein [Escherichia coli O157:H7] SEQ ID n-2572
SEQ ID n° 9737	PL-3334.1	Contig9 from 4437967 to 4438554	p 71%	gb AAAS8051.1 (U18997) ORF_f217; orfE of ECMRD, uses 2nd start [Escherichia coli] SEQ ID n-2573
SEQ ID n° 9738	PL-228.1	Contig9 from 4438551 to 4440020	p 92%	pir A65117 cytosolic axial filament protein cafA - Escherichia coli gb AAAS8050.1 (U18997) ORF_f495; orfF of ECMRD, uses 2nd start [Escherichia coli] gb AAC76279.1 (AE000404) bundles of cytoplasmic filaments [Escherichia coli K12] gb AAG58374.1 AE005552_4 (AE005552) bundles of cytoplasmic filaments [Escherichia coli O157:H7] SEQ ID n-2444
SEQ ID n° 9739	PL-227.1	Contig9 from 4440068 to 4443862	p 62%	gb AAG58373.1 AE005552_3 (AE005552) Z4604 gene product [Escherichia coli O157:H7] SEQ ID n-2433
SEQ ID n° 9740	PL-226.1	Contig9 from 4443859 to 4444716	p 61%	pir F82325 conserved hypothetical protein VC0421 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF93594.1 (AE004129) conserved hypothetical protein [Vibrio cholerae] SEQ ID n-2422

SEQ ID n° 9741	PL-225.1	Contig9 from 4444722 to 4446167	p 90%	sp P46473 TLDD_ECOLI TLDD PROTEIN pir F65116 tldd.protein - Escherichia coli (strain K-12) gb AAA58046.1 (U18997) ORF_f481 [Escherichia coli] dbj BAA07913.1 (D44451) Tldd protein [Escherichia coli] gb AAC76276.1 (AE000403) suppresses inhibitory activity of CsrA [Escherichia coli K12] SEQ ID n-1411
SEQ ID n° 9742	PL-3335.1	Contig9 from 4446210 to 4446674	p 46%	pdb 1BNE C Chain C, Barnase A43CS80C DISULFIDE MUTANT pdb 1BNE B Chain B, Barnase A43CS80C DISULFIDE MUTANT pdb 1BNE A Chain A, Barnase A43CS80C DISULFIDE MUTANT sp P46480 YHCO_ECOLI HYPOTHETICAL 10.8 KD PROTEIN IN ARGR-CAFA INTERGENIC REGION (F90) pir A65116 hypothetical protein b3239 - Escherichia coli (strain K-12) gb AAA58041.1 (U18997) ORF_f90; small but good stats [Escherichia coli] gb AAC76271.1 (AE000403) orf, hypothetical protein [Escherichia coli K12] gb AAG58367.1 AE005551_10 (AE005551) orf, hypothetical protein [Escherichia coli O157:H7] sp P26650 YJGA_ECOLI HYPOTHETICAL 21.4 KD PROTEIN IN FBP-PMBA INTERGENIC REGION (X96 PROTEIN) (F183) pir S56460 hypothetical 21.4K protein (fbp-pmba intergenic region) - Escherichia coli gb AAA24760.1 (M95096) X96 [Escherichia coli] gb AAA97131.1 (U14003) alternate gene name yjga [Escherichia coli] dbj BAA07914.1 (D44452) 21K protein [Escherichia coli] gb AAC77191.1 (AE000494) putative alpha helix protein [Escherichia coli K12] gb AAG59431.1 AE005655_10 (AE005655) putative alpha helix protein [Escherichia coli O157:H7] SEQ ID n-1400
SEQ ID n° 9743	PL-5130.1	Contig9 from 4446679 to 4446948	p 61%	#N/A
SEQ ID n° 9744	PL-224.1	Contig9 from 4446980 to 4447519	m 74%	

SEQ ID n° 9745	PL-223.1	Contig9 from 4447721 to 4449061	p 88%	sp P24231 PMBA_ECOLI PMBA PROTEIN (TLDE PROTEIN) pir S13730.pmBA protein.- Escherichia coli emb CAA38091.1 (X54152) pmBA is involved in the production of antibiotic MccB17 [Escherichia coli] gb AA97132.1 (U14003) pmBA [Escherichia coli] dbj BA07915.1 (D44452) TLDE protein [Escherichia coli] gb AAC77192.1 (AE000494) maturation of antibiotic MccB17, see tld genes [Escherichia coli K12] gb AAG59432.1 AE005655.11 (AE005655) maturation of antibiotic MccB17, see tld genes [Escherichia coli O157:H7]	SEQ ID n° 1389
SEQ ID n° 9746	PL-5132.1	Contig9 from 4449263 to 4449613	p No Hits found	ref NP_043500.1 orf29 [Bacteriophage HP1] sp P51733 Y029_BPHP1 HYPOTHETICAL 44.2 KD PROTEIN IN LYS 3'REGION (ORF29) pir S69537 hypothetical protein 29 - phage HP1 gb AAB09216.1 (U24159) orf29 [Bacteriophage HP1]	#N/A
SEQ ID n° 9747	PL-5133.1	Contig9 from 4449725 to 4450141	p 46%	ref NP_043501.1 orf30 [Bacteriophage HP1] sp P51734 Y030_BPHP1 HYPOTHETICAL 20.8 KD PROTEIN IN LYS 3'REGION (ORF30) pir S69538 hypothetical protein 30 - phage HP1 gb AAB09217.1 (U24159) orf30 [Bacteriophage HP1]	#N/A
SEQ ID n° 9748	PL-3336.1	Contig9 from 4450236 to 4450790	p 54%	ref NP_043502.1 orf31 [Bacteriophage HP1] sp P51735 VPH_BPHP1 PROBABLE TAIL FIBER PROTEIN (ORF31) pir S69539 hypothetical protein 31 - phage HP1 gb AAB09218.1 (U24159) orf31 [Bacteriophage HP1]	SEQ ID n° 2575
SEQ ID n° 9749	PL-222.1	Contig9 from 4450800 to 4452608	p 28%	ref NP_037719.1 Gp29 [Bacteriophage HK97] gb AAF31112.1 (AF069529) Gp29 [Bacteriophage HK97]	SEQ ID n° 1378
SEQ ID n° 9750	PL-5134.1	Contig9 from 4452608 to 4452880	p 33%		#N/A

SEQ ID n° 9751	PL-5135.1	Contig9 from 4452922 to 4453224	p 60%	sp P77699 TFAD_ECOLI TAIL FIBER ASSEMBLY PROTEIN HOMOLOG FROM-LAMBDOID PROPHAGE DLP12 pir G64788 ybck protein, phage protein-related Escherichia coli gb AAB40757.1 (U82598) hypothetical protein [Escherichia coli] gb AAC73662.1 (AE000161) orf, hypothetical protein [Escherichia coli K12]	#N/A
SEQ ID n° 9752	PL-5136.1	Contig9 from 4453229 to 4453381	p No Hits found		#N/A
SEQ ID n° 9753	PL-221.1	Contig9 from 4453344 to 4453952	p 42%	ref NP_043504.1 orf33 [Bacteriophage HPI] sp P51737 YO33_BPHPI HYPOTHETICAL 28.3 KD PROTEIN IN LYS 3'REGION (ORF33) pir S69541 hypothetical protein 33 - phage HPI gb AAB09220.1 (U24159) orf33 [Bacteriophage HPI]	SEQ ID n-3367
SEQ ID n° 9754	PL-3337.1	Contig9 from 4453942 to 4454460	p 55%	ref NP_043505.1 orf34 [Bacteriophage HPI] sp P51738 YO34_BPHPI HYPOTHETICAL 20.8 KD PROTEIN IN LYS 3'REGION (ORF34) pir S69542 hypothetical protein 34 - phage HPI gb AAB09221.1 (U24159) orf34 [Bacteriophage HPI]	SEQ ID n-2576
SEQ ID n° 9755	PL-220.1	Contig9 from 4454460 to 4456109	p 59%	ref NP_043506.1 orf35 [Bacteriophage HPI] sp P51739 YO35_BPHPI HYPOTHETICAL 58.7 KD PROTEIN IN LYS 3'REGION (ORF35) pir S69543 hypothetical protein 35 - phage HPI gb AAB09222.1 (U24159) orf35 [Bacteriophage HPI]	SEQ ID n-3357
SEQ ID n° 9756	PL-5138.1	Contig9 from 4457112 to 4457237	m 51%	pir P81815 Ner-like DNA-binding protein NWA1883 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB71960.1 (AJ391256) putative DNA-binding protein [Neisseria meningitidis] emb CAB85106.1 (AL162757) Ner-like DNA-binding protein [Neisseria meningitidis] Z2491]	#N/A

1037

sp|P18837|SFSB_ECOLI SUGAR FERMENTATION
 STIMULATION PROTEIN B (NER-LIKE PROTEIN)
 pir||BVECP nlp protein - Escherichia coli
 emb|CAA48736.1| (X68873) Ner-like
 protein, homologous to Ner protein of
 bacteriophages Mu and D108 [Escherichia coli]
 gb|AA57989.1| (U18997) Ner-like protein
 [Escherichia coli] gb|AAC76220.1| (AE000399)
 regulatory factor of maltose metabolism; similar
 to Ner repressor protein of phage Mu
 to [Escherichia coli K12]
 gb|AAG58322.1|AE005547_8 (AE005547) regulatory
 factor of maltose metabolism; similar to
 Ner repressor protein of phage Mu [Escherichia
 coli O157:H7]

#N/A

Contig9 from
 SEQ ID n° 9757 PL-5139.1 4457253 to m 45%
 4457381

Contig9 from
 SEQ ID n° 9758 PL-5140.1 4457438 to p No Hits found
 4457587

#N/A

sp|P40679|RNK_ECOLI REGULATOR OF NUCLEOSIDE
 DIPHOSPHATE KINASE pir||I57917 nucleoside
 diphosphate kinase regulator - Escherichia coli
 gb|AAC36933.1| (L37900) rnk gene product
 [Escherichia coli] dbj|BAA35239.1| (D90701) Rnk
 protein [Escherichia coli] dbj|BAA35248.1|
 (D90702) Rnk protein [Escherichia coli]
 gb|AAB40810.1| (U82598) regulator of nucleoside
 diphosphate kinase [Escherichia coli]
 gb|AAC73711.1| (AE000166) regulator of
 nucleoside diphosphate kinase [Escherichia
 coli K12] gb|AAG54945.1|AE005240_11 (AE005240)
 regulator of nucleoside diphosphate kinase
 [Escherichia coli O157:H7]

SEQ ID n-2577

Contig9 from
 SEQ ID n° 9759 PL-3339.1 4458122 to m 69%
 4458532

SEQ ID n° 9760	PL-5141.1	Contig9 from 4458721 to 4458993	m	62%	sp P33996 PTSO_ECOLI_PHOSPHOCARRIER_PROTEIN_NPR (NITROGEN_RELATED_HPR) pir I76722 phosphocARRIER protein Npr (nitrogen related hpr) - Escherichia coli emb CAA81621.1 (Z27094) ORFV [Escherichia coli] gb AAB60167.1 (U12684) NPr [Escherichia coli] gb AAA58008.1 (U18997) similar to nitrogen- related HPr phosphocARRIER protein of the phosphotransferase system, Swiss-Prot Accession Number P33996 [Escherichia coli] gb AAC76238.1 (AE006400) phosphocARRIER protein HPr-like NPr, nitrogen related, exchanges phosphate with Enzyme I, Hpr [Escherichia coli K12] gb AAG58340.1 (AE005548_11) (AE005548) phosphocARRIER protein HPr-like NPr, nitrogen related, exchanges phosphate with Enzyme I, Hpr [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9761	PL-219.1	Contig9 from 4458993 to 4459844	m	95%	sp P17163 YHBJ_KLEPN_HYPOTHETICAL_32.5_KD PROTEIN_IN_PTSN-PTSO_INTERGENIC_REGION (ORF4) pir S60666 probable ATP-binding protein - Klebsiella pneumoniae emb CAA90684.1 (Z50803) orfIV [Klebsiella pneumoniae] gb AAG58338.1 (AE005548_9) (AE005548) phosphotransferase system enzyme IIA, regulates N metabolism [Escherichia coli O157:H7]	SEQ ID n-1345
SEQ ID n° 9762	PL-3340.1	Contig9 from 4459928 to 4460395	m	84%	sp P17161 RP5M_KLEPN_PROBABLE_SIGMA(54) MODULATION_PROTEIN (ORF95) pir S07660 hypothetical protein 95 (rpon 3' region) - Klebsiella pneumoniae emb CAA34391.1 (X16335) ORF95 peptide (AA 1-95) [Klebsiella pneumoniae]	SEQ ID n-2579
SEQ ID n° 9763	PL-5142.1	Contig9 from 4460519 to 4460806	m	82%		#N/A

Contig9 from SEQ ID n° 9764 PL-218.1 4460830 to 4462272	m 87%	<p>gb AAG58336.1 AE005548_7 (AE005548) RNA polymerase, sigma(54 or 60) factor; nitrogen and fermentation regulation [Escherichia coli O157:H7]</p> <p>pir C65111 probable ABC transporter (nraA/rpoN 5'region) - Escherichia coli K-12) gb AA58003.1 (U18997) ORF_0241</p> <p>[Escherichia coli] gb AAC76233.1 (AE000399) putative ATP-binding component of a transport system [Escherichia coli K12]</p> <p>gb AAG58335.1 AE005548_6 (AE005548) putative ATP binding component of a transport system [Escherichia coli O157:H7]</p> <p>sp P38685 YHBN_ECOLI PROTEIN YHBN PRECURSOR pir B65111 17.3 kD protein in rpoN 5'region precursor (orf185) - Escherichia (strain K-12) gb AAB60161.1 (U12684) orf185 [Escherichia coli] gb AA58002.1 (U18997) ORF_0185 [Escherichia coli] gb AAC76232.1 (AE000399) orf, hypothetical protein [Escherichia coli K12] gb AAG58334.1 AE005548_5 (AE005548) orf, hypothetical protein [Escherichia coli O157:H7]</p> <p>sp P45397 YRBK_ECOLI HYPOTHETICAL 21.7 KD PROTEIN IN MURA-RPON INTERGENIC REGION (O191) pir A65111 hypothetical 21.7 kD protein in murZ rpoN intergenic region - Escherichia coli (strain K-12) gb AA58001.1 (U18997) ORF_0191 [Escherichia coli] gb AAC76231.1 (AE000399) orf, hypothetical protein [Escherichia coli K12] gb AAG58333.1 AE005548_4 (AE005548) orf, hypothetical protein [Escherichia coli O157:H7]</p>	SEQ ID n-2334
Contig9 from SEQ ID n° 9765 PL-217.1 4462300 to 4463025	m 91%		
Contig9 from SEQ ID n° 9766 PL-3341.1 4463032 to 4463565	m 71%		
Contig9 from SEQ ID n° 9767 PL-3342.1 4463546 to 4464124	m 72%		

SEQ ID n° 9768	PL-3343.1	Contig9 from 4464145 to 4464708	m	77%	sp P45396 YRBI_ECOLI_HYPOTHETICAL_20.0_KD PROTEIN IN MURA-RPON INTERGENIC REGION pir H65110 hypothetical 20.0 kD protein in murz. rpon intergenic region - Escherichia coli (strain K-12) gb AAC76230.1 (AE000399) orf, hypothetical protein [Escherichia coli K12] gb AAG58332.1 AE005548_3 (AE005548) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2582
SEQ ID n° 9769	PL-215.1	Contig9 from 4464726 to 4465694	m	86%	gb AAG58331.1 AE005548_2 (AE005548) putative isomerase [Escherichia coli O157:H7]
SEQ ID n° 9770	PL-214.1	Contig9 from 4465719 to 4466693	m	62%	gb AAG58330.1 AE005548_1 (AE005548) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3301
SEQ ID n° 9771	PL-213.1	Contig9 from 4466922 to 4467725	p	87%	sp P45393 YRBF_ECOLI_HYPOTHETICAL_ABC TRANSPORTER ATP-BINDING PROTEIN IN MURA-RPON INTERGENIC REGION. pir E65110 hypothetical protein b3195 - Escherichia coli (strain K-12) gb AA57996.1 (U18997) ORF_f269 [Escherichia coli] gb AAC76227.1 (AE000399) putative ATP- binding component of a transport system [Escherichia coli K12] gb AAG58329.1 AE005547_15 (AE005547) putative ATP-binding component of a transport system [Escherichia coli O157:H7] SEQ ID n-2290
SEQ ID n° 9772	PL-212.1	Contig9 from 4467736 to 4468518	p	89%	sp P45392 YRBE_ECOLI_HYPOTHETICAL_27.9_KD PROTEIN IN MURA-RPON INTERGENIC REGION (F260) pir D65110 hypothetical 27.9 kD protein in murz. rpon intergenic region - Escherichia coli (strain K-12) gb AA57995.1 (U18997) ORF_f260 [Escherichia coli] gb AAC76226.1 (AE000399) orf, hypothetical protein [Escherichia coli K12] gb AAG58328.1 AE005547_14 (AE005547) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2368

SEQ ID n° 9773 PL-3345.1	Contig9 from 4468523 to 4469029	p 77%	sp P45391 YRBD_ECOLI HYPOTHETICAL 19.6 KD	SEQ ID n-2583
			PROTEIN IN MURA-RPON INTERGENIC REGION	
SEQ ID n° 9774 PL-211.1	Contig9 from 4469063 to 4469692	p 84%	PRECUSOR (F183) pir C65110 hypothetical protein b3193 - Escherichia coli (strain K-12) gb AA57994.1 (U18997) ORF_f183 [Escherichia coli] gb AAC76225.1 (AE000399) orf, hypothetical protein [Escherichia coli K12] gb AGS8327.1 AE005547_13 (AE005547) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2257
			sp P45390 YRBC_ECOLI HYPOTHETICAL 24.0 KD PROTEIN IN MURA-RPON INTERGENIC REGION	
SEQ ID n° 9775 PL-5145.1	Contig9 from 4469694 to 4469987	p 55%	PRECUSOR (F211) pir B65110 hypothetical 24.0 KD protein in murz-rpon intergenic region - Escherichia coli (strain K-12) gb AA57993.1 (U18997) ORF_f211 [Escherichia coli] gb AAC76224.1 (AE000399) orf, hypothetical protein [Escherichia coli K12] gb AAF21249.1 AF053073_2 (AF053073) Yrbc [Shigella flexneri]	#N/A
			gb AGS8325.1 AE005547_11 (AE005547) yrbB gene product [Escherichia coli O157:H7]	
SEQ ID n° 9776 PL-5146.1	Contig9 from 4470386 to 4470640	p 83%	sp P43781 YRBA_ECOLI 9.5 KDA PROTEIN IN MURZ- RPON INTERGENIC REGION	#N/A

1042

ep P33038 MURA_ENTCL UDP-N-ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYLPIRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE TRANSFERASE) (EPT) ENOYLPIRUVYL pir s22372 UDP-N-acetylglucosamine 1- carboxyvinyltransferase (EC 2.5.1.7) - Enterobacter cloacae pdb INAW A Chain A, Enolpyruvyl Transferase pdb INAW B Chain B, Enolpyruvyl Transferase emb CAA77856.1 (Z11835) UDP-N-acetylglucosamine 1- carboxyvinyltransferase [Enterobacter cloacae] Seq ID n° 9777 PL-210.1 4470692 to 4471957 Contig9 from 4473941	92%			SEQ ID n° 2247
Seq ID n° 9778 PL-209.1 4472382 to 4473941 Contig9 from 4474045 to 4474533	88%	m	No Hits found	SEQ ID n° 2235
Seq ID n° 9779 PL-3347.1 4474700 to 4477195 Contig9 from 4478646	26%	m	No Hits found	SEQ ID n° 2584
Seq ID n° 9781 PL-207.1 4478704 to 4478817 Contig9 from 4478817	9%	m	No Hits found	SEQ ID n° 2224
Seq ID n° 9782 PL-7084.1 4478817		m	No Hits found	SEQ ID n° 2213

#N/A

1043

SEQ ID n° 9783	PL-206.1	Contig9 from 4479433 to 4480491	m	79%	<p>sp P31137 DEGS_ECOLI_PROTEASE_DEGS_PRECURSOR pir JC6052 trypsin-like proteinase (EC 3.4.21.-) hhoB - Escherichia coli gb AAC43993.1 (U15661) hhoB [Escherichia coli] gb AA58037.1 (U18997) ORF_0355 [Escherichia coli] gb AAC44006.1 (U32495) Degs [Escherichia coli] gb AAC76267.1 (AE000402) protease [Escherichia coli K12] prf 2206396B hhoB gene [Escherichia coli] SEQ ID n-2202</p>
SEQ ID n° 9784	PL-5150.1	Contig9 from 4481353 to 4481541	m	82%	<p>sp Q05459 VAGE_SAEPU-VIRULENCE-ASSOCIATED PROTEIN VAGC #N/A ref NP_052816.1 pXO1-120 [Bacillus anthracis] pir H59105 hypothetical protein pXO1-120 - Bacillus anthracis virulence plasmid pXO1 gb AAD32424.1 AAD32424 (AF065404) pXO1-120 [Bacillus anthracis] SEQ ID n-2585</p>
SEQ ID n° 9785	PL-3348.1	Contig9 from 4481746 to 4482318	p	59%	<p>dbj BAB16031.1 (AB030747) transposase [Streptococcus pyogenes] sp P39099 DEGQ_ECOLI_PROTEASE_DEGQ_PRECURSOR pir JC6051 trypsin-like proteinase (EC 3.4.21.-) hhoA precursor - Escherichia coli gb AAC43992.1 (U15661) hhoA [Escherichia coli] gb AA58036.1 (U18997) ORF_0455 [Escherichia coli] gb AAC44005.1 (U32495) DegQ [Escherichia coli] gb AAC76266.1 (AE000402) serine endoprotease [Escherichia coli K12] prf 2206396A hhoA gene [Escherichia coli] SEQ ID n-2180</p>
SEQ ID n° 9786	PL-205.1	Contig9 from 4482435 to 4483139	p	42%	
SEQ ID n° 9787	PL-204.1	Contig9 from 4483291 to 4484667	m	83%	

SEQ ID n° 9788	PL-5154.1	Contig9 from 4484905 to 4485309	m	72%	<p>sp P39436 YHCB_ECOLI_HYPOTHETICAL_15.2_KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (O134) pir [C65115 hypothetical 15.2 kD protein in rplm- hhoA intergenic region - Escherichia coli (strain K-12) gb AAA58035.1 (U18997) ORF_0134 [Escherichia coli] gb AAC76265.1 (AE000402) orf, hypothetical protein [Escherichia coli K12] gb AAG58361.1 AE005551_4 (AE005551) orf, hypothetical protein [Escherichia coli O157:H7] sp P46442 YHCB_ECOLI_HYPOTHETICAL_43.1_KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375) pir [B65115 hypothetical 43.1 kD protein in rplm- hhoA intergenic region - Escherichia coli (strain K-12) gb AAA58034.1 (U18997) ORF_F375 [Escherichia coli] gb AAC76264.1 (AE000402) orf, hypothetical protein [Escherichia coli K12] gb AAG58360.1 AE005551_3 (AE005551) yhm gene product [Escherichia coli O157:H7] sp P02410 RL13_ECOLI_50S_RIBOSOMAL_PROTEIN_L13 pir [R5EC13 ribosomal protein L13 [validated] - Escherichia coli emb CAA26041.1 (X02130) L13 (rp1M) (aa 1-129) [Escherichia coli] gb AAA58033.1 (U18997) 50S ribosomal subunit protein L13 [Escherichia coli] gb AAC76263.1 (AE000402) 50S ribosomal subunit protein L13 [Escherichia coli K12] gb AAG58359.1 AE005551_2 (AE005551) 50S ribosomal subunit protein L13 [Escherichia coli O157:H7]</p>	#N/A
SEQ ID n° 9789	PL-203.1	Contig9 from 4485653 to 4486783	p	73%		
SEQ ID n° 9790	PL-5156.1	Contig9 from 4487038 to 4487466	p	97%		

SEQ ID n-21169

SEQ ID n° 9791	PL-5158.1	Contig9 from 4487482 to 4487874	p	95%	sp P02363 RS9_ECOLI 30S RIBOSOMAL PROTEIN S9 pir R3EC9-ribosomal protein S9 [validated] - Escherichia coli_emb CAA26042.1 (X02130) S9 (rpsI) (1-130) [Escherichia coli] gb AA58032.1 (U18997) 30S ribosomal subunit protein S9 [Escherichia coli] gb AAC76262.1 (AE000402) 30S ribosomal subunit protein S9 [Escherichia coli K12] gb AGS8358.1 AE005551_1 (AE005551) 30S ribosomal subunit protein S9 [Escherichia coli O157:H7] #N/A
SEQ ID n° 9792	PL-202.1	Contig9 from 4488221 to 4488862	p	89%	gb AAG01334.1 AF288218_1 (AF288218) SspA [Providencia stuartii] sp P25663 SSPB_ECOLI STRINGENT STARVATION PROTEIN B pir JS0666 stringent starvation protein B, SspB - Escherichia coli gb AA24650.1 (M69028) stringent starvation protein [Escherichia coli] gb AA58030.1 (U18997) stringent starvation protein B [Escherichia coli] gb AAC76260.1 (AE000402) stringent starvation protein B [Escherichia coli K12] gb AGS8356.1 AE005550_9 (AE005550) stringent starvation protein B [Escherichia coli O157:H7] SEQ ID n-2588
SEQ ID n° 9793	PL-3351.1	Contig9 from 4488866 to 4489381	p	78%	gb AAG58347.1 AE005549_4 (AE005549) glutamate synthase, small subunit [Escherichia coli O157:H7] SEQ ID n-2589
SEQ ID n° 9794	PL-3352.1	Contig9 from 4489433 to 4489951	m	No Hits found	
SEQ ID n° 9795	PL-201.1	Contig9 from 4490178 to 4491596	m	89%	

SEQ ID n° 9796	PL-200.1	Contig9 from 4491606 to 4496114	m	89%	sp P09831 GLTB_ECOLI GLUTAMATE SYNTHASE [NADPH] LARGE CHAIN PRECURSOR (GLUTAMATE-SYNTHASE ALPHA SUBUNIT) (NADPH-GOGAT) (GLTS ALPHA CHAIN) pir F5112 glutamate synthase (NADPH) (EC 1.4.1.13) large chain precursor - Escherichia coli gb AAA58014.1 (U18997) glutamate synthase, large subunit [Escherichia coli] gb AAC76244.1 (AE000400) glutamate synthase, large subunit [Escherichia coli K12] SEQ ID n-1138
SEQ ID n° 9797	PL-199.1	Contig9 from 4496811 to 4499156	p	84%	emb CAA37397.1 (X53315) arcB [Escherichia coli] SEQ ID n-1125
SEQ ID n° 9798	PL-198.1	Contig9 from 4499394 to 4500047	p	77%	sp P26428 ELBB_ECOLI ENHANCING LYCOPENE BIOSYNTHESIS PROTEIN 2 (SIGMA CROSS-REACTING PROTEIN 27A) (SCR-27A) SEQ ID n-1114
SEQ ID n° 9799	PL-197.1	Contig9 from 4500052 to 4500777	p	73%	sp P46022 MTGA_ECOLI MONOFUNCTIONAL BIOSYNTHETIC PEPTIDGLYCAN TRANSGLYCOSYLASE (MONOFUNCTIONAL TGASE) pir B65112 hypothetical 27.3 kD protein in ptsO-arcB intergenic region - Escherichia coli (strain K-12) gb AAA58010.1 (U18997) ORF_f242 [Escherichia coli] gb AAC76240.1 (AE000400) putative peptidoglycan enzyme [Escherichia coli K12] SEQ ID n-1103
SEQ ID n° 9800	PL-196.1	Contig9 from 4500909 to 4501484	m	74%	sp P45467 YRAP_ECOLI HYPOTHETICAL 20.0 KD PROTEIN IN AGAI-MTR INTERGENIC REGION PRECURSOR (O191) pir B65105 hypothetical 20.0 kD protein in agai-mtr intergenic region - Escherichia coli (strain K-12) gb AAA57953.1 (U18997) ORF_o191 [Escherichia coli] gb AAC76184.1 (AE000396) putative periplasmic protein [Escherichia coli K12] gb AAG58286.1 (AE005543_16 (AE005543) putative periplasmic protein [Escherichia coli O157:H7] SEQ ID n-1092

SEQ ID n° 9801	PL-3353.1	Contig9 from 4501495 to 4502085	m	91%	<p>sp P45466 YRAO_ECOLI HYPOTHETICAL 21.1 KDA PROTEIN IN AGAI-MTR INTERGENIC REGION (O196) pir A65105 phosphoheptose isomerase homolog - Escherichia coli (strain K-12) gb AA57952.1 (U18997) ORF_o196 [Escherichia coli] gb AAC76183.1 (AE000396) orf, hypothetical protein [Escherichia coli K12] gb AAG58285.1 AE005543_15 (AE005543) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2590 sp P45465 YRAM_ECOLI HYPOTHETICAL 14.8 KDA PROTEIN IN AGAI-MTR INTERGENIC REGION (O131) pir H65104 hypothetical 14.8 kD protein in agai- mtr intergenic region - Escherichia coli (strain K-12) gb AA57951.1 (U18997) ORF_o131; overlaps o678, other starts possible [Escherichia coli] gb AAC76182.1 (AE000396) orf, hypothetical protein [Escherichia coli K12] #N/A sp P45464 YRAM_ECOLI HYPOTHETICAL 72.8 KD PROTEIN IN AGAI-MTR INTERGENIC REGION (O678) pir G65104 hypothetical 72.8 kD protein in agai- mtr intergenic region - Escherichia coli (strain K-12) gb AA57950.1 (U18997) ORF_o678 [Escherichia coli] gb AAC76181.1 (AE000396) putative glycosylase [Escherichia coli K12] sp P45528 YRAL_ECOLI HYPOTHETICAL 31.3 KD PROTEIN IN AGAI-MTR INTERGENIC REGION (F286) pir F65104 hypothetical 31.3 kD protein in agai- mtr intergenic region - Escherichia coli (strain K-12) gb AA57949.1 (U18997) ORF_f286 [Escherichia coli] gb AAC76180.1 (AE000395) orf, hypothetical protein [Escherichia coli K12] gb AAG58282.1 AE005543_12 (AE005543) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2071</p>
SEQ ID n° 9802	PL-5161.1	Contig9 from 4502110 to 4502490	m	56%	
SEQ ID n° 9803	PL-195.1	Contig9 from 4502567 to 4504360	m	58%	
SEQ ID n° 9804	PL-194.1	Contig9 from 4504373 to 4505239	p	84%	

SEQ ID n° 9805	PL-5162.1	Contig9 from 4505481 to 4505624	m 43%	<p>pir [G81001 hypothetical protein NMB2137 [imported] - Neisseria meningitidis (group B strain MD58) gb AAV42445.1 (AE002562) hypothetical protein [Neisseria meningitidis MC58]</p> <p>sp P42624 YHAK_ECOLI_HYPOTHETICAL 25.9 KD PROTEIN IN EXUR-TDCC INTERGENIC REGION (O233)</p> <p>pir [G65099 hypothetical 25.9 kD protein in exur. tdcC intergenic region - Escherichia coli (strain K-12) gb AAA57910.1 (U18997) ORF_o233 [Escherichia coli] gb AAC76141.1 (AE000392) orf, hypothetical protein [Escherichia coli K12]</p> <p>sp P42623 YHAJ_ECOLI_HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN EXUR-TDCC INTERGENIC REGION pir [F65099 hypothetical-transcription regulator exur-tdcC intergenic region - Escherichia coli (strain K-12) gb AAA57909.1 (U18997) ORF_f298 [Escherichia coli] gb AAC76140.1 (AE000392) putative transcriptional regulator LYSR-type [Escherichia coli K12]</p>	SEQ ID n-2050	#N/A
SEQ ID n° 9806	PL-192.1	Contig9 from 4505735 to 4506436	m 70%	<p>gb AAG58234.1 AE005539_11 (AE005539) orf, hypothetical protein [Escherichia coli O157:H7]</p> <p>gb AAG58233.1 AE005539_10 (AE005539) orf, hypothetical protein [Escherichia coli O157:H7]</p> <p>sp P42618 YQJE_ECOLI_HYPOTHETICAL 15.1 KD PROTEIN IN EXUR-TDCC INTERGENIC REGION</p> <p>pir [H65098 hypothetical protein yqjE - Escherichia coli (strain K-12) gb AAC76134.1 (AE000392) orf, hypothetical protein [Escherichia coli K12] gb AAG58232.1 AE005539_9 (AE005539) yqjE gene product [Escherichia coli O157:H7]</p>	SEQ ID n-2039	#N/A
SEQ ID n° 9807	PL-191.1	Contig9 from 4506547 to 4507443	p 86%			
SEQ ID n° 9808	PL-5164.1	Contig9 from 4508114 to 4508509	m 81%			
SEQ ID n° 9809	PL-5165.1	Contig9 from 4508729 to 4508989	m 39%			
SEQ ID n° 9810	PL-5166.1	Contig9 from 4508982 to 4509383	m 73%			

SEQ ID n° 9811 PL-5167.1	Contig9 from 4509385 to 4509690	m	66%	sp P42617 YQJD_ECOLI_HYPOTHETICAL_11.1_KD PROTEIN IN EXUR-TDCC INTERGENIC REGION tdcc intergenic region - Escherichia coli (strain K-12) gb AA57902.1 (U18997) ORF_0101 [Escherichia coli] gb AAC76133.1 (AE000392) orf, hypothetical protein [Escherichia coli K12] gb AG58231.1 AE005539_8 (AE005539) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
				sp P42614 YQJA_ECOLI_HYPOTHETICAL_24.6_KD PROTEIN IN EXUR-TDCC INTERGENIC REGION pir D65098 hypothetical protein b3095 - Escherichia coli (strain K-12) gb AA57899.1 (U18997) ORF_0220 [Escherichia coli] gb AAC76130.1 (AE000391) orf, hypothetical protein [Escherichia coli K12] gb AG58228.1 AE005539_5 (AE005539) orf, hypothetical protein [Escherichia coli O157:H7]	
SEQ ID n° 9812 PL-190.1	Contig9 from 4509885 to 4510556	m	85%	sp P42602 YGJU_ECOLI_HYPOTHETICAL_SYMPORER_YGJU pir F65097 hypothetical 43.5 kd protein in ebgC- exut intergenic region - Escherichia coli (strain K-12) gb AA57891.1 (U18997) ORF_0414; Geneplot suggests frameshift near start but none found [Escherichia coli] gb AAC76124.1 (AE000391) putative transport protein [Escherichia coli K12] gb AG58222.1 AE005538_9 (AE005538) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-3028 SEQ ID n-3016
SEQ ID n° 9813 PL-189.1	Contig9 from 4511208 to 4512170	p	79%	sp P42602 YGJU_ECOLI_HYPOTHETICAL_SYMPORER_YGJU pir F65097 hypothetical 43.5 kd protein in ebgC- exut intergenic region - Escherichia coli (strain K-12) gb AA57891.1 (U18997) ORF_0414; Geneplot suggests frameshift near start but none found [Escherichia coli] gb AAC76124.1 (AE000391) putative transport protein [Escherichia coli K12] gb AG58222.1 AE005538_9 (AE005538) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-3028 SEQ ID n-3016
SEQ ID n° 9814 PL-188.1	Contig9 from 4512587 to 4513834	p	83%	sp P42602 YGJU_ECOLI_HYPOTHETICAL_SYMPORER_YGJU pir F65097 hypothetical 43.5 kd protein in ebgC- exut intergenic region - Escherichia coli (strain K-12) gb AA57891.1 (U18997) ORF_0414; Geneplot suggests frameshift near start but none found [Escherichia coli] gb AAC76124.1 (AE000391) putative transport protein [Escherichia coli K12] gb AG58222.1 AE005538_9 (AE005538) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-3028 SEQ ID n-3016
SEQ ID n° 9815 PL-187.1	Contig9 from 4513954 to 4515975	m	77%	sp P42602 YGJU_ECOLI_HYPOTHETICAL_SYMPORER_YGJU pir F65097 hypothetical 43.5 kd protein in ebgC- exut intergenic region - Escherichia coli (strain K-12) gb AA57891.1 (U18997) ORF_0414; Geneplot suggests frameshift near start but none found [Escherichia coli] gb AAC76124.1 (AE000391) putative transport protein [Escherichia coli K12] gb AG58222.1 AE005538_9 (AE005538) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-3028 SEQ ID n-3016

1050

SEQ ID n° 9816	PL-186.1	Contig9 from 4516369 to 4516968	p	54%	gb AAC03422.1 (U81516) unknown [Myxococcus xanthus]	SEQ ID n-984
SEQ ID n° 9817	PL-185.1	Contig9 from 4517022 to 4517957	m	58%	sp P75829 YBUX_ECOLI HYPOTHETICAL 38.4 KDA PROTEIN IN AQPZ-CSPD INTERGENIC REGION pir E64826 yb x protein - Escherichia coli gb AAC73964.1 (AE000189) putative enzyme [Escherichia coli K12] dbj BAA35595.1 (D90725) VirK protein [Escherichia coli] sp Q9X7Q6 IDI_STRCO PROBABLE ISOPENTENYL- DIPHOSPHATE DELTA-ISOMERASE (IPP ISOMERASE) (ISOPENTENYL PYROPHOSPHATE ISOMERASE) pir T35275 probable IPP isomerase - Streptomyces coelicolor emb CAB40700.1 (AL049587) putative IPP isomerase [Streptomyces coelicolor A3(2)]	SEQ ID n-974
SEQ ID n° 9818	PL-3354.1	Contig9 from 4518535 to 4519068	p	52%	gb AAD02882.1 (AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana] ref NP_043506.1 orf35 [Bacteriophage HP1] sp P51739 YO35_BPPI1 HYPOTHETICAL 58.7 KD PROTEIN IN LYS 3'REGION (ORF35) pir S69543 hypoetical protein 35 - phage HP1 gb AAB09222.1 (U24159) orf35 [Bacteriophage HP1]	SEQ ID n-2591
SEQ ID n° 9819	PL-184.1	Contig9 from 4519206 to 4520150	p	26%		SEQ ID n-963
SEQ ID n° 9820	PL-183.1	Contig9 from 4520271 to 4521200	p	52%		
SEQ ID n° 9821	PL-5173.1	Contig9 from 4521427 to 4521603	m	No Hits found		#N/A
SEQ ID n° 9822	PL-5175.1	Contig9 from 4521802 to 4521891	m	No Hits found		#N/A
SEQ ID n° 9823	PL-5176.1	Contig9 from 4521945 to 4522046	p	No Hits found		#N/A

SEQ ID n° 9824	PL-5177.1	Contig9 from 4522214 to 4522510	m	42%	sp P37668 YTAG_ECOLI_HYPOTHETICAL_11.0_KD PROTEIN IN BISC-CSPA INTERGENIC REGION (O96) pir S47776 hypothetical_11K protein (bisc-cspa intergenic region) - Escherichia coli gb AA18532.1 (U00039) No definition line found [Escherichia coli] gb AAC76579.1 (AE000433) orf, hypothetical protein [Escherichia coli K12] gb AAGS8704.1 AE005582_7 (AE005582) orf, hypothetical protein [Escherichia coli O157:H7] pir D82455 hypothetical protein VCA0468 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96372.1 (AE004379) hypothetical protein [Vibrio cholerae] #N/A
SEQ ID n° 9825	PL-5178.1	Contig9 from 4522558 to 4522881	m	53%	gb AAGS5918.1 AE005325_11 (AE005325) putative antirepressor protein encoded by prophage CP-933N [Escherichia coli O157:H7] #N/A
SEQ ID n° 9826	PL-182.1	Contig9 from 4523265 to 4523837	p	45%	sp P07336 RPSD_SALTY_RNA-POLYMERASE_SIGMA_FACTOR RPOD (SIGMA-70) pir RNEBST transcription initiation factor sigma 70 - Salmonella typhimurium gb AAA27242.1 (M14427) rpoD protein [Salmonella typhimurium] SEQ ID n-942
SEQ ID n° 9827	PL-181.1	Contig9 from 4524660 to 4526504	m	90%	sp P02923 PRIM_ECOLI_DNA_PRIMASE_pir RYEC2_DNA primase (EC 2.7.7.-) - Escherichia coli gb AA24600.1 (J01687) DNA primase [Escherichia coli] gb AAA89146.1 (U28379) CG site No. 847; alternate gen name dnaP, parB [Escherichia coli] emb CAA23531.1 (V00274) DNA primase [Escherichia coli] gb AAC76102.1 (AE000388) DNA biosynthesis; DNA primase [Escherichia coli K12] SEQ ID n-932
SEQ ID n° 9828	PL-180.1	Contig9 from 4526675 to 4528420	m	81%	SEQ ID n-921

SEQ ID n° 9829 PL-5179.1	Contig9 from 4528541 to 4528756	m	93%		sp P02379 RS21_ECOLI 30S RIBOSOMAL PROTEIN S21 pir R3EC21 ribosomal protein S21 [validated] Escherichia coli pir R3EB21 ribosomal protein S21 - Salmonella typhimurium emb CAA23635.1 (V00346) coding sequence [Escherichia coli] gb AA24599.1 (J01687) ribosomal protein S21 [Escherichia coli] gb AA27240.1 (M14427) rpsU protein [Salmonella typhimurium] gb AA89145.1 (U28379) 30S ribosomal subunit protein S21 [Escherichia coli] gb AAC76101.1 (AE000388) 30S ribosomal subunit protein S21 [Escherichia coli K12] gb AG58199.1 AE005535_11 (AE005535) 30S ribosomal subunit protein S21 [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9830 PL-5180.1	Contig9 from 4528769 to 4528933	m		No Hits found	pir QOECR6 O-sialoglycoprotein endopeptidase (EC 3.4.24.57) - Escherichia coli gb AA89144.1 (U28379) ORF_f337 [Escherichia coli] gb AAC76100.1 (AE000388) putative O- sialoglycoprotein endopeptidase [Escherichia coli K12] sp P31056 YGIH_ECOLI HYPOTHETICAL 22.2 KD PROTEIN IN BACA-TTDA INTERGENIC REGION (O205) pir A65094 ygiH protein - Escherichia coli (strain K-12) gb AA89139.1 (U28379) alternate name ygiH; ORF_o205 [Escherichia coli] gb AAC76095.1 (AE000387) orf, hypothetical protein [Escherichia coli K12] gb AG58193.1 AE005535_5 (AE005535) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-909
SEQ ID n° 9831 PL-179.1	Contig9 from 4529051 to 4530064	p	88%			#N/A
SEQ ID n° 9832 PL-178.1	Contig9 from 4530123 to 4530779	m	78%			SEQ ID n-898

SEQ ID n° 9833	PL-5182.1	Contig9 from 4530883 to 4531236	p 74%	pir H65093 probable dihydronopterin aldolase (EC 4.1.2.25) - Escherichia coli (strain K-12) gb AAA89138.1 (U28379) alternate name ygiG; ORF_f123 [Escherichia coli] gb AAC76094.1 (AE000387) putative kinase [Escherichia coli K12]. sp P31054 BACA_ECOLI_BACITRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) pir G65093 bacitracin resistance protein baca - Escherichia coli gb AAA89137.1 (U28379) CG Site No. 29739 [Escherichia coli] gb AAC76093.1 (AE000387) bacitracin resistance; possibly phosphorylates undecaprenol [Escherichia coli K12] SEQ ID n-887
SEQ ID n° 9834	PL-177.1	Contig9 from 4531413 to 4532231	p 82%	sp P06961 CCA_ECOLI_TRNA_NUCLEOTIDYLTRANSFERASE (TRNA ADENYLYLTRANSFERASE) (TRNA PYROPHOSPHORYLASE) (CCA-ADDING ENZYME) pir RNECTA trna adenylyltransferase (EC 2.7.7.25) - Escherichia coli gb AAA23541.1 (M12788) trna nucleotidyltransferase [Escherichia coli] gb AAA89136.1 (U28379) CG Site No. 933 [Escherichia coli] gb AAC76092.1 (AE000387) trna nucleotidyl transferase [Escherichia coli K12] SEQ ID n-876
SEQ ID n° 9835	PL-176.1	Contig9 from 4532296 to 4533546	m 81%	sp P39202 YGIM_ECOLI_HYPOTHETICAL 23.1 KD PROTEIN IN GLNE-CCA INTERGENIC REGION PRECURSOR pir E65093 hypothetical protein in glne-cca intergenic region - Escherichia coli (strain K-12) (fragment) gb AAA89135.1 (U28379) alternate name ygiM; ORF_o206 [Escherichia coli] gb AAC76091.1 (AE000387) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-865
SEQ ID n° 9836	PL-175.1	Contig9 from 4533562 to 4534182	m 78%	

1054

SEQ ID n° 9837	PL-174.1	Contig9 from 4534444 to 4535382	p 53%	sp P30871 YGLF_ECOLI HYPOTHETICAL 48.4 KD PROTEIN IN GLNE-CCA INTERGENIC REGION (ORFXE) pir S37754 yglf protein - Escherichia coli emb CAA79891.1 (Z21844) open reading frame upstream glne [Escherichia coli] gb AAC76090.1 (AE000387) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-854
SEQ ID n° 9838	PL-173.1	Contig9 from 4535416 to 4538286	p 77%	sp P30870 GLNE_ECOLI GLUTAMATE-AMMONIA-LIGASE ADENYLTRANSFERASE (GLUTAMINE-SYNTHETASE ADENYLTRANSFERASE) (ATASE) pir C65093 [glutamate--ammonia-ligase] adenylyltransferase (EC 2.7.7.42) - Escherichia coli gb AAC76089.1 (AE000387) adenylylating enzyme for glutamine synthetase [Escherichia coli K12]	SEQ ID n-843
SEQ ID n° 9839	PL-172.1	Contig9 from 4538374 to 4539798	p 87%	gb AAG58186.1 AE005534_8 (AE005534) putative kinase [Escherichia coli O157:H7]	SEQ ID n-832
SEQ ID n° 9840	PL-171.1	Contig9 from 4540388 to 4541059	p 84%	pir H83639 hypothetical protein PA0045 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03435.1 AE004444_4 (AE004444) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-821
SEQ ID n° 9841	PL-5183.1	Contig9 from 4541081 to 4541440	p 61%	pir A83640 hypothetical protein PA0046 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03436.1 AE004444_5 (AE004444) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 9842	PL-170.1	Contig9 from 4541437 to 4542099	p 62%	gb AAF42718.1 AF226570_1 (AF226570) putative lipoprotein GNA1162 [Neisseria meningitidis]	SEQ ID n-810
SEQ ID n° 9843	PL-5184.1	Contig9 from 4542179 to 4542469	m 69%	gb AAG58182.1 AE005534_4 (AE005534) Z4400 gene product [Escherichia coli O157:H7]	#N/A

1055

sp P24199 RIBB_ECOLI 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE (DHBP SYNTHASE) pir S22364				
3,4-dihydroxy-2-butanone 4-phosphate synthase				
Escherichia coli emb CAA47252.1 (X66720) 3,4-dihydroxy-2-butanone 4-phosphate synthase				
[Escherichia coli] gb AAA71879.1 (M77129) luxH gene product [Escherichia coli] gb AA69209.1 (U28377) 3,4-dihydroxy-2-butanone 4-phosphate synthase [Escherichia coli]				
gb AAC76077.1 (AE000386) 3,4 dihydroxy-2-butanone-4-phosphate synthase				
[Escherichia coli K12] gb AG58181.1 AE005534_3 (AE005534) 3,4 dihydroxy-2-butanone-4-phosphate synthase				SEQ ID n-799
[Escherichia coli O157:H7]				SEQ ID n-788
gb AAG58178.1 AE005533_11 (AE005533) orf, hypothetical protein [Escherichia coli O157:H7]				
pir B83043 hypothetical protein PA4816 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG08201.1 AE004895_1 (AE004895) hypothetical protein [Pseudomonas aeruginosa]				#N/A
ref NP_052677.1 unnamed protein product [Escherichia coli] pir T00308 hypothetical protein L7011 - Escherichia coli plasmid pO157				
pir T42111 hypothetical protein L7011 - Escherichia coli plasmid pO157 dbj BAA31827.1 (AB011549) unnamed protein product [Escherichia coli] gb AAC70079.1 (AF074613) hypothetical protein [Escherichia coli O157:H7]				#N/A
Contig9 from				
SEQ ID n° 9844 PL-169.1 4542929 to 4543582	p	87%		
Contig9 from				
SEQ ID n° 9845 PL-168.1 4543777 to 4544562	p	78%		
Contig9 from				
SEQ ID n° 9846 PL-5188.1 4544629 to 4544787	p	51%		
Contig9 from				
SEQ ID n° 9847 PL-5189.1 4544801 to 4545076	m	54%		

1056

ref NP_052676.1 unnamed protein product [Escherichia coli] - pir T00307 hypothetical protein L7010 - Escherichia coli plasmid p0157 pir T42110 hypothetical protein L7010 - Escherichia coli plasmid p0157 dbj BAA31826.1 (AB011549) unnamed protein product [Escherichia coli] gb AAC70078.1 (AF074613) unknown [Escherichia coli O157:H7]				#N/A	
dbj BAB06239.1 (AP001515) transposase related protein-(20) [Bacillus halodurans]					SEQ ID n~977
sp P24196 YGIC_ECOLI HYPOTHETICAL 45.0 KD PROTEIN IN TOLC-RIBB INTERGENIC REGION (ORFA) (O386) pir S22361 hypothetical protein A - Escherichia coli gb AA71876.1 (M77129) ORFA [Escherichia coli] gb AA69206.1 (U28377) ORF_o386; alternate-name ygiC; orfa of M77129 [Escherichia coli] gb AAC76074.1 (AE000385) putative synthetase/amidase [Escherichia coli K12]					SEQ ID n~966
gb AAG58177.1 AE005533_10 (AE005533) putative synthetase/amidase [Escherichia coli O157:H7]					SEQ ID n~955
gb AAG58176.1 AE005533_9 (AE005533) orf, hypothetical protein [Escherichia coli O157:H7]					
sp P27842 YIGF_ECOLI HYPOTHETICAL 14.5 KD PROTEIN IN CORA-RARD INTERGENIC REGION (F126) pir S30707 hypothetical 14.5K protein (corA 3' region) - Escherichia coli gb AAD15039.1 (L02122) ORF [Escherichia coli] gb AA67613.1 (M87049) f126 [Escherichia coli] gb AAC76820.1 (AE000457) orf, hypothetical protein [Escherichia coli K12]					SEQ ID n~2592

Contig9 from 4545079 to 4545339	m	46%		
SEQ ID n° 9848 PL-5190.1				

Contig9 from 4545718 to 4546743	m	21%		
SEQ ID n° 9849 PL-167.1				

Contig9 from 4546897 to 4548057	m	88%		
SEQ ID n° 9850 PL-166.1				

Contig9 from 4548064 to 4548768	m	75%		
SEQ ID n° 9851 PL-165.1				

Contig9 from 4549180 to 4549593	p	39%		
SEQ ID n° 9852 PL-3356.1				

Contig9 from	pir T48674 hasA export system outer membrane	
SEQ ID n° 9853 PL-164.1	protein hasF [validated] -	
4549842 to	marcescens emb CAA671136.1 (X98513) HAS ABC	
4551215	exporter outer membrane component [Serratia	SEQ ID n-744
	marcescens]	
Contig9 from	sp P36651 ADPP_ECOLI ADP-RIBOSE PYROPHOSPHATASE	
SEQ ID n° 9854 PL-163.1	(ADP-RIBOSE DIPHOSPHATASE) (ADENOSINE	
4551575 to	DIPHOSPHORIBOSE PYROPHOSPHATASE) (ADPR-PPASE)	
4552216	(ADP-RIBOSE PHOSPHOHYDROLASE) pir H65090	
Contig9 from	hypothetical protein b3034 - Escherichia coli	
SEQ ID n° 9855 PL-162.1	(strain K-12) gb AAAG202.1 (U28377) ORF_f209	
4552316 to	[Escherichia coli] gb AAC76070.1 (AE000385)	
4553155	orf, hypothetical protein [Escherichia coli K12]	
	gb AAG58173.1 AE005533_6 (AE005533) orf,	
Contig9 from	hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-734
SEQ ID n° 9856 PL-161.1	sp P36650 ICC_ECOLI ICC PROTEIN pir P65090	
4553284 to	3',5'-cyclic-nucleotide phosphodiesterase (EC	
4553892	3.1.4.17) cpdA - Escherichia coli	
	(strain K-12) dbj BAA03989.1 (D16557) Icc	
Contig9 from	[Escherichia coli] gb AAC76068.1 (AE000385)	
SEQ ID n° 9857 PL-160.1	regulator of lacZ [Escherichia coli K12]	
4554000 to	gb AAG58171.1 AE005533_4 (AE005533) regulator of	
4554500	lacZ [Escherichia coli O157:H7]	SEQ ID n-723
Contig9 from	sp P36653 YQIA_ECOLI HYPOTHETICAL 21.6 KD	
SEQ ID n° 9858 PL-159.1	PROTEIN IN PARE-ICC INTERGENIC REGION (P193)	
4555000 to	pir B65090 hypothetical 15.2 kD protein in icc	
4555500	3'region - Escherichia coli	
Contig9 from	12) gb AAAG69199.1 (U28377) ORF_f193	
SEQ ID n° 9859 PL-158.1	[Escherichia coli] gb AAC76067.1 (AE000385)	
4556000 to	orf, hypothetical protein [Escherichia coli K12]	
4556500	gb AAG58170.1 AE005533_3 (AE005533) orf,	
Contig9 from	hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-712

SEQ ID n° 9857	PL-160.1	Contig9 from 4553965 to 4555860	P	92%	sp P20083 PARE_ECOLI_TOPOISOMERASE_IV_SUBUNIT_B pir D65090 topoisomerase IV subunit [EC 5.99.1.)- Escherichia coli. gb AA69198.1 (U28377) topoisomerase IV subunit [Escherichia coli] gb AAC76066.1 (AE000385) DNA topoisomerase IV subunit B [Escherichia coli K12] SEQ ID n-901
SEQ ID n° 9858	PL-159.1	Contig9 from 4555902 to 4558169	P	90%	gb AA690006.1 AF227958_1 (AF227958) DNA topoisomerase IV subunit [Serratia marcescens] SEQ ID n-689
SEQ ID n° 9859	PL-158.1	Contig9 from 4558192 to 4558920	P	80%	gb AAG58154.1 AE005531_7 (AE005531) 1-acyl-sn- glycerol-3-phosphate acyltransferase [Escherichia coli O157:H7] SEQ ID n-678
SEQ ID n° 9860	PL-157.1	Contig9 from 4559325 to 4560746	P	79%	gb AAG58153.1 AE005531_6 (AE005531) suppressor of ftsI [Escherichia coli O157:H7] SEQ ID n-667
SEQ ID n° 9861	PL-156.1	Contig9 from 4560881 to 4561759	M	74%	sp Q46857 YQHE_ECOLI_HYPOTHETICAL_OXIDOREDUCTASE IN METC-SUFI INTERGENIC REGION SEQ ID n-656
SEQ ID n° 9862	PL-155.1	Contig9 from 4562159 to 4562830	M	77%	sp P33196 YQHB_ECOLI_HYPOTHETICAL_24.1_KD PROTEIN IN METC-SUFI INTERGENIC REGION pir G65087 hypothetical 24.1 kD protein in metC- sufr intergenic region - Escherichia coli (strain K-12) gb AA69176.1 (U28377) ORF_0219; alternate name yghB [Escherichia coli] gb AAC76045.1 (AE000383) orf, hypothetical protein [Escherichia coli K12] gb AAG58145.1 AE005530_11 (AE005530) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-645 pir S74520 hypothetical protein slr0725 - Synechocystis sp. (strain PCC 6803) dbj BAAL6672.1 (D90899) hypothetical protein [Synechocystis sp.] gb AAG58259.1 AE005542_1 (AE005542) putative protease; htraA suppressor protein [Escherichia coli O157:H7] SEQ ID n-2594 #N/A
SEQ ID n° 9863	PL-3358.1	Contig9 from 4562975 to 4563463	M	55%	
SEQ ID n° 9864	PL-5196.1	Contig9 from 4563469 to 4563819	M	54%	

Contig9 from SEQ ID n° 9865 PL-154.1	4563968 to 4565158	m	79%	gb AAK02878.1 (AE006118) MetC [Pasteurella multocida]	SEQ ID n-834
Contig9 from SEQ ID n° 9866 PL-153.1	4565442 to 4566476	p	50%	sp P18783 EXBB_ECOLI BIOPOLYMER TRANSPORT EXBB PROTEIN pir BVECBX biopolymer transport exbb protein - Escherichia coli gb AA69173.1 (U28377) exbb gene product [Escherichia coli] gb AAC76042.1 (AE000383) uptake of enterochelin; tonB-dependent uptake of B colicins [Escherichia coli K12] gb AAG58142.1 AE005530.8 (AE005530) uptake of enterochelin; tonB-dependent uptake of E colicins [Escherichia coli O157:H7] sp P18784 EXBD_ECOLI BIOPOLYMER TRANSPORT EXBD PROTEIN pir BVECBX biopolymer transport exbd protein - Escherichia coli gb AA23733.1 (W28819) exbd peptide-[Escherichia coli] gb AA69172.1 (U28377) exbd gene product [Escherichia coli] gb AAC76041.1 (AE000383) uptake of enterochelin; tonB-dependent uptake of B colicins [Escherichia coli K12] gb AAG58141.1 AE005530.7 (AE005530) uptake of enterochelin; tonB-dependent uptake of E colicins [Escherichia coli O157:H7] pir T36177 probable DNA-binding protein - Streptomyces coelicolor emb CAB41077.1 (AL049645) putative DNA-binding protein [Streptomyces coelicolor A3(2)]	SEQ ID n-814
Contig9 from SEQ ID n° 9867 PL-151.1	4568178 to 4568777	m	No Hits found		SEQ ID n-803
Contig9 from SEQ ID n° 9870 PL-150.1	4569111 to 4570349	m	47%	gb AAG57790.1 AE005497.1 (AE005497) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-592

SEQ ID n° 9871	PL-149.1	Contig9 from 4570473 to 4571366	p	50%	gb AAD55884.1 AF130250_1 (AF130250) hypothetical protein [Ralstonia eutropha]	SEQ ID n-580
SEQ ID n° 9872	PL-148.1	Contig9 from 4571752 to 4573500	p	16%	sp Q9ZFM2 XYNB_BACST BETA-XYLOSIDASE (1,4-BETA-D- XYLAN XYLHYDROLASE) (XYLAN 1,4-BETA- XYLOSIDASE) gb AAC98129.1 (AF098273) beta- xylosidase [Bacillus stearothermophilus]	SEQ ID n-569
SEQ ID n° 9873	PL-147.1	Contig9 from 4574024 to 4575778	p	15%	sp Q9ZFM2 XYNB_BACST BETA-XYLOSIDASE (1,4-BETA-D- XYLAN XYLHYDROLASE) (XYLAN 1,4-BETA- XYLOSIDASE) gb AAC98129.1 (AF098273) beta- xylosidase [Bacillus stearothermophilus]	SEQ ID n-558
SEQ ID n° 9874	PL-5203.1	Contig9 from 4576278 to 4576709	m	80%	ref NP_052313.1 ORF C8 [Ralstonia solanacearum] dbj BAA32221.1 (AB015669) ORF C8 [Ralstonia solanacearum]	#N/A
SEQ ID n° 9875	PL-146.1	Contig9 from 4576930 to 4577850	m	No Hits found		SEQ ID n-547
SEQ ID n° 9876	PL-3359.1	Contig9 from 4577840 to 4578409	m	No Hits found		SEQ ID n-2595
SEQ ID n° 9877	PL-145.1	Contig9 from 4578625 to 4579785	m	22%	gb AAH01342.1 AAH01342 (BC001342) Unknown (protein for MGC:5623) [Homo sapiens]	SEQ ID n-936
SEQ ID n° 9878	PL-144.1	Contig9 from 4579905 to 4580816	m	87%	gb AAH18117.1 (U73857) hypothetical 34.0 kd protein in araJ-aroM intergenic region [Escherichia coli]	SEQ ID n-525
SEQ ID n° 9879	PL-143.1	Contig9 from 4581022 to 4583928	m	23%	sp Q9ZDF8 SYK_RICPR LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) pir D71694 lysine--trna ligase (EC 6.1.1.6) (lys) RP371 - Rickettsia prowazekii emb CAA14830.1 (AJ235271) LYSYL-TRNA SYNTHETASE (lys) [Rickettsia prowazekii]	SEQ ID n-514

1061

SEQ ID n° 9880	PL-142.1	Contig9 from 4584506 to 4586461	p	81%	sp P53052 CN16_YEREN 2',3'-CYCLIC-NUCLEOTIDE 2'- PHOSPHODIESTERASE PRECURSOR pir S52695 2',3'- cyclic-nucleotide-2'-phosphodiesterase (EC 3.1.4.16) precursor - Yersinia enterocolitica emb CAA59745.1 (X85742) 2',3'- cyclic-nucleotide-2'-phosphodiesterase [Yersinia enterocolitica]	SEQ ID n-903
SEQ ID n° 9881	PL-141.1	Contig9 from 4586501 to 4587319	p	45%	sp P44012 RN26_HAETIN PROBABLE RIBONUCLEASE HT0526 PRECURSOR pir C64009 ribonuclease homolog HT0526 - Haemophilus influenzae (strain Rd KW20) gb AAC22192.1 (U32735) H. influenzae predicted coding region HT0526 [Haemophilus influenzae Rd]	SEQ ID n-492
SEQ ID n° 9882	PL-140.1	Contig9 from 4587790 to 4588395	p	40%	pir T35714 hypothetical protein SC7H1.19 - Streptomyces coelicolor emb CAA16206.1 (AL021411) hypothetical protein [Streptomyces coelicolor A3(2)]	SEQ ID n-481
SEQ ID n° 9883	PL-139.1	Contig9 from 4588435 to 4589958	p	63%	pir H83486 probable MFS transporter PA1282 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04671.1 AE004557.12 (AE004557) probable MFS transporter [Pseudomonas aeruginosa]	SEQ ID n-469
SEQ ID n° 9884	PL-138.1	Contig9 from 4590504 to 4591091	p	38%	pir P83345 probable non-ribosomal peptide synthetase PA2402 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05790.1 AE004667.1 (AE004667) probable non- ribosomal peptide synthetase [Pseudomonas aeruginosa]	SEQ ID n-458
SEQ ID n° 9885	PL-5208.1	Contig9 from 4591124 to 4591306	p	No Hits found		#N/A
SEQ ID n° 9886	PL-137.1	Contig9 from 4591564 to 4593417	p	35%	emb CAC01604.1 (A2269505) peptide synthetase [Anabaena sp. 90]	SEQ ID n-448

SEQ ID n° 9887	PL-5211.1	Contig9 from 4593419 to 4593553	p	No Hits found	#N/A
SEQ ID n° 9888	PL-136.1	Contig9 from 4593604 to 4595346	p	51%	dbj BAB12211.1 (AB032549) polyketide synthase and peptide synthetase [Microcystis aeruginosa]
SEQ ID n° 9889	PL-3361.1	Contig9 from 4595476 to 4595964	p	No Hits found	SEQ ID n-438
SEQ ID n° 9890	PL-135.1	Contig9 from 4596061 to 4596930	p	49%	sp O59185 PYRD_PYRHO DIHYDROOROTATE DEHYDROGENASE (DIHYDROOROTATE OXIDASE) (DHODHASE) (DHOD) (DHOD) pir H71027 probable dihydroorotate dehydrogenase - Pyrococcus horikoshii dbj BAA30624.1 (AP000006) 303aa long hypothetical dihydroorotate dehydrogenase [Pyrococcus horikoshii] SEQ ID n-428
SEQ ID n° 9891	PL-134.1	Contig9 from 4596927 to 4597697	p	46%	pir T44251 creatininase (EC 3.5.2.10) [validated] - Arthrobacter sp. (strain TE1826) dbj BAA25929.1 (AB007122) creatininase [Arthrobacter sp.] SEQ ID n-417
SEQ ID n° 9892	PL-133.1	Contig9 from 4599955 to 4600869	p	70%	ref NP_047874.1 putative transposase [Yersinia pestis] pir T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CA855253.1 (AL117211) hypothetical protein yPMT1.71 [Yersinia pestis] SEQ ID n-406
SEQ ID n° 9893	PL-5214.1	Contig9 from 4600894 to 4601190	p	No Hits found	#N/A

SEQ ID n° 9894	PL-132.1	Contig9 from 4601300 to 4604986	m	55%	sp P13458 SBCC_ECOLI_EXONUCLEASE_SBCC pir BYECSC exonuclease (EC 3.1.15.-) sbcc - Escherichia coli_emb CAA34104.1 (X15981) sbcc (AA 1-1048) [Escherichia coli] gb AAB18121.1 (U73857) exonuclease sbcc [Escherichia coli] gb AAC73500.1 (AE000146) ATP-dependent dsDNA exonuclease [Escherichia coli K12]	SEQ ID n-995
SEQ ID n° 9895	PL-131.1	Contig9 from 4604983 to 4606218	m	72%	prf 2204364A sbcc gene [Escherichia coli] gb AAB18122.1 (U73857) exonuclease sbcc [Escherichia coli]	SEQ ID n-984
SEQ ID n° 9896	PL-130.1	Contig9 from 4606605 to 4607294	p	87%	sp P45606 PHOB_SHIDY_PHOSPHATE_REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB pir A44753 phob protein - Shigella dysenteriae gb AAA26535.1 (M31793) phosphate regulatory protein phob [Shigella dysenteriae] gb AAG54746.1 AE005219_2 (AE005219) positive and negative sensor protein for pho regulon [Escherichia coli O157:H7]	SEQ ID n-974
SEQ ID n° 9897	PL-129.1	Contig9 from 4607318 to 4608658	p	72%	sp P37011 BRNQ_ECOLI_BRANCHED-CHAIN_AMINO_ACID TRANSPORT_SYSTEM_II_CARRIER_PROTEIN (LTV-II) pir A64769 branched-chain amino acid transport system II carrier protein brnq - Escherichia coli gb AAB18125.1 (U73857) similar to S. typhimurium brnq [Escherichia coli] gb AAC73504.1 (AE000146) branched chain amino acid transport system II carrier protein [Escherichia coli K12]	SEQ ID n-362
SEQ ID n° 9898	PL-128.1	Contig9 from 4609009 to 4610340	p	77%	gb AAG54747.1 AE005219_3 (AE005219) branched chain amino acid transport system II carrier protein [Escherichia coli O157:H7]	SEQ ID n-951

SEQ ID n° 9899	PL-127.1	Contig9 from 4610471 to 4612231	m	68%	sp P36267 GGT_PSESP_GAMMA-GLUTAMYLTRANSFERASE PRECURSOR gb AAC60442.1 (S63255) gamma- glutamyltransferase, ggt {EC_2.3.2.2} [Pseudomonas, A14, Peptide, 575 aa] prf 1920225A gamma-Glu transferase [Pseudomonas sp.]	SEQ ID n-940
SEQ ID n° 9900	PL-126.1	Contig9 from 4612451 to 4613053	m	92%	gb AAK02879.1 (AE006118) TsaA [Pasteurella multocida]	SEQ ID n-929
SEQ ID n° 9901	PL-125.1	Contig9 from 4613338 to 4613934	m	64%	gb AAG54751.1 AE005219_7 (AE005219) putative glycoprotein [Escherichia coli O157:H7] sp P21516 QUEA_ECOLI_S-ADENOSYLMETHIONINE:TRNA RIBOSYLTRANSFERASE-ISOMERASE (QUEUOSINE BIOSYNTHESIS PROTEIN QUEA) pir B38530 S- adenosylmethionine--trna ribosyltransferase- isomerase (EC ----- 5.4.99.-) queA [validated] - Escherichia coli gb AA16114.1 (M37702) queuosine biosynthesis [Escherichia coli] gb AAB40161.1 (U82664) S- adenosylmethionine:trna ribosyltransferase- isomerase [Escherichia coli] gb AAC73508.1 (AE000147) synthesis of queuine in trna; probably S- adenosylmethionine:trna ribosyltransferase- isomerase [Escherichia coli K12] gb AAG54752.1 AE005220_1 (AE005220) synthesis of queuine in trna; probably S- adenosylmethionine:trna ribosyltransferase- isomerase [Escherichia coli O157:H7]	SEQ ID n-918
SEQ ID n° 9902	PL-124.1	Contig9 from 4614039 to 4615106	p	90%	sp Q54177 TGT_SHIFT_QUEUINE TRNA- RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) ENZYME (VIRULENCE-ASSOCIATED PROTEIN VACC) dbj BAA05482.1 (D26469) vacC [Shigella flexneri]	SEQ ID n-907
SEQ ID n° 9903	PL-123.1	Contig9 from 4615257 to 4616381	p	93%		

1065

SEQ ID n° 9904	PL-5216.1	Contig9 from 4616473 to 4616802	p 74%	sp P19677 YAJC_ECOLI HYPOTHETICAL 11.9 KDA PROTEIN IN TGT-SEC2 INTERGENIC REGION. (ORF12) pir D38530 preprotein translocase chain yajC - Escherichia coli gb AA24668.1 (M63939) ORF [Escherichia coli] gb AAC60468.1 (S68715) YajC [Escherichia coli, peptide, 110 aa]	
SEQ ID n° 9905	PL-122.1	Contig9 from 4616830 to 4618677	p 88%	dbj BA05483.1 (D26469) ORF [Shigella flexneri] gb AAB40163.1 (U82664) hypothetical 11.9 kd protein [Escherichia coli] gb AAC73510.1 (AE000147) orf, hypothetical protein [Escherichia coli K12] gb AAG54754.1 AE005220_3 (AE005220) orf, hypothetical protein [Escherichia coli O157:H7] prf 2005253A yacJ protein [Escherichia coli]	#N/A
SEQ ID n° 9906	PL-121.1	Contig9 from 4618688 to 4619656	p 85%	gb AAD44348.1 (AF163861) secD protein [Enterobacter aerogenes]	SEQ ID n-286
SEQ ID n° 9907	PL-3365.1	Contig9 from 4619772 to 4620221	p 92%	gb AAB40165.1 (U82664) protein-export membrane protein secF [Escherichia coli] sp P25538 YBAD_ECOLI HYPOTHETICAL 17.2 KD PROTEIN IN TSX-RIBG INTERGENIC REGION (ORF1) pir S26200 ybad protein - Escherichia coli emb CAA45734.1 (X64395) orf1 [Escherichia coli] gb AAB40169.1 (U82664) hypothetical 17.2kd protein [Escherichia coli] gb AAC73516.1 (AE000148) orf, hypothetical protein [Escherichia coli K12] gb AAG54762.1 AE005220_11 (AE005220) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG54763.1 AE005220_12 (AE005220) bifunctional pyrimidine deaminase/reductase in pathway of riboflavin synthesis	SEQ ID n-275
SEQ ID n° 9908	PL-120.1	Contig9 from 4620226 to 4621335	p 76%	[Escherichia coli O157:H7]	SEQ ID n-264

SEQ ID n° 9909	PL-3366.1	Contig9 from 4621462 to 4621932	P 84%	gb AAB40171.1 (U82664) probable riboflavin synthase beta chain [Escherichia coli]	SEQ ID n-2599
SEQ ID n° 9910	PL-5217.1	Contig9 from 4621959 to 4622375	P 80%	sp P04381 NUSB_ECOLI N UTILIZATION SUBSTANCE PROTEIN B (NUSB PROTEIN) pir I51822 nusb protein - Escherichia coli pir FJECB transcription termination factor nusb [validated] - Escherichia coli pdb 1EY1 A Chain A, Solution Structure Of Escherichia Coli Nusb pdb 1BAQ Antitermination Factor Nusb From Escherichia Coli, Nmr, 18 Structures	
SEQ ID n° 9911	PL-119.1	Contig9 from 4622476 to 4623465	P 80%	gb AA24228.1 (M26839) nusb [Escherichia coli] emb CAA45737.1 (X64395) nusb (ssyb) [Escherichia coli] emb CAA25289.1 (X00681) nusb protein [Escherichia coli] gb AAB40172.1 (U82664) N utilization substance protein B [Escherichia coli] gb AAC73519.1 (AE000148) transcription termination; L factor [Escherichia coli K12] gb AGS4765.1 AE005221_2 (AE005221) transcription termination; L factor [Escherichia coli O157:H7] prf 2111328A Nusb protein [Escherichia coli] sp P77785 THIL_ECOLI THIAMINE-MONOPHOSPHATE KINASE (THIAMINE-PHOSPHATE KINASE) pir A64771 thiamin-phosphate kinase (EC 2.7.4.16) - Escherichia coli gb AAB40173.1 (U82664) similar to H. influenzae H11305 [Escherichia coli] gb AAC73520.1 (AE000148) thiamin- monophosphate kinase [Escherichia coli K12] gb AGS4767.1 AE005221_4 (AE005221) phosphatidylglycerophosphatase [Escherichia coli O157:H7] ref NP_053144.1 ORF11 [Yersinia pestis] gb AAF05107.1 AF152923_11 (AF152923) ORF11 [Yersinia pestis]	SEQ ID n-252 SEQ ID n-2600 #N/A
SEQ ID n° 9912	PL-3367.1	Contig9 from 4623458 to 4623949	P 76%		
SEQ ID n° 9913	PL-5220.1	Contig9 from 4624229 to 4624501	P 63%		

SEQ ID n° 9914	PL-5221.1	Contig9 from 4624563 to 4624721	p	47%	sp Q47149 YAFQ_ECOLI HYPOTHETICAL 10.8 KD PROTEIN IN GMEH-DING INTERGENIC REGION pir B64747 yafQ protein - Escherichia coli dbj BAA07587.1 (D38582) YafQ [Escherichia coli] gb AAC73329.1 (AE000131) orf, hypothetical protein [Escherichia coli K12] dbj BAV7895.1 (D83336) Hypothetical protein HI0711 [Escherichia coli]	#N/A
SEQ ID n° 9915	PL-5222.1	Contig9 from 4624961 to 4625254	m	57%	emb CAA75664.1 (Y15510) transposase [Pasteurella multocida] ...	#N/A
SEQ ID n° 9916	PL-3368.1	Contig9 from 4625260 to 4625760	m	55%	gb AAG16999.1 AF184152_2 (AF184152) transposase [Piscirickettsia salmonis]	SEQ ID n-2601
SEQ ID n° 9917	PL-3369.1	Contig9 from 4625871 to 4626395	m	42%	gb AAG58523.1 AE005564_8 (AE005564) orf; hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2602
SEQ ID n° 9918	PL-5223.1	Contig9 from 4626392 to 4626670	m	50%	gb AAG58568.1 AE005569_8 (AE005569) orf; hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9919	PL-118.1	Contig9 from 4627322 to 4629187	m	89%	sp P77488 DXS_ECOLI 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) pir D64771 dxs protein - Escherichia coli gb AAB40176.1 (U82664) similar to H. influenzae HI1439 [Escherichia coli] gb AAC73523.1 (AE000148) 1-deoxyxylulose- 5-phosphate synthase; flavoprotein [Escherichia coli K12] gb AAC46162.1 (AF035440) D-1-deoxyxylulose 5-phosphate synthase [Escherichia coli] gb AAG54771.1 AE005221_8 (AE005221) geranyltranstransferase (farnesylidiphosphate synthase) [Escherichia coli O157:H7]	SEQ ID n-241
SEQ ID n° 9920	PL-117.1	Contig9 from 4629250 to 4630167	m	77%		SEQ ID n-230

1068

SEQ ID n° 9921	PL-5225.1	Contig9 from 4630172 to 4630450	m	71%	sp P22938 EX7S_ECOLI EXODEOXYRIBONUCLEASE VII SMALL SUBUNIT (EXONUCLEASE VII SMALL SUBUNIT) pir JQ0664 exodeoxyribonuclease VII (EC 3.1.11.6) small chain - Escherichia coli dbj BAA00598.1 (D00694) ORF1 [Escherichia coli] gb AB40178.1 (U82664) exodeoxyribonuclease small subunit [Escherichia coli] gb AAC73525.1 (AE000148) exonuclease VII, small subunit [Escherichia coli K12] gb AAC54772.1 AE005221_9 (AE005221) exonuclease VII, small subunit [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9922	PL-116.1	Contig9 from 4630650 to 4632098	p	90%	sp P55913 THII_SALTY THIAMINE BIOSYNTHESIS PROTEIN THII pir T46944 thiamin biosynthesis protein thii [validated] - Salmonella typhimurium gb AAB63031.1 (U94901) Thii [Salmonella typhimurium] pir H64771 hydroxymethylpyrimidine kinase (EC 2.7.1.49) - Escherichia coli gb AAA82704.1 (U34923) Thij [Escherichia coli] gb AAB40180.1 (U82664) 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein [Escherichia coli] gb AAC73527.1 (AE000148) 4- methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis [Escherichia coli K12]	SEQ ID n-219
SEQ ID n° 9923	PL-5228.1	Contig9 from 4631941 to 4632318	m	35%	sp P77728 APBA_ECOLI 2-DEHYDROPANTOATE 2- REDUCTASE (KETOPANTOATE REDUCTASE) (KPA REDUCTASE) pir A54772 ketopantoate reductase - Escherichia coli gb AAB40181.1 (U82664) similar to S. typhimurium apba [Escherichia coli] gb AAC73528.1 (AE000148) involved in thiamin biosynthesis, alternative pyrimidine biosynthesis [Escherichia coli K12]	SEQ ID n-208
SEQ ID n° 9924	PL-115.1	Contig9 from 4632315 to 4633187	m	63%		

1069

SEQ ID n° 9925	PL-3370.1	Contig9 from 4633323 to 4633814	p	76%	sp P77482 YAJQ_ECOLI PROTEIN YAJQ pir [B64772 YAJQ protein - Escherichia coli gb AAB40182.1 (U82664) similar to H. influenzae HI1034 [Escherichia coli] gb AAC73529.1 (AE000149) orf, hypothetical protein [Escherichia coli K12] gb AAG54776.1 AE005222_1 (AE005222) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-2604
SEQ ID n° 9926	PL-114.1	Contig9 from 4633938 to 4635317	m	79%	sp P77726 YAJR_ECOLI HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION pir [C64772 probable transport protein yajr - Escherichia coli gb AAB40183.1 (U82664) hypothetical protein [Escherichia coli] gb AAC73530.1 (AE000149) putative transport protein [Escherichia coli K12] SEQ ID n-197
SEQ ID n° 9927	PL-113.1	Contig9 from 4635472 to 4636356	m	87%	gb AAB40184.1 (U82664) cytochrome o ubiquinol oxidase C subunit [Escherichia coli] SEQ ID n-186
SEQ ID n° 9928	PL-5230.1	Contig9 from 4636369 to 4636701	m	79%	gb AAB40185.1 (U82664) cytochrome o ubiquinol oxidase C subunit [Escherichia coli] #N/A
SEQ ID n° 9929	PL-112.1	Contig9 from 4636701 to 4637315	m	84%	gb AAG54780.1 AE005222_5 (AE005222) cytochrome o ubiquinol oxidase subunit III [Escherichia coli O157:H7] SEQ ID n-175

SEQ ID n° 9930	PL-110.1	Contig9 from 4637305 to 4639296	m	90%	<p>sp P18401 CYOB_ECOLI_UBIQUINOL_OXIDASE POLYPEPTIDE I (CYTOCHROME O SUBUNIT 1) (OXIDASE BO(3) SUBUNIT 1) (CYTOCHROME O UBIQUINOL OXIDASE SUBUNIT 1) (UBIQUINOL OXIDASE CHAIN A) pir B42226 bo-type ubiquinol oxidase (EC 1.10.3.-) chain I - Escherichia coli pdb 1FFT A Chain A, The Structure Of Ubiquinol Oxidase From Escherichia Coli pdb 1FFT F Chain F, The Structure Of Ubiquinol Oxidase From Escherichia Coli gb AAA23632.1 (J05492) cytochrome o ubiquinol oxidase B subunit I [Escherichia coli] gb AAB40187.1 (U82664) cytochrome o ubiquinol oxidase [Escherichia coli] gb AAC73534.1 (AE000149) cytochrome o ubiquinol oxidase subunit I [Escherichia coli K12] gb AAG54781.1 AE005222_6 (AE005222) cytochrome o ubiquinol oxidase subunit I [Escherichia coli O157:H7]</p>	SEQ ID n-253
SEQ ID n° 9931	PL-109.1	Contig9 from 4639301 to 4640236	m	78%	<p>sp P18400 CYOA_ECOLI_UBIQUINOL_OXIDASE POLYPEPTIDE II PRECURSOR (CYTOCHROME O SUBUNIT 2) (OXIDASE BO(3) SUBUNIT 2) (CYTOCHROME O UBIQUINOL SUBUNIT 2) (UBIQUINOL OXIDASE CHAIN B) pir A42226 bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Escherichia coli pdb 1FFT B Chain B, The Structure Of Ubiquinol Oxidase From Escherichia Coli pdb 1FFT G Chain G, The Structure Of Ubiquinol Oxidase From Escherichia Coli gb AAA23631.1 (J05492) cytochrome o ubiquinol oxidase subunit II [Escherichia coli] gb AAB40188.1 (U82664) cytochrome o ubiquinol oxidase subunit II [Escherichia coli] gb AAC73535.1 (AE000149) cytochrome o ubiquinol oxidase subunit II [Escherichia coli K12]</p>	SEQ ID n-241

SEQ ID n° 9932	PL-108.1	m	71%	Contig9 from 4640586 to 4641347	sp P45564 YFEN_ECOLI_HYPOTHETICAL_29.2_KDA PROTEIN IN XAPA-LIG INTERGENIC REGION (ORF254) pir G65014_hypothetical_29.2K_protein b2408 - Escherichia coli (strain K-12) emb CAA52046.1 (X73828) orf254 [Escherichia coli] gb AAC75461.1 (AE000328) putative sugar hydrolase [Escherichia coli K12] dbj BAA16279.1 (D90870) similar to [SwissProt Accession Number P45564] [Escherichia coli] SEQ ID n-231
SEQ ID n° 9933	PL-107.1	m	77%	Contig9 from 4641598 to 4643076	sp P36670 AMPG_ECOLI_AMPG_PROTEIN_pir S37391 signal transducer ampG - Escherichia coli gb AAB28884.1 (S67816) AmpG [Escherichia coli] gb AAB40189.1 (U82664) beta-lactamase induction signal transducer AmpG [Escherichia coli] gb AAC73536.1 (AE000149) regulates beta- lactamase synthesis [Escherichia coli K12] gb AAG54783.1 AE005222_8 (AE005222) regulates beta-lactamase synthesis [Escherichia coli O157:H7] SEQ ID n-120
SEQ ID n° 9934	PL-106.1	m	73%	Contig9 from 4643130 to 4643708	gb AAG54784.1 AE005222_9 (AE005222) yaJG gene product [Escherichia coli O157:H7] SEQ ID n-209
SEQ ID n° 9935	PL-5232.1	p	68%	Contig9 from 4643952 to 4644266	sp P15298 BOLA_ECOLI_BOLA_PROTEIN #N/A
SEQ ID n° 9936	PL-104.1	p	89%	Contig9 from 4644645 to 4645949	sp P22257 TIG_ECOLI_TRIGGER_FACTOR (TF) pir D64773 trigger factor [validated] -- Escherichia coli gb AAB40192.1 (U82664) trigger factor [Escherichia coli] gb AAC73539.1 (AE000150) trigger factor; a molecular chaperone involved in cell division [Escherichia coli K12] gb AAG54786.1 AE005223_1 (AE005223) trigger factor; a molecular chaperone involved in cell division [Escherichia coli O157:H7] SEQ ID n-87

SEQ ID n° 9937	PL-103.1	Contig9 from 4646223 to 4646846	P 94%	sp O60107 CLPP_YEREN ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (ENDOPEPTIDASE CLP) gb AAC45782.1 (U55059)-Clpp-[Yersinia enterocolitica]	SEQ ID n-76
SEQ ID n° 9938	PL-102.1	Contig9 from 4646983 to 4648254	P 95%	sp O33873 CLPX_YEREN ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT.CLPX--gb AAC45783.1 (U66330) Clpx [Yersinia enterocolitica]	SEQ ID n-85
SEQ ID n° 9939	PL-101.1	Contig9 from 4648463 to 4650817	P 95%	gb AAB40195.1 (U82664) ATP-dependent protease LA [Escherichia coli]	SEQ ID n-55
SEQ ID n° 9940	PL-5235.1	Contig9 from 4651046 to 4651321	P 80%	sp P02341 DBHB_ECOLI DNA-BINDING PROTEIN HU-BETA (NS1) (HU-1) pir [DNECS1 DNA-binding protein HU- 1 - Escherichia coli emb CAA34539.1 (X16540) HU-1 protein (AA 1-90) [Escherichia coli] gb AAB40196.1 (U82664) DNA-binding protein NS1 [Escherichia coli] gb AAC73543.1 (AE000150) DNA-binding protein HU-beta, NS1 (HU-1) [Escherichia coli K12]	#N/A
SEQ ID n° 9941	PL-100.1	Contig9 from 4651615 to 4653486	P 67%	gb AAG54790.1 AE005223_5 (AE005223) DNA-binding protein HU-beta, NS1 (HU-1) [Escherichia coli O157:H7] sp P77241 PPID_ECOLI PEPTIDYL-PROLYL CIS-TRANS ISOMERASE D (PPIASE D) (ROTAMASE D) pir [A64774 ybaU protein - Escherichia coli dbj BAAL1645.1 (D82943) YbaU [Escherichia coli] gb AAB40197.1 (U82664) similar to H. influenzae HI1004 [Escherichia coli] gb AAC73544.1 (AE000150) putative protease maturation protein [Escherichia coli K12]	SEQ ID n-84
SEQ ID n° 9942	PL-3371.1	Contig9 from 4653637 to 4654011	P 41%	gb AAG54792.1 AE005223_7 (AE005223) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2605

SEQ ID n° 9943	PL-5236.1	Contig9 from 4654165 to 4654572	p	66%	sp P77712 YBAW_ECOLI HYPOTHETICAL 15.1 KD PROTEIN IN HUPB-COF INTERGENIC REGION pir C64774.ybaw protein - Escherichia coli dbj BAAL1647.1 (D82943) Ybaw [Escherichia coli] gb AAB40199.1 (U82664) hypothetical protein [Escherichia coli] gb AAC73546.1 (AE000150) orf, hypothetical protein [Escherichia coli K12] #N/A	SEQ ID n-3845
SEQ ID n° 9944	PL-99.1	Contig9 from 4654601 to 4655299	m	83%	gb AAG54794.1 AE005223_9 (AE005223) orf, hypothetical protein [Escherichia coli O157:H7] pir G82247 cysteine synthase/cystathionine beta- synthase family protein VCI061	
SEQ ID n° 9945	PL-98.1	Contig9 from 4655332 to 4656384	m	82%	[imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94220.1 (AE004187) cysteine synthase/cystathionine beta-synthase family protein [Vibrio cholerae] pir G64774 regulatory protein b0447 - Escherichia coli gb AAB40203.1 (U82664) similar to Z. mobilis glutamate uptake regulatory protein [Escherichia coli] gb AAC73550.1 (AE000151) putative LRP-like transcriptional regulator [Escherichia coli K12]	SEQ ID n-3834
SEQ ID n° 9946	PL-3372.1	Contig9 from 4656512 to 4656973	p	84%	sp P77265 MDLA_ECOLI MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDLA pir H64774 ABC-type transport protein mdla - Escherichia coli gb AAB40204.1 (U82664) multidrug resistance- like ATP-binding protein Mdl [Escherichia coli] gb AAC73551.1 (AE000151) ATP-binding component of a transport system [Escherichia coli K12]	SEQ ID n-2606
SEQ ID n° 9947	PL-97.1	Contig9 from 4657060 to 4658829	p	81%	gb AAB40205.1 (U82664) multidrug resistance- like ATP-binding protein Mdl [Escherichia coli]	SEQ ID n-3823
SEQ ID n° 9948	PL-96.1	Contig9 from 4658822 to 4660606	p	81%		SEQ ID n-3812

SEQ ID n° 9949	PL-5238.1	Contig9 from 4660787 to 4661125	p 83%	gb AAB40206.1 (U82664) glutamine synthetase activity regulation protein [Escherichia coli] - sp P37905 AMTB_ECOLI PROBABLE AMMONIUM TRANSPORTER pir C64775 ammonium transport protein amtB - Escherichia coli gb AAD14837.1 (U40429) AmtB [Escherichia coli] gb AAB40207.1 (U82664) putative ammonium transporter [Escherichia coli] gb AAC73554.1 (AE000151) probable ammonium transporter [Escherichia coli K12] gb AAG54801.1 AE005224_6 (AE005224) probable ammonium transporter [Escherichia coli O157:H7] SEQ ID n-9801	#N/A
SEQ ID n° 9950	PL-95.1	Contig9 from 4661112 to 4662431	p 72%	sp P23911 TESB_ECOLI ACYL-COA THIOESTERASE II (TEII) pir D64775 acyl-CoA thioesterase (EC 3.1.2.-) II - Escherichia coli gb AAA24665.1 (M63308) thioesterase II [Escherichia coli] gb AAB40208.1 (U82664) acyl-CoA thioesterase II [Escherichia coli] gb AAC73555.1 (AE000151) acyl-CoA thioesterase II [Escherichia coli K12] gb AAG54802.1 AE005224_7 (AE005224) acyl-CoA thioesterase II [Escherichia coli O157:H7] gb AAG54803.1 AE005224_8 (AE005224) glycoprotein/polysaccharide metabolism [Escherichia coli O157:H7] SEQ ID n-2607	#N/A
SEQ ID n° 9951	PL-94.1	Contig9 from 4662504 to 4663367	m 79%	sp P27720 YMOA_YEREN MODULATING PROTEIN YMOA (HISTONE-LIKE PROTEIN) pir S15291 modulating protein ymoA - Yersinia enterocolitica emb CAA41091.1 (X58058) ymoA [Yersinia enterocolitica] SEQ ID n-9790	#N/A
SEQ ID n° 9952	PL-3373.1	Contig9 from 4663618 to 4664064	p 64%		
SEQ ID n° 9953	PL-5239.1	Contig9 from 4664376 to 4664579	m 90%		

SEQ ID n° 9954	PL-93.1	Contig9 from 4665634 to 4668783	m	89%	sp P31224 ACRB_ECOLI ACRIFLAVIN RESISTANCE PROTEIN B pir B36938 acriflavine resistance protein acrb - Escherichia coli gb AAA3411.1 (M94248) acriflavine resistance protein [Escherichia coli] gb AAA67135.1 (U00734) 114 kDa protein [Escherichia coli] gb ABA40216.1 (U82664) probable transmembrane protein AcrE [Escherichia coli] gb AAC73564.1 (AE000152) acridine efflux pump [Escherichia coli K12] sp P31223 ACRA_ECOLI ACRIFLAVIN RESISTANCE PROTEIN A PRECURSOR pir A36938 acriflavine resistance protein acra precursor - Escherichia coli gb AAA23410.1 (M94248) acriflavine resistance protein [Escherichia coli] gb AAA67134.1 (U00734) 42 kDa protein [Escherichia coli] gb ABA40217.1 (U82664) lipoprotein Acra precursor [Escherichia coli] gb AAC73565.1 (AE000152) acridine efflux pump [Escherichia coli K12] gb AAG54812.1 AE005225_6 (AE005225) acridine efflux pump [Escherichia coli O157:H7] SEQ ID n-9779
SEQ ID n° 9955	PL-92.1	Contig9 from 4668111 to 4670004	m	82%	gb AAG54813.1 AE005225_7 (AE005225) acraB operon repressor [Escherichia coli O157:H7] pir B75270 ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1) gb AAF12012.1 AE002076_4 (AE002076) ABC transporter, ATP-binding protein [Deinococcus radiodurans] pir A75270 conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb AAF12011.1 AE002076_3 (AE002076) conserved hypothetical protein [Deinococcus radiodurans] SEQ ID n-9735
SEQ ID n° 9956	PL-91.1	Contig9 from 4670134 to 4670775	p	70%	
SEQ ID n° 9957	PL-90.1	Contig9 from 4671189 to 4671863	p	77%	
SEQ ID n° 9958	PL-89.1	Contig9 from 4671860 to 4672489	p	63%	

SEQ ID n° 9959	PL-3374.1	Contig9 from 4672530 to 4673078	p	71%	pir C75270 probable biotin synthase - Deinococcus radiodurans (strain R1) gb AAE12013.1 AE002076_5 (AE002076) biotin synthase, putative [Deinococcus radiodurans] SEQ ID n-2608
SEQ ID n° 9960	PL-88.1	Contig9 from 4673197 to 4673961	m	54%	gb AAF17282.1 (AF204805) unknown [Nostoc sp. GSV224] SEQ ID n-9724
SEQ ID n° 9961	PL-3375.1	Contig9 from 4674084 to 4674521	p	36%	ref NP_070641.1 hypothetical protein [Archaeoglobus fulgidus] pir E69476 hypothetical protein AF1814 - Archaeoglobus fulgidus gb AAB89439.1 (AE000977) A. fulgidus predicted coding region AF1814 [Archaeoglobus fulgidus] SEQ ID n-2609
SEQ ID n° 9962	PL-5243.1	Contig9 from 4674650 to 4674817	m	46%	gb AAG54815.1 AE005225_9 (AE005225) Z0583 gene product [Escherichia coli O157:H7] #N/A
SEQ ID n° 9963	PL-3376.1	Contig9 from 4674840 to 4675382	m	52%	sp P23862 PRIC_ECOLI PRIMOSOMAL REPLICATION PROTEIN N" pir JQ1149 primosomal replication factor N pric [validated] - Escherichia coli dbj BAA03055.1 (D13958) primosomal replication protein n' (gtg start codon) [Escherichia coli] gb AAB40221.1 (U82664) primosomal replication protein n [Escherichia coli] gb AAC73569.1 (AE000153) primosomal replication protein N'' [Escherichia coli K12] SEQ ID n-2610
SEQ ID n° 9964	PL-3377.1	Contig9 from 4675526 to 4676077	p	83%	gb AAB40223.1 (U82664) adenine phosphoribosyltransferase [Escherichia coli] SEQ ID n-2611
SEQ ID n° 9965	PL-87.1	Contig9 from 4676174 to 4678150	p	76%	gb AAG54819.1 AE005226_2 (AE005226) DNA polymerase III; tau and gamma subunits; DNA elongation factor III [Escherichia coli O157:H7] SEQ ID n-9714

SEQ ID n° 9966	PL-5244.1	Contig9 from 4678207 to 4678536	P 93%	sp P17577 YBAB_ECOLI_HYPOTHETICAL_12.0_KDA PROTEIN IN DNAX-RECR INTERGENIC REGION pir QGCZG ybaB_protein - Escherichia coli gb AA233458.1 (M38777) orf12 ORF [Escherichia coli] gb AAC73573.1 (AE000153) orf, hypothetical protein [Escherichia coli K12] gb AAG54820.1 AE005226_3 (AE005226) orf, hypothetical protein [Escherichia coli O157:H7] sp P12727 RECR_ECOLI_RECOMBINATION_PROTEIN_REC pir BVECR recombination protein recr - Escherichia coli emb CAA33768.1 (X15761) recr product (AA 1-201) [Escherichia coli] gb AAB40226.1 (U82664) recr [Escherichia coli] gb AAC73574.1 (AE000153) recombination and repair [Escherichia coli K12] gb AAG54821.1 AE005226_4 (AE005226) recombination and repair [Escherichia coli O157:H7]	#N/A
SEQ ID n° 9967	PL-86.1	Contig9 from 4678536 to 4679141	P 90%	sp P44523 HXCI_HAEM_HEME-HEMOPEXIN_UTILIZATION PROTEIN C PRECURSOR pir B64049 outer membrane protein hxC homolog - Haemophilus influenzae (strain Rd KW20) gb AAC21789.1 (U32696) hemin receptor (hemR) [Haemophilus influenzae Rd] sp P10413 HTPG_ECOLI_HEAT_SHOCK_PROTEIN_HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C62.5) pir HHEC62 heat shock protein C62.5 - Escherichia coli gb AA23460.1 (M38777) htpG ORF [Escherichia coli] gb AAB40227.1 (U82664) heat shock protein HtpG [Escherichia coli] gb AAC73575.1 (AE000153) chaperone Hsp90, heat shock protein C 62.5 [Escherichia coli K12] gb AAB40228.1 (U82664) adenylate kinase [Escherichia coli]	SEQ ID n-9703 SEQ ID n-9692 SEQ ID n-9681 SEQ ID n-9670
SEQ ID n° 9968	PL-85.1	Contig9 from 4679538 to 4681610	M 43%		
SEQ ID n° 9969	PL-84.1	Contig9 from 4682135 to 4684027	P 91%		
SEQ ID n° 9970	PL-83.1	Contig9 from 4684210 to 4684854	P 88%		

SEQ ID n° 9971	PL-82.1	Contig9 from 4685031 to 4686008	p	76%	sp P43413 HEMZ_YEREN FERROCHELATASE (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) pir S70735 ferrochelataase (EC 4.99.1.1) - Yersinia enterocolitica emb CAAB7697.1 (Z47767) ferrochelataase [Yersinia enterocolitica] emb CAB63286.1 (AJ251713) O-antigen chain length determinant-like protein	SEQ ID n-3660
SEQ ID n° 9972	PL-81.1	Contig9 from 4686192 to 4687295	p	65%	[Yersinia pestis] sp P22937 INGK_ECOLI INOSINE-GUANOSINE KINASE pir JQ0812 inosine kinase (EC 2.7.1.73) - Escherichia coli dbj BA00690.1 (D00798) inosine-guanosine kinase [Escherichia coli] gb AAB40231.1 (U82664) inosine kinase [Escherichia coli] gb AAC73579.1 (AE000154) inosine-guanosine kinase [Escherichia coli K12] gb AAG54826.1 AE005226_9 (AE005226) inosine- guanosine kinase [Escherichia coli O157:H7] pir C55543 cmaU protein - Pseudomonas syringae pv. syringae gb AAC46034.1 (U14657) CmaU [Pseudomonas syringae]	SEQ ID n-3649
SEQ ID n° 9973	PL-80.1	Contig9 from 4687394 to 4688704	p	89%	gb AAB40231.1 (U82664) inosine kinase [Escherichia coli] gb AAC73579.1 (AE000154) inosine-guanosine kinase [Escherichia coli K12] gb AAG54826.1 AE005226_9 (AE005226) inosine- guanosine kinase [Escherichia coli O157:H7] pir C55543 cmaU protein - Pseudomonas syringae pv. syringae gb AAC46034.1 (U14657) CmaU [Pseudomonas syringae]	SEQ ID n-3638
SEQ ID n° 9974	PL-79.1	Contig9 from 4689854 to 4690465	p	42%		SEQ ID n-9626
SEQ ID n° 9975	PL-5247.1	Contig9 from 4690663 to 4690881	m	No Hits found	#N/A	
SEQ ID n° 9976	PL-78.1	Contig9 from 4690878 to 4692584	m	83%	gb AAG54827.1 AE005227_1 (AE005227) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-3615
SEQ ID n° 9977	PL-77.1	Contig9 from 4692826 to 4694043	m	83%	gb AAG54828.1 AE005227_2 (AE005227) fosmidomycin resistance protein [Escherichia coli O157:H7]	SEQ ID n-3604
SEQ ID n° 9978	PL-76.1	Contig9 from 4694434 to 4696092	p	80%	pir JC7221 UDP(uridine 5'-diphosphate)-sugar hydrolase (EC 3.-.-.-) - aerogenes gb AAF12718.1 AF068226_1 (AF068226) UDP-sugar hydrolase precursor [Enterobacter aerogenes]	SEQ ID n-3594

1079

SEQ ID n° 9979	PL-3378.1	Contig9 from 4696154 to 4696630	m	69%	sp P37175 YBAK_ECOLI PROTEIN YBAK pir H64778 ybak protein - Escherichia coli gb AAB40235.1 (U82664)-similar to H ₂ -influenzae HI1434 [Escherichia coli] gb AAC73583.1 (AE000154) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-3612
SEQ ID n° 9980	PL-75.1	Contig9 from 4696831 to 4697643	m	63%	sp P77301 YBAP_ECOLI HYPOTHETICAL 29.9 KD PROTEIN IN USHA-TESA INTERGENIC REGION pir A64779 ybap protein - Escherichia coli gb AAB40236.1 (U82664) hypothetical protein [Escherichia coli] gb AAC73584.1 (AE000154) putative ligase [Escherichia coli K12] SEQ ID n-3583
SEQ ID n° 9981	PL-5249.1	Contig9 from 4697925 to 4698242	p	No Hits found	#N/A
SEQ ID n° 9982	PL-74.1	Contig9 from 4698369 to 4701104	m	77%	gb AAG54833.1 AE005227_7 (AE005227) putative ATPase [Escherichia coli O157:H7] sp P77565 YBBI_ECOLI HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN USHA-TESA INTERGENIC REGION pir F64779 probable transcription regulator ybbi - Escherichia coli gb AAB40241.1 (U82664) similar to H ₂ influenzae HI0293 [Escherichia coli] gb AAC73589.1 (AE000155) putative transcriptional regulator [Escherichia coli K12] SEQ ID n-3572
SEQ ID n° 9983	PL-5250.1	Contig9 from 4701246 to 4701647	p	77%	#N/A
SEQ ID n° 9984	PL-3379.1	Contig9 from 4701641 to 4702096	m	61%	sp P75709 YBBJ_ECOLI HYPOTHETICAL 16.8 KD PROTEIN IN USHA-TESA INTERGENIC REGION pir G64779 probable membrane protein ybbJ - Escherichia coli gb AAC73590.1 (AE000155) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-2613

SEQ ID n° 9985	PL-73.1	Contig9 from 4702099 to 4703019	m	88%	sp P77367 YBBK_ECOLI_HYPOTHETICAL_33.7_KD PROTEIN IN USHA-TESA INTERGENIC REGION pir H64779 probable membrane-protein-ybbk - Escherichia coli gb AAB40243.1 (U82664) similar to M. tuberculosis MTCV277.09 [Escherichia coli] gb AAC73591.1 (AE000155) putative protease [Escherichia coli K12] gb AAG54846.1 AE005230_6 (AE005230) putative protease [Escherichia coli O157:H7] gb AAG54849.1 AE005230_9 (AE005230) putative thioredoxin-like protein [Escherichia coli O157:H7]	SEQ ID n-3562
SEQ ID n° 9986	PL-72.1	Contig9 from 4703044 to 4703901	m	77%	sp AAG54850.1 AE005230_10 (AE005230) putative oxidoreductase [Escherichia coli O157:H7]	SEQ ID n-3552
SEQ ID n° 9987	PL-71.1	Contig9 from 4703970 to 4704755	m	78%	gb AAB40248.1 (U82664) acyl-coA thioesterase I precursor [Escherichia coli]	SEQ ID n-3541
SEQ ID n° 9988	PL-70.1	Contig9 from 4704806 to 4705441	m	65%	sp P31219 YBBA_ECOLI_HYPOTHETICAL_ABC TRANSPORTER ATP-BINDING PROTEIN YBBA pir F64780 probable ABC-type transport protein ybbA - Escherichia coli gb AAB40249.1 (U82664) hypothetical abc transporter [Escherichia coli] gb AAC73597.1 (AE000155) putative ATP-binding component of a transport system [Escherichia coli K12]	SEQ ID n-3530
SEQ ID n° 9989	PL-69.1	Contig9 from 4705409 to 4706095	p	85%	gb AAG54852.1 AE005230_12 (AE005230) putative ATP-binding component of a transport system [Escherichia coli O157:H7]	SEQ ID n-3519
SEQ ID n° 9990	PL-68.1	Contig9 from 4706092 to 4708524	p	78%	sp P77504 YBBP_ECOLI_HYPOTHETICAL_89.3_KD PROTEIN IN TESA-RHSD INTERGENIC REGION pir G64780 probable membrane protein ybbp - Escherichia coli gb AAB40250.1 (U82664) hypothetical protein [Escherichia coli] gb AAC73598.1 (AE000155) putative oxidoreductase [Escherichia coli K12]	SEQ ID n-3508

Contig9 from SEQ ID n° 9991	PL-67.1 4708744 to 4709808	m	52%	pir [B64843 hypothetical protein b1012 - Escherichia coli gb AAC74097.1 (AE000202) orf, hypothetical protein [Escherichia coli K12] dbj BAA35789.1 (D90738) Hypothetical 49.3 kd protein in idh-deor intergenic region. [Escherichia coli] sp P37482 YVCB_BACSU HYPOTHETICAL 43.2 KD PROTEIN IN DNAC-RPLI INTERGENIC REGION pir [S65973 transport protein homolog yycB - Bacillus subtilis dbj BAA05179.1 (D26185) unknown [Bacillus subtilis] emb CAB16085.1 (Z99124) similar to ABC transporter (permease) [Bacillus subtilis] pir [C83625 hypothetical protein PA0165 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03555.1 AE004454.7 (AE004454) hypothetical protein [Pseudomonas aeruginosa] sp P45273 RISA_HAEIN RIBOFLAVIN SYNTHASE ALPHA CHAIN pir [E64132 riboflavin synthase (EC 2.5.1.9) alpha chain - Haemophilus influenzae gb AAC23257.1 (U32834) riboflavin synthase, alpha chain (ribe) [Haemophilus influenzae Rd] gb AAF81206.1 AF247502_1 (AF247502) Yt12 [Salmonella dublin] ref NP_047874.1 putative transposase [Yersinia pestis] pir [T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CAB55253.1 (AL117211) hypothetical protein YPMT1.71 [Yersinia pestis]	SEQ ID n-9498
Contig9 from SEQ ID n° 9992	PL-66.1 4709869 to 4711143	m	38%	pir [S65973 transport protein homolog yycB - Bacillus subtilis dbj BAA05179.1 (D26185) unknown [Bacillus subtilis] emb CAB16085.1 (Z99124) similar to ABC transporter (permease) [Bacillus subtilis] pir [C83625 hypothetical protein PA0165 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03555.1 AE004454.7 (AE004454) hypothetical protein [Pseudomonas aeruginosa] sp P45273 RISA_HAEIN RIBOFLAVIN SYNTHASE ALPHA CHAIN pir [E64132 riboflavin synthase (EC 2.5.1.9) alpha chain - Haemophilus influenzae gb AAC23257.1 (U32834) riboflavin synthase, alpha chain (ribe) [Haemophilus influenzae Rd] gb AAF81206.1 AF247502_1 (AF247502) Yt12 [Salmonella dublin] ref NP_047874.1 putative transposase [Yersinia pestis] pir [T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CAB55253.1 (AL117211) hypothetical protein YPMT1.71 [Yersinia pestis]	SEQ ID n-9488
Contig9 from SEQ ID n° 9993	PL-65.1 4711199 to 4712113	m	33%	pir [S65973 transport protein homolog yycB - Bacillus subtilis dbj BAA05179.1 (D26185) unknown [Bacillus subtilis] emb CAB16085.1 (Z99124) similar to ABC transporter (permease) [Bacillus subtilis] pir [C83625 hypothetical protein PA0165 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03555.1 AE004454.7 (AE004454) hypothetical protein [Pseudomonas aeruginosa] sp P45273 RISA_HAEIN RIBOFLAVIN SYNTHASE ALPHA CHAIN pir [E64132 riboflavin synthase (EC 2.5.1.9) alpha chain - Haemophilus influenzae gb AAC23257.1 (U32834) riboflavin synthase, alpha chain (ribe) [Haemophilus influenzae Rd] gb AAF81206.1 AF247502_1 (AF247502) Yt12 [Salmonella dublin] ref NP_047874.1 putative transposase [Yersinia pestis] pir [T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CAB55253.1 (AL117211) hypothetical protein YPMT1.71 [Yersinia pestis]	SEQ ID n-9477
Contig9 from SEQ ID n° 9994	PL-64.1 4713134 to 4713799	p	53%	pir [S65973 transport protein homolog yycB - Bacillus subtilis dbj BAA05179.1 (D26185) unknown [Bacillus subtilis] emb CAB16085.1 (Z99124) similar to ABC transporter (permease) [Bacillus subtilis] pir [C83625 hypothetical protein PA0165 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03555.1 AE004454.7 (AE004454) hypothetical protein [Pseudomonas aeruginosa] sp P45273 RISA_HAEIN RIBOFLAVIN SYNTHASE ALPHA CHAIN pir [E64132 riboflavin synthase (EC 2.5.1.9) alpha chain - Haemophilus influenzae gb AAC23257.1 (U32834) riboflavin synthase, alpha chain (ribe) [Haemophilus influenzae Rd] gb AAF81206.1 AF247502_1 (AF247502) Yt12 [Salmonella dublin] ref NP_047874.1 putative transposase [Yersinia pestis] pir [T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CAB55253.1 (AL117211) hypothetical protein YPMT1.71 [Yersinia pestis]	SEQ ID n-9466
Contig9 from SEQ ID n° 9995	PL-63.1 4714501 to 4715463	p	70%	pir [S65973 transport protein homolog yycB - Bacillus subtilis dbj BAA05179.1 (D26185) unknown [Bacillus subtilis] emb CAB16085.1 (Z99124) similar to ABC transporter (permease) [Bacillus subtilis] pir [C83625 hypothetical protein PA0165 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03555.1 AE004454.7 (AE004454) hypothetical protein [Pseudomonas aeruginosa] sp P45273 RISA_HAEIN RIBOFLAVIN SYNTHASE ALPHA CHAIN pir [E64132 riboflavin synthase (EC 2.5.1.9) alpha chain - Haemophilus influenzae gb AAC23257.1 (U32834) riboflavin synthase, alpha chain (ribe) [Haemophilus influenzae Rd] gb AAF81206.1 AF247502_1 (AF247502) Yt12 [Salmonella dublin] ref NP_047874.1 putative transposase [Yersinia pestis] pir [T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CAB55253.1 (AL117211) hypothetical protein YPMT1.71 [Yersinia pestis]	SEQ ID n-9455
Contig9 from SEQ ID n° 9996	PL-5253.1 4715614 to 4715817	p	49%	pir [S65973 transport protein homolog yycB - Bacillus subtilis dbj BAA05179.1 (D26185) unknown [Bacillus subtilis] emb CAB16085.1 (Z99124) similar to ABC transporter (permease) [Bacillus subtilis] pir [C83625 hypothetical protein PA0165 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03555.1 AE004454.7 (AE004454) hypothetical protein [Pseudomonas aeruginosa] sp P45273 RISA_HAEIN RIBOFLAVIN SYNTHASE ALPHA CHAIN pir [E64132 riboflavin synthase (EC 2.5.1.9) alpha chain - Haemophilus influenzae gb AAC23257.1 (U32834) riboflavin synthase, alpha chain (ribe) [Haemophilus influenzae Rd] gb AAF81206.1 AF247502_1 (AF247502) Yt12 [Salmonella dublin] ref NP_047874.1 putative transposase [Yersinia pestis] pir [T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CAB55253.1 (AL117211) hypothetical protein YPMT1.71 [Yersinia pestis]	SEQ ID n-9455
Contig9 from SEQ ID n° 9997	PL-6968.1 4716279 to 4716374	p	No Hits found		#N/A
					#N/A

sp|P09029|PURK_ECOLI
 PHOSPHORIBOSYLAMINOIMIDAZOLE-CARBOXYLASE ATPASE
 SUBUNIT (AIR) CARBOXYLASE) (AIRC)
 pir||DCECPK phosphoribosylaminoimidazole
 carboxylase (EC 4.1.1.21) carbon
 dioxide-fixation chain - Escherichia coli
 gb|AA24450.1| (M19657) 5'-phosphoribosyl-5-
 amino-4-imidazole carboxylase II
 (purK, EC 4.1.1.21) [Escherichia coli]
 gb|AAB40275.1| (U82664) 5'-phosphoribosyl-5-
 amino-4-imidazole carboxylase II
 [Escherichia coli] gb|AAC73624.1| (AE000158)
 phosphoribosylaminoimidazole carboxylase = AIR
 carboxylase, CO(2)-fixing subunit [Escherichia
 coli K12] SEQ ID n-3444
 sp|P09028|PUR6_ECOLI
 PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE
 CATALYTIC SUBUNIT (AIR) CARBOXYLASE)
 (AIRC) pir||DECPE phosphoribosylaminoimidazole
 carboxylase (EC 4.1.1.21) catalytic
 chain - Escherichia coli emb|CAA31420.1|
 (X12982) purE gene product (catalytic subunit)
 (AA 1- 169) [Escherichia coli]
 gb|AA24449.1| (M19657) 5'-phosphoribosyl-5-
 amino-4-imidazole carboxylase I (purE,
 EC 4.1.1.21) [Escherichia coli] gb|AAB40276.1|
 (U82664) phosphoribosylaminoimidazole
 carboxylase [Escherichia coli]
 gb|AAC73625.1| (AE000158)
 phosphoribosylaminoimidazole carboxylase = AIR
 carboxylase, catalytic subunit [Escherichia coli
 K12] gb|AG54880.1|AE005233_6 (AE005233)
 phosphoribosylaminoimidazole carboxylase = AIR
 carboxylase, catalytic subunit [Escherichia coli
 O157:H7] SEQ ID n-2615

Contig9 from
 SEQ ID n° 9998 PL-62.1 4716730 to m 76%
 4717827

Contig9 from
 SEQ ID n° 9999 PL-3380.1 4717824 to m 82%
 4718354

SEQ ID n° 10000	PL-61.1	Contig9 from 4718502 to 4719224	m	68%	gb AAG54881.1 AE005233_7 (AE005233)orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-9434
SEQ ID n° 10001	PL-3381.1	Contig9 from 4719235 to 4719729	m	77%	gb AAG54882.1 AE005233_8 (AE005233)peptidyl- prolyl cis-trans isomerase B (rotamase B) [Escherichia coli O157:H7] SEQ ID n-2616
SEQ ID n° 10002	PL-5254.1	Contig9 from 4719604 to 4719735	p	70%	gb AAB40278.1 (U82664)hypothetical protein [Escherichia coli] #N/A
SEQ ID n° 10003	PL-60.1	Contig9 from 4719997 to 4721382	p	85%	sp P21888 SYC_ECOLI_CYSSTEINYL-TRNA SYNTHETASE (CYSSTEINE--TRNA LIGASE) (CYRS) pir YYEC cysteine--trna ligase (EC 6.1.1.16) - Escherichia coli emb CAA41983.1 (X59293) cysteinyl-trna synthetase [Escherichia coli] gb AAA23658.1 (M59381)transfer RNA-Cys synthetase [Escherichia coli] gb AAB40279.1 (U82664) cysteinyl-trna synthetase [Escherichia coli] gb AAC73628.1 (AE000158) cysteine trna synthetase [Escherichia coli K12] prf 1714234A Cys-trna synthetase [Escherichia coli] SEQ ID n-9423
SEQ ID n° 10004	PL-59.1	Contig9 from 4721451 to 4723304	m	22%	pir D42463 hypothetical protein Bcv' (pinB 5' region) - Shigella boydii (fragment) SEQ ID n-3411
SEQ ID n° 10005	PL-58.1	Contig9 from 4723734 to 4724651	m	58%	pir E71694 hypothetical protein RP372 - Rickettsia prowazekii emb CAA14831.1 (AJ235271) unknown [Rickettsia prowazekii] SEQ ID n-9400
SEQ ID n° 10006	PL-57.1	Contig9 from 4724664 to 4725668	m	35%	pir T36184 probable oxygenase - Streptomyces coelicolor emb CAB38880.1 (AL035707) putative oxygenase [Streptomyces coelicolor A3(2)] SEQ ID n-3390

SEQ ID n° 10007	PL-56.1	Contig9 from 4726512 to 4727171	m	72%	<p>sp P76459 ATOA_ECOLI_ACETATE_COA-TRANSFERASE BETA SUBUNIT (ACETYL-COA:ACETOACETATE COA TRANSFERASE BETA SUBUNIT) -pir D64992 butyrate- acetoacetate CoA-transferase (EC 2.8.3.9) large chain homolog atoa [similarity] - Escherichia coli (strain K-12) dbj BAA16018.1 (D90851) Acetyl-CoA:acetoacetyl- CoA transferase b subunit (EC 2.8.3.-). [Escherichia coli] gb AAC75282.1 (AE000311) acetyl-CoA:acetoacetyl-CoA transferase beta subunit [Escherichia coli K12] SEQ ID n-3379</p>
SEQ ID n° 10008	PL-55.1	Contig9 from 4727174 to 4727833	m	82%	<p>sp P76458 ATOD_ECOLI_ACETATE_COA-TRANSFERASE ALPHA SUBUNIT (ACETYL-COA:ACETOACETATE COA TRANSFERASE ALPHA SUBUNIT) -pir C64992 atod protein - Escherichia coli (strain K-12) dbj BAA16017.1 (D90851) Acetyl-CoA:acetoacetyl- CoA transferase a subunit (EC 2.8.3.-). [Escherichia coli] gb AAC75281.1 (AE000311) acetyl-CoA:acetoacetyl-CoA transferase alpha subunit [Escherichia coli K12] SEQ ID n-3368</p> <p>sp Q06065 ATOC_ECOLI_ACETOACETATE_METABOLISM REGULATORY PROTEIN ATOC (ORNITHINE/ARGININE DECARBOXYLASE INHIBITOR) (ORNITHINE DECARBOXYLASE ANTIZYME) -pir B64992 acetoacetate metabolism regulatory protein atoc - Escherichia coli gb AAAG0332.1 (U17902) NtrC/NtrA-like protein regulator [Escherichia coli] dbj BAA16016.1 (D90851) Acetoacetate metabolism regulatory protein Atoc (Ornithine / Arginine decarboxylase inhibitor) (Ornithine decarboxylase antizyme). [Escherichia coli] gb AAC75280.1 (AE000311) response regulator of ato, ornithine decarboxylase antizyme (sensor ATOS) [Escherichia coli K12] #N/A</p>
SEQ ID n° 10009	PL-5257.1	Contig9 from 4727830 to 4728234	m	66%	

SEQ ID n°	Contig9 from	PL	Contig9 from	m	No Hits	found	SEQ ID n-3357
SEQ ID n° 10010	4728459 to	PL-54.1	4729538	m	No Hits	found	SEQ ID n-3357
SEQ ID n° 10011	4730381 to	PL-53.1	4731478	p	62%		
SEQ ID n° 10012	4732125 to	PL-3382.1	4732574	p	No Hits	found	SEQ ID n-3346
SEQ ID n° 10013	4733044 to	PL-52.1	4734072	m	No Hits	found	SEQ ID n-3617
SEQ ID n° 10014	4735646 to	PL-5259.1	4736083	p	No Hits	found	SEQ ID n-3335
SEQ ID n° 10015	4736961 to	PL-51.1	4737794	m	No Hits	found	#N/A
SEQ ID n° 10016	4738647 to	PL-5260.1	4738829	p	No Hits	found	SEQ ID n-3324
SEQ ID n° 10017	4739280 to	PL-5261.1	4739495	p	71%		#N/A
SEQ ID n° 10018	4739724 to	PL-5362.1	4740116	m	69%		#N/A
SEQ ID n° 10019	4740113 to	PL-50.1	4741096	m	63%		#N/A

Contig9 from
 4728459 to 4729538
 Contig9 from
 4730381 to 4731478
 Contig9 from
 4732125 to 4732574
 Contig9 from
 4733044 to 4734072
 Contig9 from
 4735646 to 4736083
 Contig9 from
 4736961 to 4737794
 Contig9 from
 4738647 to 4738829
 Contig9 from
 4739280 to 4739495
 Contig9 from
 4739724 to 4740116
 Contig9 from
 4740113 to 4741096

pir||S46408 hypothetical protein - Aeromonas salmonicida gb|AA72049.1| (t27156) [Aeromonas salmonicida gene, complete cds.] gene product
 gb|AAB40924.1| (U82821) major cold shock protein CSP22 [Yersinia enterocolitica]
 ref|NP_052386.1| YopT chaperone SycT [Yersinia enterocolitica] gb|AAD16809.1| (AF102990) YopT chaperone SycT [Yersinia enterocolitica]
 ref|NP_054620.1| unknown [Yersinia pestis]
 ref|NP_047619.1| Yop targeted effector [Yersinia pestis] pir||T43601 yop targeted effector yopT yersinia pestis plasmid pCD1 gb|AAC62582.1| (AF053946) unknown [Yersinia pestis]
 gb|AAC69833.1| (AF074612) Yop targeted effector [Yersinia pestis] emb|CAB54897.1| (AL117189) putative cytotoxic effector protein [Yersinia pestis]

SEQ ID n-3313

SEQ ID n° 10020 PL-49.1	Contig9 from 4741251 to 4741868	m 79%	gb AAC37030.1 (M74011) putative [Yersinia enterocolitica]	SEQ ID n-3301
SEQ ID n° 10021 PL-48.1	Contig9 from 4741847 to 4742473	m 45%	pir D83431 type III export protein PscK PA1724 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05113.1 AE004598_12 (AE004598) type III export protein PscK [Pseudomonas aeruginosa]	SEQ ID n-3290
SEQ ID n° 10022 PL-47.1	Contig9 from 4742473 to 4743210	m 86%	gb AAC44781.1 (U56077) PscJ [Pseudomonas aeruginosa]	SEQ ID n-3279
SEQ ID n° 10023 PL-5266.1	Contig9 from 4743217 to 4743555	m 70%	pir B83431 type III export protein PscI PA1722 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05111.1 AE004598_10 (AE004598) type III export protein PscI [Pseudomonas aeruginosa] #N/A	
SEQ ID n° 10024 PL-46.1	Contig9 from 4743631 to 4744197	m 38%	ref NP_054587.1 Yop proteins translocation... protein H homolog [Yersinia pestis] ref NP_047581.1 secreted protein [Yersinia pestis] sp Q00929 YSCY_YERPS YOP PROTEINS TRANSLOCATION PROTEIN H (LOW CALCIUM RESPONSE LOCUS PROTEIN P) pir T43568 translocation protein H homolog - Yersinia pestis plasmid pCD1 gb AA27649.1 (M83986) lcrP [Yersinia pseudotuberculosis] gb AAC62547.1 (AF053946) Yop proteins translocation protein H homolog [Yersinia pestis] gb AAC69828.1 (AF074612) secreted protein [Yersinia pestis] emb CAB54934.1 (AL117189) putative type III secretion protein [Yersinia pestis]	SEQ ID n-3268

SEQ ID n° 10025 PL-5267.1	Contig9 from 4744190 to 4744543	m 58%	ref NP_054588.1 Yop proteins translocation protein G homolog [Yersinia pestis] ref NP_047582.1 type III secretion protein [Yersinia pestis] pir T43569 translocation protein G homolog - Yersinia pestis plasmid pCD1 gb AAC62548.1 (AF053946) Yop proteins translocation protein G homolog [Yersinia pestis] gb AAC69777.1 (AF074612) type III secretion protein [Yersinia pestis] emb CAB54933.1 (AL117189) putative type III secretion protein [Yersinia pestis] pir G83430 type III export protein PscF PA1719 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAC44777.1 (U56077) PscF [Pseudomonas aeruginosa] gb AAG05108.1 AE004598_7 (AE004598) type III export protein PscF [Pseudomonas aeruginosa] ref NP_054590.1 Yop proteins translocation protein E homolog [Yersinia pestis] ref NP_047584.1 type III secretion protein [Yersinia pestis] pir T43571 type III secretion protein yscE - Yersinia pestis plasmid pCD1 gb AAC62550.1 (AF053946) Yop proteins translocation protein E homolog [Yersinia pestis] gb AAC69779.1 (AF074612) type III secretion protein [Yersinia pestis] emb CAB54931.1 (AL117189) putative type III secretion protein [Yersinia pestis] pir E83430 type III export protein PscD PA1717 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05106.1 AE004598_5 (AE004598) type III export protein PscD [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 10026 PL-5268.1	Contig9 from 4744546 to 4744800	m 60%		#N/A
SEQ ID n° 10027 PL-5269.1	Contig9 from 4744784 to 4745002	m 48%		#N/A
SEQ ID n° 10028 PL-45.1	Contig9 from 4745002 to 4746270	m 65%		#N/A

SEQ ID n° 3257

SEQ ID n° 10029	PL-44.1	Contig9 from 4746267 to 4748135	m	73%	ref NP_052413.1 secretin YscC [Yersinia enterocolitica] sp Q01244 YSCC_YEREN YOP- PROTEINS TRANSLOCATION PROTEIN C_PRECURSOR pir C40361 virC-region hypothetical protein yscC precursor - Yersinia enterocolitica plasmid pXV gb AAC37020.1 (M74011) yscC gene product [Yersinia enterocolitica] gb AAD16836.1 (AF102990) secretin YscC [Yersinia enterocolitica] pir C83430 type III export apparatus protein PA1715 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05104.1 AE004598_3 (AE004598) type III export apparatus protein [Pseudomonas aeruginosa] pir B83430 hypothetical protein PA1714 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05103.1 AE004598_2 (AE004598) hypothetical protein [Pseudomonas aeruginosa] sp P26993 EXSA_PSEAE EXOENZYME S SYNTHESIS REGULATORY PROTEIN EXSA pir A83430 transcription regulator ExsA PA1713 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05102.1 AE004598_1 (AE004598) transcriptional regulator ExsA [Pseudomonas aeruginosa] pir B83434 translocation protein in type III secretion PA1690 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05079.1 AE004596_5 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa]	SEQ ID n-3246
SEQ ID n° 10030	PL-3384.1	Contig9 from 4748108 to 4748530	m	48%		SEQ ID n-2618
SEQ ID n° 10031	PL-43.1	Contig9 from 4748545 to 4749378	m	53%		SEQ ID n-3237
SEQ ID n° 10032	PL-42.1	Contig9 from 4749493 to 4750311	m	75%		SEQ ID n-3226
SEQ ID n° 10033	PL-41.1	Contig9 from 4751211 to 4752266	m	79%		SEQ ID n-3215

SEQ ID n° 10034	PL-40.1	Contig9 from 4752263 to 4753051	m	86%	<p>pir C83434 translocation protein in type III secretion PA1691 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05080.1 AE004596_6 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa] ref NP_052406.1 YSCS [Yersinia enterocolitica] ref NP_054599.1 Yop proteins translocation protein S homolog [Yersinia pestis] ref NP_047593.1 type III secretion protein [Yersinia pestis] sp P40298 YSCS_YERPS YOP PROTEINS TRANSLOCATION PROTEIN S pir T43580 type III secretion protein yscs - Yersinia pestis plasmid pCD1 gb AA27679.1 (L25667) yscs [Yersinia pseudotuberculosis] gb AAC62559.1 (AF053946) Yop proteins translocation protein S homolog [Yersinia pestis] gb AAC69786.1 (AF074612) type III secretion protein [Yersinia pestis] gb AAD16829.1 (AF102990) YSCS [Yersinia enterocolitica] emb CAB54922.1 (AL117189) putative type III secretion protein [Yersinia pestis] #N/A</p>	SEQ ID n-3155
SEQ ID n° 10035	PL-5272.1	Contig9 from 4753048 to 4753314	m	76%	<p>pir E83434 translocation protein in type III secretion PA1693 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05082.1 AE004596_8 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa] ref NP_052404.1 YSCQ [Yersinia enterocolitica] gb AAD16827.1 (AF102990) YSCQ [Yersinia enterocolitica]</p>	SEQ ID n-9067
SEQ ID n° 10036	PL-39.1	Contig9 from 4753317 to 4753970	m	87%		
SEQ ID n° 10037	PL-38.1	Contig9 from 4753967 to 4754899	m	60%		SEQ ID n-2976

SEQ ID n° 10038 PL-37.1
 Contig9 from 4754896 to 4756026 m 42%
 pir||G83434 translocation protein in type III secretion PA1695 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05084.1|AE004596_10 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa] ref|NP_054603.1|Yop proteins translocation protein O [Yersinia pestis] ref|NP_047597.1|type III secretion protein [Yersinia pestis] pir||T43584 type III secretion protein yscO - Yersinia pestis plasmid pCD1 gb|AAB72198.1| (AF020214) YscO [Yersinia pestis] gb|AAC62563.1| (AF053946) Yop proteins translocation protein O [Yersinia pestis] gb|AAC69790.1| (AF074612) type III secretion protein [Yersinia pestis] emb|CAB54918.1| (AL117189) putative type-III secretion protein [Yersinia pestis] ref|NP_052401.1|ATPase YscN [Yersinia enterocolitica] sp|P40290|YSCN_YBREN PROBABLE ATP SYNTHASE YSCN (YOPS SECRETION ATPASE) pir||A55520 yscN protein - Yersinia enterocolitica gb|AAD16824.1| (AF102990) ATPase YscN [Yersinia enterocolitica] pir||G83431 outer membrane protein PopN PA1698 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAC45939.1| (AF010150) PopN [Pseudomonas aeruginosa] gb|AAG05087.1|AE004597_1 (AE004597) outer membrane protein PopN [Pseudomonas aeruginosa]

SEQ ID n° 10039 PL-3385.1
 Contig9 from 4756038 to 4756499 m 58%
 pir||G83434 translocation protein in type III secretion PA1695 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05084.1|AE004596_10 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa] ref|NP_054603.1|Yop proteins translocation protein O [Yersinia pestis] ref|NP_047597.1|type III secretion protein [Yersinia pestis] pir||T43584 type III secretion protein yscO - Yersinia pestis plasmid pCD1 gb|AAB72198.1| (AF020214) YscO [Yersinia pestis] gb|AAC62563.1| (AF053946) Yop proteins translocation protein O [Yersinia pestis] gb|AAC69790.1| (AF074612) type III secretion protein [Yersinia pestis] emb|CAB54918.1| (AL117189) putative type-III secretion protein [Yersinia pestis] ref|NP_052401.1|ATPase YscN [Yersinia enterocolitica] sp|P40290|YSCN_YBREN PROBABLE ATP SYNTHASE YSCN (YOPS SECRETION ATPASE) pir||A55520 yscN protein - Yersinia enterocolitica gb|AAD16824.1| (AF102990) ATPase YscN [Yersinia enterocolitica] pir||G83431 outer membrane protein PopN PA1698 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAC45939.1| (AF010150) PopN [Pseudomonas aeruginosa] gb|AAG05087.1|AE004597_1 (AE004597) outer membrane protein PopN [Pseudomonas aeruginosa]

SEQ ID n° 10040 PL-36.1
 Contig9 from 4756499 to 4757821 m 89%
 pir||G83434 translocation protein in type III secretion PA1695 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05084.1|AE004596_10 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa] ref|NP_054603.1|Yop proteins translocation protein O [Yersinia pestis] ref|NP_047597.1|type III secretion protein [Yersinia pestis] pir||T43584 type III secretion protein yscO - Yersinia pestis plasmid pCD1 gb|AAB72198.1| (AF020214) YscO [Yersinia pestis] gb|AAC62563.1| (AF053946) Yop proteins translocation protein O [Yersinia pestis] gb|AAC69790.1| (AF074612) type III secretion protein [Yersinia pestis] emb|CAB54918.1| (AL117189) putative type-III secretion protein [Yersinia pestis] ref|NP_052401.1|ATPase YscN [Yersinia enterocolitica] sp|P40290|YSCN_YBREN PROBABLE ATP SYNTHASE YSCN (YOPS SECRETION ATPASE) pir||A55520 yscN protein - Yersinia enterocolitica gb|AAD16824.1| (AF102990) ATPase YscN [Yersinia enterocolitica] pir||G83431 outer membrane protein PopN PA1698 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAC45939.1| (AF010150) PopN [Pseudomonas aeruginosa] gb|AAG05087.1|AE004597_1 (AE004597) outer membrane protein PopN [Pseudomonas aeruginosa]

SEQ ID n° 10041 PL-35.1
 Contig9 from 4758251 to 4759123 p 75%
 pir||G83434 translocation protein in type III secretion PA1695 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG05084.1|AE004596_10 (AE004596) translocation protein in type III secretion [Pseudomonas aeruginosa] ref|NP_054603.1|Yop proteins translocation protein O [Yersinia pestis] ref|NP_047597.1|type III secretion protein [Yersinia pestis] pir||T43584 type III secretion protein yscO - Yersinia pestis plasmid pCD1 gb|AAB72198.1| (AF020214) YscO [Yersinia pestis] gb|AAC62563.1| (AF053946) Yop proteins translocation protein O [Yersinia pestis] gb|AAC69790.1| (AF074612) type III secretion protein [Yersinia pestis] emb|CAB54918.1| (AL117189) putative type-III secretion protein [Yersinia pestis] ref|NP_052401.1|ATPase YscN [Yersinia enterocolitica] sp|P40290|YSCN_YBREN PROBABLE ATP SYNTHASE YSCN (YOPS SECRETION ATPASE) pir||A55520 yscN protein - Yersinia enterocolitica gb|AAD16824.1| (AF102990) ATPase YscN [Yersinia enterocolitica] pir||G83431 outer membrane protein PopN PA1698 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAC45939.1| (AF010150) PopN [Pseudomonas aeruginosa] gb|AAG05087.1|AE004597_1 (AE004597) outer membrane protein PopN [Pseudomonas aeruginosa]

SEQ ID n-2886

SEQ ID n-2619

SEQ ID n-2797

SEQ ID n-2714

Seq ID n° 10042 PL-5276.1	Contig9 from 4759104 to 4759391	p 70%	pir H83431 conserved hypothetical protein in type III secretion PAL699 Pseudomonas aeruginosa (strain PAO1) gb AAC45940.1 (AF010150) Pcr1 [Pseudomonas aeruginosa] gb AAG05088.1 AE004597_2 (AE004597) conserved hypothetical protein in type III secretion [Pseudomonas aeruginosa] #N/A
Seq ID n° 10043 PL-5277.1	Contig9 from 4759388 to 4759759	p 69%	ref NP_052398.1 YopN chaperone SycN [Yersinia enterocolitica] gb AAA98431.1 (M32097) unknown protein [Plasmid pYV03] gb AAD16821.1 (AF102990) YopN chaperone SycN [Yersinia enterocolitica] #N/A
Seq ID n° 10044 PL-5278.1	Contig9 from 4759756 to 4760121	p 61%	pir B83432 conserved hypothetical protein in type III secretion PAL701 Pseudomonas aeruginosa (strain PAO1) gb AAC45942.1 (AF010150) Pcr3 [Pseudomonas aeruginosa] gb AAG05090.1 AE004597_4 (AE004597) conserved hypothetical protein in type III secretion [Pseudomonas aeruginosa] #N/A
Seq ID n° 10045 PL-5279.1	Contig9 from 4760124 to 4760453	p 56%	gb AAC45943.1 (AF010150) Pcr4 [Pseudomonas aeruginosa] #N/A
Seq ID n° 10046 PL-34.1	Contig9 from 4760450 to 4762567	p 88%	dbj BAA01770.1 (D10998) low calcium response protein [Yersinia enterocolitica] #N/A
Seq ID n° 10047 PL-5281.1	Contig9 from 4762564 to 4762998	p 68%	pir E83432 transcription regulator protein PcrR PAL704 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAC45945.1 (AF010150) PcrR [Pseudomonas aeruginosa] gb AAG05093.1 AE004597_7 (AE004597) transcriptional regulator protein PcrR [Pseudomonas aeruginosa] #N/A

SEQ ID n° 2630

SEQ ID n° 10048 PL-5283.1	Contig9 from 4763039 to 4763317	p 61%	pir F83432 regulator in type III secretion PAL705 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AA05094.1 AE004597_8 (AE004597) regulator in type III secretion [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 10049 PL-33.1	Contig9 from 4763329 to 4764243	p 67%	sp P21206 LCRV_YERPE VIRULENCE-ASSOCIATED V ANTIGEN (LOW CALCIUM RESPONSE LOCUS PROTEIN V) pir B33601 lcrV protein - Yersinia pestis	SEQ ID n-2545
SEQ ID n° 10050 PL-3386.1	Contig9 from 4764253 to 4764756	p 81%	gb AAC45936.1 (AF010149) PcrH [Pseudomonas aeruginosa]	SEQ ID n-2620
SEQ ID n° 10051 PL-32.1	Contig9 from 4764743 to 4765921	p 61%	gb AAC46212.1 (AF035922) PepB [Pseudomonas aeruginosa]	SEQ ID n-2450
SEQ ID n° 10052 PL-31.1	Contig9 from 4765933 to 4766817	p 63%	gb AAC46213.1 (AF035922) PepD [Pseudomonas aeruginosa]	SEQ ID n-2339
SEQ ID n° 10053 PL-5285.1	Contig9 from 4766836 to 4767207	p No Hits found	sp P26995 EXSC_PSEAE EXOENZYME S SYNTHESIS PROTEIN C PRECURSOR pir A41047 exsC protein - Pseudomonas aeruginosa pir C83433 exoenzyme S synthesis protein C precursor PAL710 [imported] Pseudomonas aeruginosa (strain PAO1) gb AAA25814.1 (M64975) S synthesis trans- regulatory protein [Pseudomonas aeruginosa] gb AA05099.1 AE004597_13 (AE004597) exoenzyme S synthesis protein C precursor [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 10054 PL-5286.1	Contig9 from 4767204 to 4767641	p 75%		
SEQ ID n° 10055 PL-5287.1	Contig9 from 4767638 to 4767871	p No Hits found		#N/A

Contig9 from SEQ ID n° 10056 PL-5288.1	4767868 to 4768254	p 60%	ref NP_052409.1 lipoprotein Virg (YscW) [Yersinia enterocolitica] gb AAD16832.1 (AF102990) lipoprotein Virg (YscW) [Yersinia enterocolitica] prf 2117313A lipoprotein [Yersinia enterocolitica] sp P11290 YIBD_ECOLI_HYPOTHETICAL 40.5 KDA PROTEIN IN SEC-B-TDH INTERGENIC REGION pir S47836 hypothetical protein f344 - Escherichia coli pir Q3ECTH hypothetical 40.5K protein (secB-tdh 5' region) - Escherichia coli gb AA18592.1 (U00039) alternate gene name yibD [Escherichia coli] gb AAC76639.1 (AE000439) putative regulator [Escherichia coli K12] ref NP_037752.1 holin [Bacteriophage HK97] gb AAF31096.1 AF069529_9 (AF069529) holin [Bacteriophage HK97] ref NP_049909.1 structural protein P5 [Alteromonas phage PM2] gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2] emb CAA09702.1 (AJ011579) gp15 [bacteriophage PS3] sp P37479 YYCE_BACSU_HYPOTHETICAL 15.6 KD PROTEIN IN PURA-DNAC INTERGENIC REGION pir S65969 YYCE protein - Bacillus subtilis dbj BAA05175.1 (D26185) unknown [Bacillus subtilis] emb CAB16080.1 (Z99124) YYCE [Bacillus subtilis] sp Q48450 YC04_KLEPN_PUTATIVE CAPSULE POLYSACCHARIDE EXPORT PROTEIN PRECURSOR (ORF4) pir B56146 probable polysaccharide export protein precursor - Klebsiella pneumoniae dbj BAA04775.1 (D21242) ORF4 [Klebsiella pneumoniae]	#N/A	SEQ ID n-2229
Contig9 from SEQ ID n° 10057 PL-30.1	4769131 to 4770120	p 39%	ref NP_049909.1 structural protein P5 [Alteromonas phage PM2] gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2] emb CAA09702.1 (AJ011579) gp15 [bacteriophage PS3] sp P37479 YYCE_BACSU_HYPOTHETICAL 15.6 KD PROTEIN IN PURA-DNAC INTERGENIC REGION pir S65969 YYCE protein - Bacillus subtilis dbj BAA05175.1 (D26185) unknown [Bacillus subtilis] emb CAB16080.1 (Z99124) YYCE [Bacillus subtilis] sp Q48450 YC04_KLEPN_PUTATIVE CAPSULE POLYSACCHARIDE EXPORT PROTEIN PRECURSOR (ORF4) pir B56146 probable polysaccharide export protein precursor - Klebsiella pneumoniae dbj BAA04775.1 (D21242) ORF4 [Klebsiella pneumoniae]	#N/A	SEQ ID n-2621
Contig9 from SEQ ID n° 10058 PL-5289.1	4770485 to 4770811	p 63%	ref NP_049909.1 structural protein P5 [Alteromonas phage PM2] gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2] emb CAA09702.1 (AJ011579) gp15 [bacteriophage PS3] sp P37479 YYCE_BACSU_HYPOTHETICAL 15.6 KD PROTEIN IN PURA-DNAC INTERGENIC REGION pir S65969 YYCE protein - Bacillus subtilis dbj BAA05175.1 (D26185) unknown [Bacillus subtilis] emb CAB16080.1 (Z99124) YYCE [Bacillus subtilis] sp Q48450 YC04_KLEPN_PUTATIVE CAPSULE POLYSACCHARIDE EXPORT PROTEIN PRECURSOR (ORF4) pir B56146 probable polysaccharide export protein precursor - Klebsiella pneumoniae dbj BAA04775.1 (D21242) ORF4 [Klebsiella pneumoniae]	#N/A	SEQ ID n-2622
Contig9 from SEQ ID n° 10059 PL-5290.1	4770821 to 4771222	p 59%	ref NP_049909.1 structural protein P5 [Alteromonas phage PM2] gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2] emb CAA09702.1 (AJ011579) gp15 [bacteriophage PS3] sp P37479 YYCE_BACSU_HYPOTHETICAL 15.6 KD PROTEIN IN PURA-DNAC INTERGENIC REGION pir S65969 YYCE protein - Bacillus subtilis dbj BAA05175.1 (D26185) unknown [Bacillus subtilis] emb CAB16080.1 (Z99124) YYCE [Bacillus subtilis] sp Q48450 YC04_KLEPN_PUTATIVE CAPSULE POLYSACCHARIDE EXPORT PROTEIN PRECURSOR (ORF4) pir B56146 probable polysaccharide export protein precursor - Klebsiella pneumoniae dbj BAA04775.1 (D21242) ORF4 [Klebsiella pneumoniae]	#N/A	SEQ ID n-2118
Contig9 from SEQ ID n° 10060 PL-3387.1	4771232 to 4771681	p 58%	ref NP_049909.1 structural protein P5 [Alteromonas phage PM2] gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2] emb CAA09702.1 (AJ011579) gp15 [bacteriophage PS3] sp P37479 YYCE_BACSU_HYPOTHETICAL 15.6 KD PROTEIN IN PURA-DNAC INTERGENIC REGION pir S65969 YYCE protein - Bacillus subtilis dbj BAA05175.1 (D26185) unknown [Bacillus subtilis] emb CAB16080.1 (Z99124) YYCE [Bacillus subtilis] sp Q48450 YC04_KLEPN_PUTATIVE CAPSULE POLYSACCHARIDE EXPORT PROTEIN PRECURSOR (ORF4) pir B56146 probable polysaccharide export protein precursor - Klebsiella pneumoniae dbj BAA04775.1 (D21242) ORF4 [Klebsiella pneumoniae]	#N/A	SEQ ID n-2118
Contig9 from SEQ ID n° 10061 PL-3388.1	4771770 to 4772165	m 40%	ref NP_049909.1 structural protein P5 [Alteromonas phage PM2] gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2] emb CAA09702.1 (AJ011579) gp15 [bacteriophage PS3] sp P37479 YYCE_BACSU_HYPOTHETICAL 15.6 KD PROTEIN IN PURA-DNAC INTERGENIC REGION pir S65969 YYCE protein - Bacillus subtilis dbj BAA05175.1 (D26185) unknown [Bacillus subtilis] emb CAB16080.1 (Z99124) YYCE [Bacillus subtilis] sp Q48450 YC04_KLEPN_PUTATIVE CAPSULE POLYSACCHARIDE EXPORT PROTEIN PRECURSOR (ORF4) pir B56146 probable polysaccharide export protein precursor - Klebsiella pneumoniae dbj BAA04775.1 (D21242) ORF4 [Klebsiella pneumoniae]	#N/A	SEQ ID n-2118
Contig9 from SEQ ID n° 10062 PL-29.1	4772846 to 4773991	p 75%	ref NP_049909.1 structural protein P5 [Alteromonas phage PM2] gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2] emb CAA09702.1 (AJ011579) gp15 [bacteriophage PS3] sp P37479 YYCE_BACSU_HYPOTHETICAL 15.6 KD PROTEIN IN PURA-DNAC INTERGENIC REGION pir S65969 YYCE protein - Bacillus subtilis dbj BAA05175.1 (D26185) unknown [Bacillus subtilis] emb CAB16080.1 (Z99124) YYCE [Bacillus subtilis] sp Q48450 YC04_KLEPN_PUTATIVE CAPSULE POLYSACCHARIDE EXPORT PROTEIN PRECURSOR (ORF4) pir B56146 probable polysaccharide export protein precursor - Klebsiella pneumoniae dbj BAA04775.1 (D21242) ORF4 [Klebsiella pneumoniae]	#N/A	SEQ ID n-2118

1094

SEQ ID n° 10063 PL-5292.1	Contig9 from 4773991 to 4774419	p	71%	sp Q46630 AMSI_ERWAM PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE AMSI pir S52140 protein-tyrosine-phosphatase (EC 3.1.3.48), low molecular weight - Erwinia amylovora emb CAA54881.1 (X77921) acid phosphatase [Erwinia amylovora]	#N/A
SEQ ID n° 10064 PL-28.1	Contig9 from 4774481 to 4776628	p	68%	gb AAD21564.1 (AF104912) putative transmembrane protein Wzc [Escherichia coli]	SEQ ID n-2009
SEQ ID n° 10065 PL-27.1	Contig9 from 4776876 to 4777733	p	66%	pir T47009 hypothetical protein tehB [imported] - Yersinia pestis emb CAA21352.1 (AL031866) ORF29, len: 295 aa, probable tellurite resistance protein (tehB), highly similar to many, eg. P25397 TEHB_ECOLI (197 aa). 61.3% identity in 191 aa overlap Fasta scores:opt: 792, -E(): 0 or U32807_6 Haemophilus influenzae (286 a a), 58.2% ide>	SEQ ID n-1898
SEQ ID n° 10066 PL-26.1	Contig9 from 4777778 to 4779370	m	62%	emb CAB81024.1 (AL161576) putative protein [Arabidopsis thaliana]	SEQ ID n-1791
SEQ ID n° 10067 PL-25.1	Contig9 from 4780110 to 4781477	p	71%	pir F83328 probable sodium:alanine symporter PA2533 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05921.1 AE004681_3 (AE004681) probable sodium:alanine symporter [Pseudomonas aeruginosa]	SEQ ID n-1684
SEQ ID n° 10068 PL-24.1	Contig9 from 4781523 to 4783007	m	65%	gb AAD45415.1 (U65001) salicylaldehyde dehydrogenase [Sphingomonas sp.]	SEQ ID n-1574
SEQ ID n° 10069 PL-23.1	Contig9 from 4783573 to 4784709	m	39%	gb AAK03233.1 (AE006155) unknown [Pasteurella multocida]	SEQ ID n-1466
SEQ ID n° 10070 PL-3389.1	Contig9 from 4785112 to 4785558	p	No Hits found		SEQ ID n-2623

1095

SEQ ID n° 10071	PL-22.1	Contig9 from 4785981 to 4787051	p - 77%	gb AAA85578.1 (U23806) extended ORF of mgte gene; transcription from this start point is unlikely [Providencia stuartii] pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) SEQ ID n-2356
SEQ ID n° 10072	PL-21.1	Contig9 from 4787565 to 4788230	m - 38%	gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) SEQ ID n-2246
SEQ ID n° 10073	PL-20.1	Contig9 from 4789354 to 4790028	p - 44%	gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-2137
SEQ ID n° 10074	PL-5296.1	Contig9 from 4790057 to 4790266	m - NO Hits found	#N/A
SEQ ID n° 10075	PL-19.1	Contig9 from 4790259 to 4791260	p - 60%	pir G82090 transcription regulator LacI family VC2337 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95481.1 (AE004303) transcriptional regulator, LacI family [Vibrio cholerae] sp Q57007 YB07_HAEIN_HYPOTHETICAL NA+/H+ ANTIPORTER H1107_pir I54182 Na+/H+-exchanging protein homolog - Haemophilus influenzae (strain Rd KW20) gb AAC22762.1 (U32790) Na+/H+ antiporter (nhaC) [Haemophilus influenzae Rd] SEQ ID n-2027
SEQ ID n° 10076	PL-18.1	Contig9 from 4791418 to 4792872	p - 67%	SEQ ID n-920

1096

SEQ ID n° 10077	PL-17.1	Contig9 from 4792859 to 4794037	p	54%	sp Q08432 PATE_BACSU PUTATIVE AMINOTRANSFERASE B pir S32934 aminotransferase patB - Bacillus subtilis emb CAB07910.1 (Z93933) aminotransferase [Bacillus subtilis] emb CAB07924.1 (Z93934) aminotransferase [Bacillus subtilis] gb AAB61979.1 (U63302) patB [Bacillus subtilis] emb CAB15133.1 (Z99120) aminotransferase [Bacillus subtilis]	SEQ ID n-809
SEQ ID n° 10078	PL-5300.1	Contig9 from 4794171 to 4794383	m	82%	gb AAF22961.1 AF157489_1 (AF157489) Pln [Photorhabdus luminescens]	#N/A
SEQ ID n° 10079	PL-3390.1	Contig9 from 4795073 to 4795639	p	39%	pir B82381 transcription regulator luxR family VCAL078 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96971.1 (AE004433) transcriptional regulator, luxR family [Vibrio cholerae]	SEQ ID n-2625
SEQ ID n° 10080	PL-16.1	Contig9 from 4795682 to 4796707	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-700
SEQ ID n° 10081	PL-15.1	Contig9 from 4797245 to 4798144	m	69%	gb AAG56458.1 AE005372_3 (AE005372) putative transcriptional regulator LYSR-type [Escherichia coli O157:H7]	SEQ ID n-391
SEQ ID n° 10082	PL-14.1	Contig9 from 4798419 to 4799741	p	75%	sp P77357 ABGA_ECOLI AMINOENZOYL-GLUTAMATE UTILIZATION PROTEIN A	SEQ ID n-480
SEQ ID n° 10083	PL-13.1	Contig9 from 4799734 to 4801182	p	73%	gb AAG56460.1 AE005372_5 (AE005372) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-973
SEQ ID n° 10084	PL-12.1	Contig9 from 4801292 to 4802818	p	82%	sp P46133 ABGT_ECOLI AMINOENZOYL-GLUTAMATE TRANSPORT PROTEIN pir C64883 membrane protein ydaH - Escherichia coli gb AAC74418.1 (AE000231) putative pump protein (transport) [Escherichia coli K12]	SEQ ID n-263

1097

SEQ ID n° 10085	PL-5304.1	Contig9 from 4803096 to 4803530	p	41%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] #N/A
SEQ ID n° 10086	PL-11.1	Contig9 from 4803563 to 4804588	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans] SEQ ID n-252
SEQ ID n° 10087	PL-10.1	Contig9 from 4805130 to 4805822	p	41%	pir C83477 probable transcription regulator PAL347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa] SEQ ID n-43
SEQ ID n° 10088	PL-9.1	Contig9 from 4805876 to 4806556	p	43%	pir B82381 transcription regulator LuxR family VCA1078 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96971.1 (AE004433) transcriptional regulator, luxR family [Vibrio cholerae] SEQ ID n-9746
SEQ ID n° 10089	PL-5306.1	Contig9 from 4806598 to 4806909	p	No Hits found	#N/A
SEQ ID n° 10090	PL-8.1	Contig9 from 4807365 to 4809029	p	56%	pir F82543 outer membrane hemolysin activator protein XF2550 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF85347.1 AE004062_2 (AE004062) outer membrane hemolysin activator protein [Xylella fastidiosa] SEQ ID n-9637
SEQ ID n° 10091	PL-6.1	Contig9 from 4809078 to 4818161	p	35%	pir F81045 hemagglutinin/hemolysin-related protein NMB1768 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF42109.1 (AE002526) hemagglutinin/hemolysin-related protein [Neisseria meningitidis MC58] SEQ ID n-3422

SEQ ID n° 10092 PL-5311.1	Contig9 from 4818176 to 4818523	p 44%	pir D81221 hypothetical protein NMB0237 [imported] - Neisseria meningitidis (group B strain MD58) gb AA040692.1 (AB002381) hypothetical protein [Neisseria meningitidis MC58]	#N/A
SEQ ID n° 10093 PL-5312.1	Contig9 from 4818576 to 4818903	m 43%	sp P39394 YJII_ECOLI_HYPOTHETICAL 14.6 KD PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132) pir S56573 hypothetical 14.6K protein (mcrB-hsdS intergenic region) - Escherichia coli gb AA097244.1 (U14003) ORF_F132 [Escherichia coli] gb AAC77303.1 (AE000505) orf, hypothetical protein [Escherichia coli K12]	#N/A
SEQ ID n° 10094 PL-7363.1	Contig9 from 4818876 to 4819271	m 34%	pir C83640 probable transcription regulator PA0048 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03438.1 AB004444-7- (AB004444) probable transcriptional regulator [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 10095 PL-7362.1	Contig9 from 4819371 to 4822688	p 16%	sp P47762 PRIM_LISMO DNA PRIMASE gb AAC43305.1 (UL3165) DNA primase [Listeria monocytogenes] prf 2104269B DNA primase [Listeria monocytogenes]	#N/A
SEQ ID n° 10096 PL-3129.2	Contig9 from 4822675 to 4823805	p 31%	gb AAF89876.1 (AF173869) putative site-specific recombinase xerD [Staphylococcus aureus]	#N/A
SEQ ID n° 10097 PL-6889.1	Contig9 from 4823998 to 4824129	p No Hits found		#N/A
SEQ ID n° 10098 PL-5649.4	Contig9 from 4824159 to 4824353	m No Hits found		#N/A
SEQ ID n° 10099 PL-3497.5	Contig9 from 4824337 to 4825719	m 57%	pdb 1F3I A Chain A, Crystal Structure Of Tn5 Transposase Complexed With Transposon End Dna	#N/A

SEQ ID n° 10100 PL-6896.2	Contig9 from 4825792 to 4826235	m	22%	gb AAD27742.1 AF132967.1 (AF132967) CGI-33 protein [Homo sapiens]	#N/A
SEQ ID n° 10101 PL-3186.2	Contig9 from 4826146 to 4827153	p	No Hits found		#N/A
SEQ ID n° 10102 PL-6912.2	Contig9 from 4827317 to 4827625	m	No Hits found		#N/A
SEQ ID n° 10103 PL-3187.2	Contig9 from 4827539 to 4828351	p	18%	gb AAFS1932.1 (AE003601) CGI4677 gene product [Drosophila melanogaster]	#N/A
SEQ ID n° 10104 PL-6929.1	Contig9 from 4828348 to 4828665	p	No Hits found		#N/A
SEQ ID n° 10105 PL-6486.1	Contig9 from 4828710 to 4828952	m	38%	sp P39394 YJTW_ECOLI_HYPOTHETICAL 14.6 KD PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132) pir [S56573 hypothetical 14.6K protein (mcrB-hsds intergenic region) - Escherichia coli gb AAA97244.1 (U14003) ORF_f132 [Escherichia coli] gb AAC77303.1 (AE000505) orf, hypothetical protein [Escherichia coli K12] sp O34419 RSR1_VIBCH_CRYPTIC PHAGE CTXPHI TRANSCRIPTIONAL REPRESSOR RSTR pir [H82197 transcription repressor Rstr VCI464 VCI455 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAB81724.1 (U83795) Rstr [Vibrio cholerae] gb AAB81728.1 (U83796) Rstr [Vibrio cholerae] gb AAF94612.1 (AE004224) transcriptional repressor Rstr [Vibrio cholerae] gb AAF94621.1 (AE004224) transcriptional repressor Rstr [Vibrio cholerae]	#N/A
SEQ ID n° 10106 PL-6898.2	Contig9 from 4829045 to 4829416	m	48%	dbj BAB05094.1 (AP001511) DNA primase [Bacillus halodurans]	#N/A
SEQ ID n° 10107 PL-3126.4	Contig9 from 4829516 to 4832830	p	15%		#N/A

SEQ ID n° 10108	PL-2.3	Contig9 from 4832817 to 4833947	p 37%	pir F83177 integrase/recombinase XerD PA3738 [imported] - Pseudomonas aeruginosa (strain PA01) gb AA07125.1 AE004793_2 (AE004793) integrase/recombinase XerD [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 10109	PL-7360.1	Contig9 from 4834218 to 4834319	m No Hits found		#N/A
SEQ ID n° 10110	PL-7359.1	Contig9 from 4834304 to 4835017	m 22%	gb AAH11625.1 AAH11625 (BC011625) Similar to hypothetical-protein-FLJ14299 [Homo sapiens]	#N/A
SEQ ID n° 10111	PL-7356.1	Contig9 from 4834907 to 4835719	p 17%	gb AAF51932.1 (AE003601) CG14677 gene product [Drosophila melanogaster]	#N/A
SEQ ID n° 10112	PL-6922.1	Contig9 from 4835716 to 4836033	p No Hits found		#N/A
SEQ ID n° 10113	PL-5719.1	Contig9 from 4836078 to 4836320	m 38%	sp P39394 YJIW_ECOLI HYPOTHETICAL 14.6 KD PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132) pir S56573 hypothetical 14.6K protein (mcrB-hsdS intergenic region) - Escherichia coli gb AA97244.1 (U14003) ORF_f132 [Escherichia coli] gb AAC77303.1 (AE000505) orf, hypothetical protein [Escherichia coli K12] sp O34419 RSR1_VIBCH CRYPTIC PHAGE CTXPHI TRANSCRIPTIONAL REPRESSOR RSTR pir H82197 transcription repressor Rstr VC1464 VC1455 [imported] - Vibrio cholerae (group O1 strain N16961) gb AA81724.1 (U83795) Rstr [Vibrio cholerae] gb AA81728.1 (U83796) Rstr [Vibrio cholerae] gb AAF94612.1 (AE004224) transcriptional repressor Rstr [Vibrio cholerae] gb AAF94621.1 (AE004224) transcriptional repressor Rstr [Vibrio cholerae]	#N/A
SEQ ID n° 10114	PL-5720.1	Contig9 from 4836413 to 4836784	m 48%		#N/A

1101

SEQ ID n° 10115 PL-3159.2	Contigs from 4836884 to 4840198	p	17%	sp P47762 PRIM_LISMO DNA PRIMASE gb AAC43305.1 (U13165) DNA primase [Listeria monocytogenes] prf 2104269B DNA primase [Listeria monocytogenes] pir F83177 integrase/recombinase XerD PA3738 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG07125.1 AE004793_2 (AE004793) integrase/recombinase XerD [Pseudomonas aeruginosa]	#N/A	SEQ ID n-2281
SEQ ID n° 10116 PL-3047.1	Contigs from 4840185 to 4841297	p	38%			
SEQ ID n° 10117 PL-6941.1	Contigs from 4841586 to 4841687	m	No Hits found		#N/A	
SEQ ID n° 10118 PL-4044.1	Contigs from 4841672 to 4842109	m	No Hits found			SEQ ID n-3192
SEQ ID n° 10119 PL-5706.1	Contigs from 4842373 to 4842642	p	No Hits found		#N/A	
SEQ ID n° 10120 PL-3048.1	Contigs from 4843051 to 4843635	m	69%	gb AAG58075.1 AE005525_1 (AE005525) sprt gene product [Escherichia coli O157:H7] sp P04384 METK_ECOLI S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) pir SYEC5M methionine adenosyltransferase (EC 2.5.1.6) [validated] - Escherichia coli gb AA69109.1 (U28377) CG Site No. 507 [Escherichia coli] gb AAC75979.1 (AE000377) methionine adenosyltransferase 1 (AdoMet synthetase); methyl and propylamine donor, corepressor of met genes [Escherichia coli K12] gb AAG58073.1 AE005524_9 (AE005524) methionine adenosyltransferase 1 (AdoMet synthetase); methyl and propylamine donor, corepressor of met genes [Escherichia coli O157:H7]	SEQ ID n-2282	
SEQ ID n° 10121 PL-3049.1	Contigs from 4843784 to 4844956	m	92%			SEQ ID n-2283

SEQ ID n°	Contig9 from	P	No Hits found	#N/A
10122 PL-5705.1	4845249 to 4845461			
10123 PL-3050.1	4845588 to 4847492	P	88%	
				Seq ID n-2385
10124 PL-3051.1	4847662 to 4848585	P	88%	
				Seq ID n-2285
10125 PL-3052.1	4848848 to 4849561	m	87%	
				Seq ID n-2287
10126 PL-3053.2	4849654 to 4850340	m	80%	
				#N/A
10127 PL-3054.2	4850925 to 4852586	m	72%	
				#N/A

pir||A65079 arginine decarboxylase (EC 4.1.1.19)
 - Escherichia coli gb|AA69105.1| (U28377) CG
 Site No. 161 [Escherichia coli] gb|AAC75975.1|
 (AE000377) biosynthetic arginine decarboxylase
 [Escherichia coli K12]
 sp|P16936|SPEB_ECOLI AGMATINASE (AGMATINASE
 UREOHYDROLASE) (AUH) pir||C42604 agmatinase (EC
 3.5.3.11) [validated] - Escherichia coli
 gb|AA83909.1| (M32363) agmatine ureohydrolase
 [Escherichia coli] gb|AA69104.1| (U28377)
 agmatine ureohydrolase [Escherichia coli]
 gb|AAC75974.1| (AE000377) agmatinase
 [Escherichia coli K12] gb|AA658067.1|AE005524_3
 (AE005524) agmatinase [Escherichia coli O157:H7] SEQ ID n-2285
 sp|Q46931|YGDQ_ECOLI HYPOTHETICAL 26.2 KD
 PROTEIN IN MUTH-TAS INTERGENIC REGION
 pir||A65066 hypothetical protein b2832 -
 Escherichia coli (strain K-12) gb|AA840479.1|
 (U29581) ORF_0237 [Escherichia coli]
 gb|AAC75871.1| (AE000367) putative transport
 protein [Escherichia coli K12]
 gb|AAG57943.1|AE005512_2 (AE005512) methyl-
 directed mismatch repair [Escherichia coli
 O157:H7 EDL933] gb|BAB37111.1| (AP002563)
 methyl-directed mismatch repair [Escherichia
 coli O157:H7]
 sp|P33595|YABN_ECOLI HYPOTHETICAL 63.9 KDA
 PROTEIN IN TBPA-LEUD INTERGENIC REGION
 (ORF103)

SEQ ID n° 10128 PL-3055.1	Contig9 from 4853031 to 4853636	m 79%	sp P30126 LEUD_ECOLI 3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI) pir S40585 3-isopropylmalate dehydratase (EC 4.2.1.33) small chain - Escherichia coli dbj BAA01340.1 (D10483) leud protein homolog (PIR:S07306) [Escherichia coli] gb AAC73182.1 (AE000117) isopropylmalate isomerase subunit [Escherichia coli K12] pir H64728 3-isopropylmalate dehydratase (EC 4.2.1.33) alpha chain - Escherichia coli gb AAC73183.1 (AE000117) 3- isopropylmalate isomerase (dehydratase) subunit [Escherichia coli K12] SEQ ID n-2290
SEQ ID n° 10129 PL-3056.1	Contig9 from 4853645 to 4855054	m 89%	sp P37412 LEU3_SALTY 3-ISOPROPYLMALATE DEHYDROGENASE (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) pdb 1CNZ A Chain A, 3- isopropylmalate Dehydrogenase (Ipmdh) From Salmonella typhimurium pdb 1CNZ B Chain B, 3-Isopropylmalate Dehydrogenase (Ipmdh) From Salmonella Typhimurium gb AAB60185.1 (U20795) 3-isopropylmalate dehydrogenase [Salmonella typhimurium] sp P09151 LEU1_ECOLI 2-ISOPROPYLMALATE SYNTHASE (ALPHA-ISOPROPYLMALATE SYNTHASE) (ALPHA-IPM SYNTHETASE) pir B64729 2- isopropylmalate synthase (EC 4.1.3.12) - Escherichia coli gb AAC73185.1 (AE000117) 2- isopropylmalate synthase [Escherichia coli K12] SEQ ID n-2291
SEQ ID n° 10130 PL-3057.1	Contig9 from 4855056 to 4856147	m 85%	gb AAB60185.1 (U20795) 3-isopropylmalate dehydrogenase [Salmonella typhimurium] sp P09151 LEU1_ECOLI 2-ISOPROPYLMALATE SYNTHASE (ALPHA-ISOPROPYLMALATE SYNTHASE) (ALPHA-IPM SYNTHETASE) pir B64729 2- isopropylmalate synthase (EC 4.1.3.12) - Escherichia coli gb AAC73185.1 (AE000117) 2- isopropylmalate synthase [Escherichia coli K12] SEQ ID n-2292
SEQ ID n° 10131 PL-3058.1	Contig9 from 4856150 to 4857712	m 84%	gb AAD26693.1 AF117227_5 (AF117227) Leuo [Salmonella typhimurium] SEQ ID n-2293
SEQ ID n° 10132 PL-3059.1	Contig9 from 4858670 to 4859614	p 70%	gb AAD26693.1 AF117227_5 (AF117227) Leuo [Salmonella typhimurium] SEQ ID n-2294

SEQ ID n° 10133 PL-2771.2	Contig9 from 4859849 to 4861651	p	72%	pir H82069 probable long-chain-fatty-acid--CoA ligase VC2484 [imported] - cholerae (group O1 strain N16961) gb AAF95626.1 (AE004318) long-chain-fatty-acid- CoA ligase, putative [Vibrio cholerae] #N/A
SEQ ID n° 10134 PL-3514.1	Contig9 from 4861972 to 4862541	p	49%	pir H69778 hypothetical protein ydeN - Bacillus subtilis dbj BAAL9361.1 (AB001488) FUNCTION UNKNOWN. [Bacillus subtilis] emb CAB12333.1 (Z99106) ydeN [Bacillus subtilis] #N/A
SEQ ID n° 10135 PL-2770.1	Contig9 from 4862698 to 4863324	m	31%	pir G71856 hypothetical protein jhg1045 - Helicobacter pylori (strain J99) gb AAD06623.1 (AE001532) putative [Helicobacter pylori J99] SEQ ID n-1977
SEQ ID n° 10136 PL-2769.2	Contig9 from 4863334 to 4864599	m	24%	sp P55126 FRPA_NEIMC IRON-REGULATED PROTEIN FRPA pir A47058 Fe-regulated RTX cytotoxin homolog FtpA - Neisseria meningitidis gb AAA25454.1 (L06302) iron-regulated protein [Neisseria meningitidis] #N/A
SEQ ID n° 10137 PL-3513.2	Contig9 from 4864678 to 4865115	m	25%	pir F81828 probable periplasmic type I secretion system protein NWA1995 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB85214.1 (AL162757) putative periplasmic type I secretion system protein [Neisseria meningitidis Z2491] #N/A
SEQ ID n° 10138 PL-7352.1	Contig9 from 4865606 to 4865689	m	No Hits found	#N/A
SEQ ID n° 10139 PL-2768.1	Contig9 from 4865998 to 4867752	p	86%	pir YCEC31 acetolactate synthase (EC 4.1.3.18) III large chain - Escherichia coli gb AAC73188.1 (AE000118) acetolactate synthase III, valine sensitive, large subunit [Escherichia coli K12] #N/A
SEQ ID n° 10140 PL-3512.1	Contig9 from 4867755 to 4868246	p	89%	gb AAF65177.1 AF117227_2 (AF117227) ILvH [Salmonella typhimurium] SEQ ID n-2724

1105

SEQ ID n° 10141 PL-2767.1	Contig9 from 4868334 to 4869341	p 90%	sp P21930 FRUR_SALTY FRUCTOSE REPRESSOR (CATABOLITE REPRESSOR/ACTIVATOR) pir S15941 PEP--fructosephosphotransferase system repressor - Salmonella typhimurium emb CAA39103.1 (X55456) PEP:fructose phosphotransferase system repressor [Salmonella typhimurium] gb AAF65176.1 AF117227_1 (AF117227) FruR [Salmonella typhimurium] prf 1712316P fruR gene [Salmonella typhimurium] SEQ ID n-2973
SEQ ID n° 10142 PL-3511.1	Contig9 from 4869973 to 4870431	p 79%	gb AAG54385.1 AE005185_2 (AE005185) orf, hypothetical protein [Escherichia coli O157:H7] pir QQECFT yabc protein - Escherichia coli dbj BA01348.1 (D10483) ORF [Escherichia coli] sp P22187 FTSL_ECOLI_CELL DIVISION PROTEIN FTSL pir A45278 cell division protein ftSL - Escherichia coli emb CAA38860.1 (X55034) OrfA protein [Escherichia coli] gb AAA24299.1 (K00137) orfA gene [Escherichia coli] gb AAB24309.1 (S49875) FtsL=cytoplasmic membrane cell division protein [Escherichia coli, Peptide, 121 aa] gb AAB24311.1 (S49802) MrAR=cell cycle regulator [Escherichia coli, Peptide, 121 aa] gb AAC73194.1 (AE000118) cell division protein; ingrowth of wall at septum [Escherichia coli K12] gb AAG54387.1 AE005185_4 (AE005185) cell division protein; ingrowth of wall at septum [Escherichia coli O157:H7] prf 1904252A ftsL gene [Escherichia coli] SEQ ID n-2972
SEQ ID n° 10143 PL-2766.1	Contig9 from 4870434 to 4871378	p 82%	
SEQ ID n° 10144 PL-5699.1	Contig9 from 4871378 to 4871695	p 82%	#N/A

sp P04286 PBP3_ECOLI PENICILLIN-BINDING PROTEIN 3 PRECURSOR (PBP-3) pir ZPECP3 penicillin- binding protein 3 precursor - Escherichia coli emb CAA38861.1 (X55034) Pbp3 protein [Escherichia coli] gb AAA24300.1 (K00137) penicillin-binding protein 3 [Escherichia coli] dbj BA01349.1 (D10483) penicillin-binding protein 3 precursor [Escherichia coli] gb AAC73195.1 (AE000118) septum formation; penicillin-binding protein 3; peptidoglycan synthetase [Escherichia coli K12] gb AAG54388.1 AE005185_5 (AE005185) septum formation; penicillin-binding protein 3; peptidoglycan synthetase [Escherichia coli O157:H7]	Contig9 from 4871724 to 4873490	SEQ ID n° 10145 PL-2765.1	p 89%	SEQ ID n-1971
sp P11880 MURF_ECOLI UDP-N-ACETYLMURAMOYLALANYL- D-GLUTAMYL-2, 6-DIAMINOPIMELATE--D- ALANYL-D-ALANYL LIGASE (UDP-MURNAC- PENTAPEPTIDE SYNTHETASE) ALANINE-ADDING ENZYME) pir F64730 UDP-N- acetylmuramoylalanyl-D-glutamyl-2, 6- diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli gb AAC44657.1 (U67891) UDP-MurNAC-Tripeptide:D- Ala-D-Ala-Adding enzyme [Escherichia coli] gb AAC73197.1 (AE000118) D-alanine:D- alanine-adding enzyme [Escherichia coli K12] gb AAG54391.1 AE005185_8 (AE005185) phospho-N- acetylmuramoyl-pentapeptide transferase? [Escherichia coli O157:H7]	Contig9 from 4873477 to 4874964	SEQ ID n° 10146 PL-2764.1	p 82%	SEQ ID n-1970
Contig9 from 4874961 to 4876340	SEQ ID n° 10147 PL-2763.1	p 73%	SEQ ID n-1969	
Contig9 from 4876334 to 4877416	SEQ ID n° 10148 PL-2762.1	p 90%	SEQ ID n-1968	

sp|P14900|MURD_ECOLI_UDP-N-ACETYL-MURAMOYLALANINE-
 -D-GLUTAMATE LIGASE (UDP-N-
 ACETYL-MURAMOYL-L-ALANYL-D-GLUTAMATE SYNTHETASE)
 (D-GLUTAMIC ACID ADDING ENZYME) pir||CEECME UDP-
 N-acetylmuramoylalanine-D-glutamate ligase (EC
 6.3.2.9) - Escherichia coli
 emb|CAA38865.1|(X55034) UDP-MurNac-L-Ala-D-Glu
 (MurD) (AA 1-438) [Escherichia coli]
 emb|CAA35933.1|(X51584) murD gene product (AA 1-
 438) [Escherichia coli] dbj|BAA01353.1|
 (D10483) UDP-N-acetylmuramoylalanine-D-glutamate
 ligase [Escherichia coli]
 gb|AAC73199.1|(AE000118) UDP-N-
 acetylmuramoylalanine-D-glutamate ligase
 [Escherichia coli K12] SEQ ID n-3967
 sp|P16457|FTSW_ECOLI_CELL_DIVISION_PROTEIN_FTSW
pir||CEECFW cell division protein ftsw -
 Escherichia coli emb|CAA38866.1|(X55034) FtsW
 protein [Escherichia coli] gb|AA83859.1|
 (M30807) cell division protein [Escherichia
 coli] dbj|BAA01354.1|(D10483) cell division
 protein ftsW [Escherichia coli] gb|AAC73200.1|
 (AE000118) cell division; membrane protein
 involved in shape determination
 [Escherichia coli K12]
 gb|AAG54393.1|AE005185_10 (AE005185) cell
 division; membrane protein involved in shape
 determination [Escherichia coli O157:H7] SEQ ID n-3966
 pdb|1FOK|A Chain A, The 1.9 Angstrom Crystal
 Structure Of E. Coli Murg pdb|1FOK|B Chain B,
 The 1.9 Angstrom Crystal Structure Of E. Coli
 Murg
 Contig9 from
 SEQ ID n° 10149 PL-2761.1 4877419 to p 76%
 4878729
 Contig9 from
 SEQ ID n° 10150 PL-2760.1 4878729 to p 87%
 4879922
 Contig9 from
 SEQ ID n° 10151 PL-2759.1 4879919 to p 83%
 4880986

sp|P17952|MURC_ECOLI UDP-N-ACETYL-MURAMATE--
 ALANINE LIGASE (UDP-N-ACETYL-MURAMOYL-
 L-ALANINE SYNTHETASE) pir||CECCAM UDP-N-
 acetylmuramate--alanine ligase (EC 6.3.2.8) -
 Escherichia coli emb|CAA38868.1|
 (X55034) UDP-N-acetylmuramate--alanine ligase
 [Escherichia coli] emb|CAA36868.1| (X52644)
 (UDP-N-acetylmuramate: L-alanine ligase) (AA 1-
 491) [Escherichia coli]
 dbj|BAA01356.1| (D10483) UDP-N-acetylmuramate-
 alanine ligase [Escherichia coli]
 gb|AAC73202.1| (AE000118) L-alanine adding
 enzyme, UDP-N-acetyl-muramate:alanine
 ligase [Escherichia coli K12] prf||1808265A
 murC gene [Escherichia coli]
 sp|P07862|DDL_B_ECOLI D-ALANINE--D-ALANINE LIGASE
 B (D-ALANYLALANINE SYNTHETASE) (D-ALA-
 D-ALA LIGASE) pir||CECDL D-alanine--D-alanine
 ligase (EC 6.3.2.4) B - Escherichia coli
 pdb|1IOV| Complex Of D-Ala:d-Ala Ligase With
 Adp And A Phosphoryl Phosphate
 pdb|2DLN| Mol_id: 1; Molecule: D-Alanine--D-
 Alanine Ligase; Chain: Null; EC:
 6.3.2.4 emb|CAA38869.1| (X55034) D-Ala:D-Ala
 ligase (ddl) [Escherichia coli] gb|AA23672.1|
 (M14029) ddl cell wall enzyme [Escherichia coli]
 gb|AA23815.1| (K02668) D-alanine:D-alanine
 ligase [Escherichia coli] dbj|BAA01357.1|
 (D10483) D-alanine-D-alanine ligase [Escherichia
 coli] gb|AAC73203.1| (AE000118) D-alanine-D-
 alanine ligase B, affects cell division
 [Escherichia coli K12]

Contig9 from
 SEQ ID n° 10152 PL-2758.1 4881042 to P 84%
 4882517

Contig9 from
 SEQ ID n° 10153 PL-2757.1 4882510 to P 82%
 4883430

SEQ ID n-1963

SEQ ID n-1962

Contig9 from SEQ ID n° 10154 PL-2756.1 4883432 to 4884238	p 74%	<p>sp P06136 FTSQ_ECOLI CELL DIVISION PROTEIN FTSQ pir CECQ cell division protein ftsq - Escherichia coli emb CAA38870.1 (X55034) FTSQ protein [Escherichia coli] emb CAA26589.1 (X02821) put. ftsa protein [Escherichia coli] gb AA23816.1 (X02668) ftsq protein [Escherichia coli] dbj BAA01358.1 (D10483) cell division protein ftsq [Escherichia coli] gb AAC73204.1 (AE000118) cell division protein; ingrowth of wall at septum [Escherichia coli K12] SEQ ID n-3961</p>
Contig9 from SEQ ID n° 10155 PL-2755.1 4884280 to 4885536	p 94%	<p>sp P06137 FTSA_ECOLI CELL DIVISION PROTEIN FTSA pir CECA cell division protein ftsa - Escherichia coli emb CAA38871.1 (X55034) FTSA protein [Escherichia coli] emb CAA26590.1 (X02821) ftsa protein [Escherichia coli] dbj BAA01359.1 (D10483) cell division-protein ftsA [Escherichia coli] gb AAC73205.1 (AE000118) ATP-binding cell division protein; septation process, complexes with ftsZ, associated with junctions of inner and outer membranes [Escherichia coli K12] gb AAG54398.1 AE005186_4 (AE005186) ATP-binding cell division protein, septation process, complexes with FtsZ, associated with junctions of inner and outer membranes [Escherichia coli O157:H7] SEQ ID n-3960</p>
Contig9 from SEQ ID n° 10156 PL-2754.1 4885599 to 4886759	p 93%	<p>pir CECZ cell division protein ftsZ - Escherichia coli gb AAC73206.1 (AE000119) cell division; forms circumferential ring; tubulin- like GTP-binding protein and GTPase [Escherichia coli K12] gb AAG54399.1 AE005186_5 (AE005186) cell division; forms circumferential ring; tubulin-like GTP-binding protein and GTPase [Escherichia coli O157:H7] SEQ ID n-3959</p>

1110

SEQ ID n° 10157 PL-2753.1	4886843 to 4887775	p	93%	Contig9 from	sp P07652 LPXC_ECOLI_UDP-3-O-[3-HYDROXYMYRISTOYL] N-ACETYLGLUCOSAMINE DEACETYLASE (ENVA PROTEIN)	SEQ ID n-2958
					pir BVECEA_UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (EC 3.5.1.-) - Escherichia coli emb CAA38873.1 (X55034) EnvA protein [Escherichia coli] gb AA83849.1 (M19211) ell permeability-cell separation protein [Escherichia coli] dbj BAA01361.1 (D10483) envA protein [Escherichia coli] gb AAC73207.1 (AE000119) UDP-3-O-acyl N-acetylglucosamine deacetylase; lipid A biosynthesis [Escherichia coli K12] gb AAG54400.1 AE005186_6 (AE005186) UDP-3-O-acyl N-acetylglucosamine deacetylase; lipid A biosynthesis [Escherichia coli O157:H7]	
SEQ ID n° 10158 PL-2752.1	4887903 to 4888430	m	39%	Contig9 from	pir G82080 hypothetical protein VC2395 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95538.1 (AE004310) hypothetical protein [Vibrio cholerae]	SEQ ID n-2957
					gb AAG54401.1 AE005186_7 (AE005186) orf, hypothetical protein [Escherichia coli O157:H7]	
SEQ ID n° 10159 PL-3506.1	4888529 to 4888987	p	57%	Contig9 from	gb AAG54402.1 AE005186_8 (AE005186) preprotein translocase; secretion protein [Escherichia coli O157:H7]	SEQ ID n-2721
					gb AAG54403.1 AE005186_9 (AE005186) 7,8-dihydro-8-oxoguanine-triphosphatase, prefers dGTP, causes AT-GC transversions [Escherichia coli O157:H7]	
SEQ ID n° 10160 PL-2751.1	4889071 to 4891782	p	93%	Contig9 from	pir E64732 yacG protein - Escherichia coli (strain K-12) gb AAC73212.1 (AE000119) orf, hypothetical protein [Escherichia coli K12] gb AAG54405.1 AE005186_11 (AE005186) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2956
SEQ ID n° 10161 PL-5693.1	4891903 to 4892295	p	69%	Contig9 from		#N/A
SEQ ID n° 10162 PL-5691.1	4892334 to 4892531	m	76%	Contig9 from		#N/A

1111

Contig9 from 4892562 to 4893314	sp P36680 YACF_ECOLI_HYPOTHETICAL_28.3_KD PROTEIN IN MUTT-GUAC INTERGENIC REGION pir F64732_hypothetical protein b0102 - Escherichia coli (strain K-12) gb AAC73213.1 (AE000119) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n~1955
Contig9 from 4893307 to 4893930	sp P36679 YACE_ECOLI_22.6_KDA_PROTEIN_IN_MUTT- GUAC_INTERGENIC_REGION_pir G64732_yace protein - Escherichia coli (strain K-12) gb AAC73214.1 (AE000119) putative DNA repair protein [Escherichia coli K12]	SEQ ID n~1953
Contig9 from 4894022 to 4895221	gb AAG54407.1 AE005186_13 (AE005186) putative DNA repair protein [Escherichia coli O157:H7] gb AAG54410.1 AE005187_3 (AE005187) putative integral membrane protein involved in biogenesis of fimbriae, protein transport, DNA uptake [Escherichia coli O157:H7]	SEQ ID n~1952
Contig9 from 4895224 to 4896666	gb AAG54411.1 AE005187_4 (AE005187) putative integral membrane protein involved in biogenesis of fimbriae, protein transport, DNA uptake [Escherichia coli O157:H7]	SEQ ID n~1951
Contig9 from 4896834 to 4897256	emb CAB89833.1 (AJ242516) Ppdd protein [Salmonella typhimurium]	SEQ ID n~2720
Contig9 from 4897454 to 4898344	emb CAB89834.1 (AJ242516) NadC protein [Salmonella typhimurium]	SEQ ID n~2950
Contig9 from 4898840 to 4899694	gb AAG54415.1 AE005187_8 (AE005187) regulates ampC [Escherichia coli O157:H7]	SEQ ID n~1949
Contig9 from 4899821 to 4900021		#N/A

1112

sp P30130 FIMD_ECOLI OUTER MEMBRANE USHER PROTEIN FIMD PRECURSOR pir S56542 outer membrane usher protein fimd precursor - Escherichia coli gb AAA97213.1 (U14003) CG Site No. 18349 [Escherichia coli] gb AAC77273.1 (AE000502) outer membrane protein; export and assembly of type 1 fimbriae, interrupted [Escherichia coli K12]					SEQ ID n-1948
Contig9 from SEQ ID n° 10171 PL-2744.1 4900263 to 4901249	m	51%	No Hits found	#N/A	
Contig9 from SEQ ID n° 10172 PL-5688.1 4901332 to 4901469	m	No Hits found		#N/A	
Contig9 from SEQ ID n° 10173 PL-5687.1 4901580 to 4901795	m	No Hits found		#N/A	
Contig9 from SEQ ID n° 10174 PL-2743.1 4901806 to 4902522	m	47%	gb AAG55424.1 AE005284_2 (AE005284) putative chaperone [Escherichia coli O157:H7]	SEQ ID n-1947	
Contig9 from SEQ ID n° 10175 PL-5686.1 4902625 to 4902819	m	No Hits found		#N/A	
Contig9 from SEQ ID n° 10176 PL-5685.1 4902852 to 4903238	m	No Hits found		#N/A	
Contig9 from SEQ ID n° 10177 PL-5684.1 4903551 to 4903694	m	No Hits found		#N/A	
Contig9 from SEQ ID n° 10178 PL-3504.1 4904213 to 4904791	p	53%	pir F82969 hypothetical protein PA5402 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG08787.1 AE004953_1 (AE004953) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2719	

SEQ ID n° 2719

SEQ ID n° 10179 PL-5681.1	Contig9 from 4904800 to 4905021	p 71%	pir G82969 probable transcription regulator PA5403 [imported] - pseudomonas aeruginosa (strain PAO1) gb AAG08788.1 AE004953_2 (AE004953) probable transcriptional regulator [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 10180 PL-7349.1	Contig9 from 4905291 to 4905638	p No Hits found		#N/A
SEQ ID n° 10181 PL-5679.1	Contig9 from 4905740 to 4906054	p No Hits found		#N/A
SEQ ID n° 10182 PL-2742.1	Contig9 from 4906786 to 4907550	p 87%	emb CAB89840.1 (A7242516) PdhR protein [Salmonella typhimurium] sp P06958 ODPI_ECOLI PYRUVATE DEHYDROGENASE E1 COMPONENT pir DEECPV pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) - Escherichia coli gb AAC73225.1 (AE000120) pyruvate dehydrogenase (decarboxylase component) [Escherichia coli K12] gb AAG54418.1 AE005187_11 (AE005187) pyruvate dehydrogenase (decarboxylase component) [Escherichia coli O157:H7]	SEQ ID n-1946 SEQ ID n-1945
SEQ ID n° 10183 PL-2741.1	Contig9 from 4907740 to 4910403	p 93%		

sp P06959 ODP2_ECOLI_DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE... DEHYDROGENASE COMPLEX (E2)... pir [XXECDP dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) aceF [validated]																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

1115

SEQ ID n° 10191 PL-2735.1	Contig9 from 4918819 to 4919691	p	79%	sp O52401 YGG_B_EWIC_HYPOTHETICAL_30.6_KDA PROTEIN IN ICIA-FBA INTERGENIC REGION gb AAB92571.1 (AF037440) putative 30.6 kDa protein [Edwardsiella ictaluri]	SEQ ID n-1938
SEQ ID n° 10192 PL-3503.1	Contig9 from 4920121 to 4920651	m	No Hits found		SEQ ID n-2718
SEQ ID n° 10193 PL-2734.1	Contig9 from 4920648 to 4921946	m	34%	gb AAG56271.1 AE005355_5 (AE005355) putative enzyme [Escherichia coli O157:H7] sp P11667 YGG_ECOLI_HYPOTHETICAL_23.2_KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 5) pir QOEC5A hypothetical 23K protein (sbm-fba intergenic region) - Escherichia coli gb AAG5090.1 (U28377) ORF_f211; alternate name yggA; orf5 of X14436 [Escherichia coli] gb AAC75960.1 (AE000375) orf, hypothetical protein [Escherichia coli K12] sp P11668 YGG_ECOLI_HYPOTHETICAL_26.6_KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 6) (F246) pir A65077 hypothetical 26.6K protein (sbm-fba intergenic region) - Escherichia coli gb AAAG69089.1 (U28377) ORF_f246; alternate name yggE; orf6 of X14436 [Escherichia coli] gb AAC75959.1 (AE000375) putative actin [Escherichia coli K12] gb AAG58048.1 AE005522_6 (AE005522) putative actin [Escherichia coli O157:H7]	SEQ ID n-1937
SEQ ID n° 10194 PL-2733.1	Contig9 from 4922864 to 4923487	p	68%		SEQ ID n-1936
SEQ ID n° 10195 PL-2732.1	Contig9 from 4923601 to 4924323	p	68%		
SEQ ID n° 10196 PL-2731.1	Contig9 from 4924320 to 4925222	m	91%	sp O52399 ICIA_EWIC_CHROMOSOME_INITIATION INHIBITOR (ORIC REPLICATION INHIBITOR) gb AAB92569.1 (AF037440) inhibitor of chromosome initiation [Edwardsiella ictaluri]	SEQ ID n-1935
SEQ ID n° 10197 PL-5669.1	Contig9 from 4925320 to 4925514	m	No Hits found		SEQ ID n-1934

#N/A

SEQ ID n° 10198 PL-3502.1	Contig9 from 4925603 to 4926157	p	No Hits found	SEQ ID n-2717	#N/A
SEQ ID n° 10199 PL-5668.1	Contig9 from 4926476 to 4926637	p	No Hits found		
SEQ ID n° 10200 PL-1262.1	Contig9 from 4926929 to 4927588	p	90%	SEQ ID n-932	
SEQ ID n° 10201 PL-1261.1	Contig9 from 4927861 to 4929102	p	88%		
SEQ ID n° 10202 PL-5667.2	Contig9 from 4929151 to 4929366	m	77%	SEQ ID n-931	#N/A

sp|052398|RP1A EDWIC RIBOSE 5-PHOSPHATE
 ISOMERASE A (PHOSPHORIBOISOMERASE A)
 gb|AAB92568.1| (AF037440) ribose-5-phosphate
 isomerase [Edwardsiella ictaluri]
 sp|P08328|SERA_ECOLI D-3-PHOSPHOGLYCERATE
 DEHYDROGENASE (PGDH) pir||DEBCFG
 phosphoglycerate dehydrogenase (EC 1.1.1.95) -
 Escherichia coli gb|AA24625.1| (L29397)
 phosphoglycerate dehydrogenase [Escherichia
 coli] gb|AA69080.1| (U28377) D-3-
 phosphoglycerate dehydrogenase [Escherichia
 coli] gb|AAC75950.1| (AE000374) D-3-
 phosphoglycerate dehydrogenase [Escherichia coli
 K12] gb|AAG58040.1|AE005521_8 (AE005521) D-3-
 phosphoglycerate dehydrogenase [Escherichia coli
 O157:H7]
 gb|AAG58038.1|AE005521_6 (AE005521) putative
 ligase [Escherichia coli O157:H7 EDL933]

Contig9 from SEQ ID n° 10203-PL-5666.2 4929382 to 4929795	m	50%	<p>sp P09160 YGFA_ECOLI_HYPOTHETICAL_21.1_KDA PROTEIN IN SSR-SERA INTERGENIC REGION (O182) pir QQEC2K_hypothetical_21.1K_protein(ssr-sera intergenic region) - Escherichia coli gb AA24651.1 (M12965) 22-kDa protein [Escherichia coli] gb AA69079.1 (U28377) ORF_0182; two upstream start codons, one within ssr [Escherichia coli] gb AAC75949.1 (AE000374) putative ligase [Escherichia coli K12] dbj BAB37205.1 (AP002563) putative ligase [Escherichia coli O157:H7]</p>	#N/A
Contig9 from SEQ ID n° 10204-PL-5665.1 4930082 to 4930411	m	76%	<p>sp P45580 YGFE_ECOLI_HYPOTHETICAL_12.6_KD PROTEIN IN PEPP-SSR INTERGENIC REGION (O109) pir F65075_hypothetical_12.7_KD_protein_in_pepp. ssr_intergenic_region - Escherichia coli (strain K-12) gb AA69078.1 (U28377) ORF_0109 [Escherichia coli] gb AAC75948.1 (AE000374) orf, hypothetical protein [Escherichia coli K12] gb AAG58037.1 AE005521_5 (AE005521) orf, hypothetical protein [Escherichia coli O157:H7]</p>	#N/A
Contig9 from SEQ ID n° 10205-PL-3501.1 4930601 to 4931176	p	70%	<p>sp P25533 YGFB_ECOLI_HYPOTHETICAL_21.5_KD PROTEIN IN PEPP-SSR INTERGENIC REGION (ORF194) (F194) pir A47020_hypothetical_21.5K_protein (pepp-ssr_intergenic_region) - Escherichia coli dbj BAAL4324.1 (D90281) ORF194 protein [Escherichia coli] gb AA69077.1 (U28377) ORF_f194 [Escherichia coli] gb AAC75947.1 (AE000374) orf, hypothetical protein [Escherichia coli K12] gb AAG58036.1 AE005521_4 (AE005521) orf, hypothetical protein [Escherichia coli O157:H7]</p>	SEQ ID n° 2716
Contig9 from SEQ ID n° 10206-PL-1260.1 4931223 to 4932539	p	84%	<p>gb AAG58035.1 AE005521_3 (AE005521) proline aminopeptidase P II [Escherichia coli O157:H7]</p>	SEQ ID n° 330

SEQ ID n° 10207 PL-1259.1	Contig9 from 4932547 to 4933725	P 74%	<p>pir [C65075 probable 2-octaprenyl-6-methoxyphenol 4-monooxygenase (EC 1.14.13.-)] ubiH - Escherichia coli (strain K-12)</p> <p>gb AAA69075.1 (U28377) ORF_f392 [Escherichia coli] gb AAC75945.1 (AE000374) 2-octaprenyl-6-methoxyphenol--> 2-octaprenyl-6-methoxy-1, 4-benzoquinone [Escherichia coli K12]</p>	SEQ ID n-328
SEQ ID n° 10208 PL-1258.1	Contig9 from 4933764 to 4934984	P 71%	<p>gb AAG58033.1 AE005521.1 (AE005521) orf, hypothetical-protein-[Escherichia coli O157:H7]</p> <p>sp P27248 GCST_ECOLI AMINOMETHYLTRANSFERASE (GLYCINE CLEAVAGE SYSTEM T PROTEIN) pir [A56689 aminomethyltransferase (EC 2.1.2.10) [validated] - Escherichia coli gb AAC36843.1 (M97263) T-protein [Escherichia coli] emb CAA52144.1 (X73958) aminomethyltransferase [Escherichia coli] gb AAA69073.1 (U28377) ORF_f364 [Escherichia coli] gb AAC75943.1 (AE000374) aminomethyltransferase (T protein; tetrahydrofolate-dependent) of glycine cleavage system [Escherichia coli K12]</p> <p>sp P27248 GCST_ECOLI AMINOMETHYLTRANSFERASE (GLYCINE CLEAVAGE SYSTEM T PROTEIN) pir [A56689 aminomethyltransferase (EC 2.1.2.10) [validated] - Escherichia coli gb AAC36843.1 (M97263) T-protein [Escherichia coli] emb CAA52144.1 (X73958) aminomethyltransferase [Escherichia coli] gb AAA69073.1 (U28377) ORF_f364 [Escherichia coli] gb AAC75943.1 (AE000374) aminomethyltransferase (T protein; tetrahydrofolate-dependent) of glycine cleavage system [Escherichia coli K12]</p>	SEQ ID n-327
SEQ ID n° 10209 PL-1257.1	Contig9 from 4935343 to 4936239	P 79%		
SEQ ID n° 10210 PL-5662.1	Contig9 from 4936154 to 4936438	P 71%		

#N/A

[illegible]

1120

SEQ ID n° 10216 PL-5656.1	Contig9 from 4948487 to 4948627	m	33%	sp P39394 YJTW_ECOLI_HYPOTHETICAL_14.6_KD PROTEIN IN MCRB-HSDS INTERGENIC REGION (F132) pir S56573 hypothetical 14.6K protein (mcrB-hds intergenic region) - Escherichia coli gb AA97244.1 (U14003) ORF f132 [Escherichia coli] gb AAC77303.1 (AE000505) orf, hypothetical protein [Escherichia coli K12] #N/A
SEQ ID n° 10217 PL-5655.1	Contig9 from 4948832 to 4949218	m	42%	sp O85264 RSR2_VIBCH_CRYPTIC_PHAGE_CTXPHI TRANSCRIPTIONAL REPRESSOR RSTR gb AAC24223.1 (AF055890) repressor [Vibrio cholerae 569B] gb AAF29541.1 AF220606_1 (AF220606) RSTR [Vibrio cholerae] gb AAG38011.1 AF262318_2 (AF262318) Rstr classical [Vibrio phage CTX] #N/A
SEQ ID n° 10218 PL-1253.1	Contig9 from 4949320 to 4952634	p	16%	dbj BAB05094.1 (AP001511) DNA primase [Bacillus halodurans] SEQ ID n° 322
SEQ ID n° 10219 PL-1252.1	Contig9 from 4952621 to 4953751	p	37%	pir F83177 integrase/recombinase XerD PA3738 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07125.1 AE004793_2 (AE004793) integrase/recombinase XerD [Pseudomonas aeruginosa] SEQ ID n° 321
SEQ ID n° 10220 PL-5651.2	Contig9 from 4953945 to 4954076	p	No Hits found	#N/A
SEQ ID n° 10221 PL-7345.1	Contig9 from 4954106 to 4954189	m	No Hits found	#N/A
SEQ ID n° 10222 PL-7344.1	Contig9 from 4954283 to 4955665	m	57%	pdb 1F3I A Chain A, Crystal Structure Of Tn5 Transposase Complexed With Transposon End Dna #N/A
SEQ ID n° 10223 PL-5647.2	Contig9 from 4955676 to 4956071	m	No Hits found	#N/A

1121

SEQ ID n° 10224 PL-2218.3	Contig9 from 4955987 to 4958773	p 35%	pir C83339 hypothetical protein PA2462 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG05850.1 AE004673.10 (AE004673) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 10225 PL-5644.1	Contig9 from 4958791 to 4958994	p No Hits found		#N/A
SEQ ID n° 10226 PL-2219.1	Contig9 from 4959381 to 4959959	p 28%	gb AAF62314.1 (AE002420) MafB-related protein [Neisseria meningitidis MC58]	SEQ ID n-2377
SEQ ID n° 10227 PL-5643.1	Contig9 from 4959969 to 4960286	p 50%	pir H81173 hypothetical protein NMB0654 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF41074.1 (AE002420) hypothetical protein [Neisseria meningitidis MC58]	#N/A
SEQ ID n° 10228 PL-2220.1	Contig9 from 4960349 to 4961581	p 21%	emb CAB72079.1 (AJ391284) hypothetical protein [Neisseria meningitidis]	SEQ ID n-2379
SEQ ID n° 10229 PL-3496.1	Contig9 from 4961653 to 4962042	p No Hits found		SEQ ID n-2712
SEQ ID n° 10230 PL-5642.1	Contig9 from 4962113 to 4962391	p No Hits found		#N/A
SEQ ID n° 10231 PL-5641.1	Contig9 from 4962427 to 4962576	p No Hits found		#N/A
SEQ ID n° 10232 PL-5639.1	Contig9 from 4964042 to 4964206	p No Hits found		#N/A
SEQ ID n° 10233 PL-2221.1	Contig9 from 4964340 to 4966019	p 60%	gb AAC31980.1 (L39897) HecB [Pectobacterium chrysanthemi]	SEQ ID n-2380

SEQ ID n° 10234 PL-2222.1	Contig9 from 4966883 to 4967524	m	17%	emb CAB39044.1 (AL034559) HesB-like domain protein [Plasmodium falciparum]	SEQ ID n-2381
SEQ ID n° 10235 PL-2223.1	Contig9 from 4967521 to 4968546	m	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-2382
SEQ ID n° 10236 PL-2224.1	Contig9 from 4970413 to 4971846	p	61%	pir S30159 N-formimidoyl fortimicin A synthase Micromonospora olivasterospora dbj BAA00940.1 (D10050) formimidoyl fortimicin A synthetase [Micromonospora olivasterospora]	SEQ ID n-2383
SEQ ID n° 10237 PL-2225.1	Contig9 from 4971843 to 4972694	p	41%	emb CAB94532.1 (AL359152) putative methylase [Streptomyces coelicolor A3(2)]	SEQ ID n-2384
SEQ ID n° 10238 PL-2226.1	Contig9 from 4972719 to 4973993	p	41%	pir F75017 probable glycine C-acetyltransferase (EC 2.3.1.29) PAB1244 - Pyrococcus abyssi (strain Orsay) emb CAB50590-1 (AJ248288) 5-AMINOLEVULINIC ACID SYNTHASE (8 AMINO-7-OXONENANOATE SYNTHASE) [Pyrococcus abyssi]	SEQ ID n-2385
SEQ ID n° 10239 PL-5635.1	Contig9 from 4974037 to 4974396	p	36%	gb AAC44868.1 (U60417) PapB [Streptomyces pristinaespiralis]	#N/A
SEQ ID n° 10240 PL-2227.1	Contig9 from 4974434 to 4976452	p	58%	gb AAC44866.1 (U60417) PapA [Streptomyces pristinaespiralis]	SEQ ID n-2386
SEQ ID n° 10241 PL-2228.1	Contig9 from 4976445 to 4977332	p	40%	gb AAC44867.1 (U60417) PapC [Streptomyces pristinaespiralis]	SEQ ID n-2387
SEQ ID n° 10242 PL-2229.1	Contig9 from 4977354 to 4978886	p	63%	gb AAC43550.1 (U40487) proton antiporter efflux pump [Mycobacterium smegmatis] prf 2207392A efflux pump [Mycobacterium smegmatis] pir B70806 hypothetical glycine-rich protein Rv3507 - Mycobacterium tuberculosis (strain H37RV) emb CAA17744.1 (AL022022) PE_PGRS [Mycobacterium tuberculosis]	SEQ ID n-2388
SEQ ID n° 10243 PL-2230.1	Contig9 from 4979482 to 4980777	p	22%		SEQ ID n-2390

1123

SEQ ID n° 10244 PL-5631.1	Contig9 from 4980941 to 4981039	p	No Hits found	#N/A
SEQ ID n° 10245 PL-2231.1	Contig9 from 4981457 to 4982761	p	24%	pir H70846 hypothetical glycine-rich protein RV3345c - Mycobacterium tuberculosis (strain H37RV) emb CAA17117.1 (AL021841) PE_PGRS [Mycobacterium tuberculosis] SEQ ID n-1391
SEQ ID n° 10246 PL-2232.1	Contig9 from 4983693 to 4984298	m	48%	pir E75485 hypothetical protein - Deinococcus radiodurans (strain R1) gb AAFL0288.1 AE001927_7 (AE001927) hypothetical protein [Deinococcus radiodurans] SEQ ID n-1392
SEQ ID n° 10247 PL-2233.1	Contig9 from 4984310 to 4985299	m	79%	sp P39179 UPI4_ECOLI UNKNOWN PROTEIN FROM 2D- PAGE (SPOT PR51) pir B65074 hypothetical protein b2898 - Escherichia coli (strain K-12) gb AAA83079.1 (U28375) ORF_0326 [Escherichia coli] gb AAC75936.1 (AE000373) orf, hypothetical protein [Escherichia coli K12] sp Q46825 YGFY_ECOLI HYPOTHETICAL 10.5 KD PROTEIN IN FLDB-BGLA INTERGENIC REGION pir A65074 hypothetical protein b2897 - Escherichia coli (strain K-12) gb AAA83078.1 (U28375) ORF_f88 [Escherichia coli] gb AAC75935.1 (AE000373) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-1393
SEQ ID n° 10248 PL-5629.1	Contig9 from 4985471 to 4985743	p	84%	gb AAG58025.1 AE005520_3 (AE005520) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 10249 PL-5628.1	Contig9 from 4985724 to 4986140	p	57%	gb AAG58024.1 AE005520_2 (AE005520) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 10250 PL-3490.1	Contig9 from 4986162 to 4986683	m	78%	pir G65073 flavodoxin II - Escherichia coli gb AAA83076.1 (U28375) ORF_0173 [Escherichia coli] gb AAC75933.1 (AE000373) flavodoxin 2 [Escherichia coli K12] gb AAG58023.1 AE005520_1 (AE005520) flavodoxin 2 [Escherichia coli O157:H7] SEQ ID n-2706

SEQ ID n° 10251 PL-2234.1	Contig9 from 4986788 to 4987699	p 86%	gb AAB87499.1 (AF033497) site-specific recombinase [Proteus mirabilis]	SEQ ID n-1394
SEQ ID n° 10252 PL-2235.1	Contig9 from 4987723 to 4988430	p 66%	sp P39691 DSBC_ERWCH_THIOL:DISULFIDE INTERCHANGE PROTEIN DSBC PRECURSOR pir S44444 protein disulfide-isomerase (EC 5.3.4.1) dsbc precursor Erwinia chrysanthemi emb CAA54108.1 (X76687) dsbc [Erwinia chrysanthemi] gb AAG58020.1 AE005519_6 (AE005519) ssDNA exonuclease, 5' --> 3' specific [Escherichia coli] OT57:H7	SEQ ID n-1395
SEQ ID n° 10253 PL-2236.1	Contig9 from 4988430 to 4990163	p 83%	sp P07012 RF2_ECOLI PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) pir FCECR2 translation releasing factor RF-2 - Escherichia coli (strain K-12) gb AAC75929.1 (AE000372) peptide chain release factor RF-2 [Escherichia coli K12] prf 1806195A peptide chain-releasing factor:ISOTYPE-2 [Escherichia coli] pdb 1BBU A Chain A, Lysyl-Trna Synthetase (Lyss) Complexed With Lysine pdb 1BBW A Chain A, Lysyl- Trna Synthetase (Lyss)	SEQ ID n-1396
SEQ ID n° 10254 PL-2237.1	Contig9 from 4990385 to 4991419	p 94%	pir B82482 antibiotic acetyltransferase VCA0253 [imported] - Vibrio cholerae O1 strain N16961 gb AAF96164.1 (AB004365) antibiotic acetyltransferase [Vibrio cholerae] ref NP_073263.1 orf39 [Salmonella enterica serovar Choleraesuis] dbj BAB20546.1 (AB040415) orf39 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-1397
SEQ ID n° 10255 PL-2238.1	Contig9 from 4991429 to 4992943	p 88%	pir B82482 antibiotic acetyltransferase VCA0253 [imported] - Vibrio cholerae O1 strain N16961 gb AAF96164.1 (AB004365) antibiotic acetyltransferase [Vibrio cholerae] ref NP_073263.1 orf39 [Salmonella enterica serovar Choleraesuis] dbj BAB20546.1 (AB040415) orf39 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-1398
SEQ ID n° 10256 PL-2239.1	Contig9 from 4993419 to 4994042	p 81%	pir B82482 antibiotic acetyltransferase VCA0253 [imported] - Vibrio cholerae O1 strain N16961 gb AAF96164.1 (AB004365) antibiotic acetyltransferase [Vibrio cholerae] ref NP_073263.1 orf39 [Salmonella enterica serovar Choleraesuis] dbj BAB20546.1 (AB040415) orf39 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-1399
SEQ ID n° 10257 PL-2240.1	Contig9 from 4994246 to 4995253	p 73%	pir B82482 antibiotic acetyltransferase VCA0253 [imported] - Vibrio cholerae O1 strain N16961 gb AAF96164.1 (AB004365) antibiotic acetyltransferase [Vibrio cholerae] ref NP_073263.1 orf39 [Salmonella enterica serovar Choleraesuis] dbj BAB20546.1 (AB040415) orf39 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-1401
SEQ ID n° 10258 PL-7340.1	Contig9 from 4995859 to 4995981	p No Hits found		#N/A
SEQ ID n° 10259 PL-2241.1	Contig9 from 4996002 to 4996769	m 40%	pir T35272 hypothetical protein SC5F2A.30 - Streptomyces coelicolor emb CAB40697.1 (AL049587) hypothetical protein [Streptomyces coelicolor A3(2)]	SEQ ID n-1402

SEQ ID n° 10260-PL-2242-1	Contig9 from 4997077 to 4998048	p	57%	pir A83414 probable transcription regulator PAL850 [imported] - Pseudomonas aeruginosa (strain PAO1)	SEQ ID n-2403
SEQ ID n° 10261-PL-2243.1	Contig9 from 4998062 to 4999729	m	71%	gb AA05239.1 AE004611.4 (AE004611) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-2404
SEQ ID n° 10262-PL-2244.1	Contig9 from 5000062 to 5000952	p	86%	sp P74839 PRPR_SALTY PROPIONATE CATABOLISM OPERON REGULATORY PROTEIN gb AAC44813.1 (U51879) PrpR [Salmonella typhimurium] sp Q56062 CPPM_SALTY PUTATIVE CARBOXYVINYL- CARBOXYPHOSPHONATE PHOSPHORYLMUTASE (CPEP PHOSPHONOMUTASE) gb AAC44814.1 (U51879) PrpB [Salmonella typhimurium]	SEQ ID n-2405
SEQ ID n° 10263-PL-2245.1	Contig9 from 5001013 to 5002179	p	82%	sp P31660 CISZ_ECOLI METHYLCITRATE SYNTHASE --(CITRATE SYNTHASE 2) pir E64760 citrate (si)-- synthase (EC 4.1.3.7) - Escherichia coli gb AA18057.1 (U73857) similar to E. coli gltA citrate synthase [Escherichia coli] gb AAC73436.1 (AE000140) putative citrate synthase; propionate metabolism? [Escherichia coli K12] sp P74840 PRPD_SALTY PRPD PROTEIN gb AAC44816.1 (U51879) PrpD [Salmonella typhimurium]	SEQ ID n-2406
SEQ ID n° 10264-PL-2246.1	Contig9 from 5002234 to 5003685	p	88%	gb AAC44817.2 (U51879) PrpE [Salmonella typhimurium]	SEQ ID n-2407
SEQ ID n° 10265-PL-2248.1	Contig9 from 5003758 to 5005644	p	81%	dbj BAB04638.1 (AP001510) diaminobutyric acid aminotransferase [Bacillus halodurans]	SEQ ID n-2409
SEQ ID n° 10266-PL-2249.1	Contig9 from 5006797 to 5008107	p	60%	dbj BAB10550.1 (AB008265) gene_id:MDC12.4-unknown protein [Arabidopsis thaliana]	SEQ ID n-2410
SEQ ID n° 10267-PL-2250.1	Contig9 from 5008124 to 5008981	p	30%		SEQ ID n-2412

SEQ ID n° 10268 PL-3489.1	Contig9 from 5009000 to p 46%	pir G83130 spermidine acetyltransferase PA4114 [imported] - Pseudomonas aeruginosa (strain PAO1) gb ARG07501.1 AE004828_2 (AE004828) spermidine acetyltransferase [Pseudomonas aeruginosa] SEQ ID n-2704
SEQ ID n° 10269 PL-2251.1	Contig9 from 5009515 to p 53%	pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] SEQ ID n-2413
SEQ ID n° 10270 PL-2252.1	Contig9 from 5019372 to p 53%	pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] SEQ ID n-2414
SEQ ID n° 10271 PL-2253.1	Contig9 from 5029187 to p 52%	gb AAF17280.1 (AF204805) NOSC [Nostoc sp. GSV224] SEQ ID n-2415
SEQ ID n° 10272 PL-2254.1	Contig9 from 5032585 to p 52%	gb AAF17280.1 (AF204805) NOSC [Nostoc sp. GSV224] SEQ ID n-2416
SEQ ID n° 10273 PL-2255.1	Contig9 from 5042436 to p 12%	gb AAA48767.1 (J03860) fatty acid synthase (EC 3.2.1.23) [Gallus gallus] SEQ ID n-2417
SEQ ID n° 10274 PL-2256.1	Contig9 from 5044315 to p 50%	gb ARG57346.1 AE005453_3 (AE005453) putative ATP binding component of a transport system [Escherichia coli O157:H7] gb AAE50779.1 (S83325) aspartyl(asparaginyl)beta-hydroxylase, HAAH [human, hepatoblastoma cell line HepG2, Peptide, 758 aa] [Homo sapiens] SEQ ID n-2418
SEQ ID n° 10275 PL-2257.1	Contig9 from 5046095 to p 34%	emb CAB92259.1 (AL356595) putative oxygenase [Streptomyces coelicolor A3(2)] SEQ ID n-2419
SEQ ID n° 10276 PL-2258.1	Contig9 from 5047071 to p 35%	emb CAB92259.1 (AL356595) putative oxygenase [Streptomyces coelicolor A3(2)] SEQ ID n-2420

SEQ ID n° 10277 PL-2259.1	Contig9 from 5048054 to 5050477	p	44%	pir H83348 probable acylase PA2385 [imported] - Pseudomonas aeruginosa (strain PA01) gb AA05773.1 AE004664_10 (AE004664) probable acylase [Pseudomonas aeruginosa]	SEQ ID n-1421
SEQ ID n° 10278 PL-2260.1	Contig9 from 5050659 to 5051492	p	37%	gb AAF71807.1 AC013430_16 (AC013430) F3F9.18 [Arabidopsis thaliana]	SEQ ID n-1423
SEQ ID n° 10279 PL-5618.1	Contig9 from 5051686 to 5051832	p	No Hits found		#N/A
SEQ ID n° 10280 PL-5617.1	Contig9 from 5051855 to 5052040	m	No Hits found		#N/A
SEQ ID n° 10281 PL-2261.1	Contig9 from 5052069 to 5053034	p	No Hits found		SEQ ID n-1424
SEQ ID n° 10282 PL-5616.1	Contig9 from 5053021 to 5053248	p	No Hits found		#N/A
SEQ ID n° 10283 PL-2151.2	Contig9 from 5053239 to 5054969	p	38%	pir C70091 conserved hypothetical protein yydD Bacillus subtilis dbj BA11278.1 (D78193) yydD [Bacillus subtilis] emb CAE16057.1 (Z99124) similar to hypothetical proteins [Bacillus subtilis] pir B83170 hypothetical protein PA3791 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07178.1 AE004798_1 (AE004798) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-1303
SEQ ID n° 10284 PL-3488.1	Contig9 from 5055466 to 5055972	p	36%	pir F83173 outer membrane protein OprC PA3790 [imported] - Pseudomonas aeruginosa (strain PA01) dbj BAA05664.1 (D28119) outer membrane protein C [Pseudomonas aeruginosa] gb AAG07177.1 AE004797_12 (AE004797) outer membrane protein OprC [Pseudomonas aeruginosa]	SEQ ID n-2703
SEQ ID n° 10285 PL-2150.1	Contig9 from 5056180 to 5058210	p	67%		SEQ ID n-1302

1128

SEQ ID n° 10286 PL-2149.1	Contig9 from 5058258 to 5059052	m	28%	emb CAC14352.1 (AL445945) putative secreted hydrolase [Streptomyces coelicolor]	SEQ ID n-1300
SEQ ID n° 10287 PL-2148.1	Contig9 from 5059665 to 5060939	m	88%	pir E83018 homocysteine synthase PA5025 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG08410.1 AE004915_5 (AE004915) homocysteine synthase [Pseudomonas aeruginosa]	SEQ ID n-1299
SEQ ID n° 10288 PL-2147.1	Contig9 from 5061621 to 5062982	p	54%	pir H82186 probable multidrug resistance protein Norm VC1540 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94694.1 (AE004232) multidrug resistance protein Norm, putative [Vibrio cholerae]	SEQ ID n-1298
SEQ ID n° 10289 PL-2146.1	Contig9 from 5063871 to 5064617	p	20%	gb AAC44892.1 (U73112) hemoglobin-haptoglobin utilization protein A [Neisseria meningitidis]	SEQ ID n-1297
SEQ ID n° 10290 PL-2145.1	Contig9 from 5064700 to 5066199	p	39%	gb AAK03599.1 (AE006188) unknown [Pasteurella multocida]	SEQ ID n-1296
SEQ ID n° 10291 PL-2144.1	Contig9 from 5066456 to 5069500	p	25%	pir C83035 hypothetical protein PA4897 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG08282.1 AE004902_10 (AE004902) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-1295
SEQ ID n° 10292 PL-2143.1	Contig9 from 5069583 to 5070350	p	57%	gb AAC83227.1 (AF070473) TonB [Pasteurella multocida] gb AAK03272.1 (AE006158) TonB [Pasteurella multocida]	SEQ ID n-1294
SEQ ID n° 10293 PL-3487.1	Contig9 from 5070417 to 5070878	m	55%	pir C83467 conserved hypothetical protein PA1428 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04817.1 AE004572_5 (AE004572) conserved hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-12702

SEQ ID n° 10294 PL-2142.1	Contig9 from 5071312 to 5073261	p 82%	sp P40601 LIP1_PHOU_LIPASE_1 PRECURSOR (TRIACYLGLYCEROL LIPASE) pir A47081 triacylglycerol lipase (EC 3.1.1.3) - Xenorhabdus luminescens emb CAA47020.1 (X66379) triacylglycerol lipase [Xenorhabdus luminescens]	SEQ ID n-2293
SEQ ID n° 10295 PL-3486.1	Contig9 from 5073387 to 5073842	m 41%	pir T36821 hypothetical protein SCI35.08c - Streptomyces coelicolor emb CAA20797.1 (AL031541) hypothetical protein SCI35.08c [Streptomyces coelicolor A3(2)]	SEQ ID n-2701
SEQ ID n° 10296 PL-5612.1	Contig9 from 5074050 to 5074325	m No Hits found	#N/A	
SEQ ID n° 10297 PL-5611.1	Contig9 from 5074986 to 5075390	p 35%	sp P13421 FMA_SERMA_FIMBRIA_A PROTEIN PRECURSOR pir A31096 fimbrial protein precursor, mannose- resistant - Serratia marcescens (strain US46) gb AA26576.1 (W21161) Smfa protein [Serratia marcescens]	#N/A
SEQ ID n° 10298 PL-2141.1	Contig9 from 5076311 to 5076796	p 65%	emb CAA03911.1 (AJ000084) Ccm1 protein [Proteus mirabilis]	SEQ ID n-2292
SEQ ID n° 10299 PL-3483.1	Contig9 from 5077006 to 5077536	p 70%	emb CAA03913.1 (AJ000084) putative acetyl transferase [Proteus mirabilis]	SEQ ID n-2700
SEQ ID n° 10300 PL-3482.1	Contig9 from 5077616 to 5078098	p No Hits found		SEQ ID n-2699
SEQ ID n° 10301 PL-2140.1	Contig9 from 5078106 to 5078690	p 58%	gb AAG58469.1 AE005559_5 (AE005559) induced in stationary phase, recognized by rpoS, affects cell division [Escherichia coli O157:H7]	SEQ ID n-2291
SEQ ID n° 10302 PL-5610.1	Contig9 from 5079718 to 5080005	p 54%	dbj BAB03228.1 (AB046380) tail fiber protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 10303 PL-7296.1	Contig9 from 5080231 to 5080443	m 42%	dbj BAA35849.1 (D90742) Hypothetical 7.5 kd protein in mdoH-msyB intergenic region. [Escherichia coli]	#N/A

1130

Contig9 from SEQ ID n° 10304 PL-3481.1 5080963	m	No Hits found	pir C83007 probable transcription regulator PA5116 [imported] - Pseudomonas aeruginosa (strain PAO1) #N/A	SEQ ID n° 2698
Contig9 from SEQ ID n° 10305 PL-5609.1 5081331	p	46%	gb AAG08501.1 AE004924.6 (AE004924) probable transcriptional regulator [Pseudomonas aeruginosa]	
Contig9 from SEQ ID n° 10306 PL-2139.1 5083523	p	43%	ref NP_043502.1 orf31 [Bacteriophage HPI] sp P51735 VPH_BPHP1 PROBABLE TAIL FIBER PROTEIN (ORF31) pir S69539 hypothetical protein 31 - phage HPI gb AAB09218.1 (U24159) orf31 [Bacteriophage HPI]	SEQ ID n° 2289
Contig9 from SEQ ID n° 10307 PL-2138.1 5084299	p	36%	gb AAG56009.1 AE005333.6 (AE005333) putative tail fiber protein of prophage CP-933X [Escherichia coli O157:H7]	SEQ ID n° 2288
Contig9 from SEQ ID n° 10308 PL-2137.1 5084870	p	42%	ref NP_043504.1 orf33 [Bacteriophage HPI] sp P51737 Y033_BPHP1 HYPOTHETICAL 28.3 KD PROTEIN IN LYS 3' REGION (ORF33) pir S69541 hypothetical protein 33 - phage HPI gb AAB09220.1 (U24159) orf33 [Bacteriophage HPI]	SEQ ID n° 2287
Contig9 from SEQ ID n° 10309 PL-3480.1 5085378	p	55%	ref NP_043505.1 orf34 [Bacteriophage HPI] sp P51738 Y034_BPHP1 HYPOTHETICAL 20.8 KD PROTEIN IN LYS 3' REGION (ORF34) pir S69542 hypothetical protein 34 - phage HPI gb AAB09221.1 (U24159) orf34 [Bacteriophage HPI]	SEQ ID n° 2697
Contig9 from SEQ ID n° 10310 PL-2136.1 5086877	p	61%	ref NP_043506.1 orf35 [Bacteriophage HPI] sp P51739 Y035_BPHP1 HYPOTHETICAL 58.7 KD PROTEIN IN LYS 3' REGION (ORF35) pir S69543 hypothetical protein 35 - phage HPI gb AAB09222.1 (U24159) orf35 [Bacteriophage HPI]	SEQ ID n° 2286

SEQ ID n° 10311 PL-5607.1	Contig9 from 5086835 to 5087026	p	No Hits found	#N/A
SEQ ID n° 10312 PL-5606.1	Contig9 from 5087146 to 5087319	p	No Hits found	#N/A
SEQ ID n° 10313 PL-3478.1	Contig9 from 5087316 to 5087783	p	68%	sp P76107 YDCQ_ECOLI_HYPOTHETICAL_16.1_KD PROTEIN IN TEHB-ANSP INTERGENIC REGION pir A64896 hypothetical protein b1438 - Escherichia coli gb AAC74520.1 (AE000241) orf, hypothetical protein [Escherichia coli K12] sp P18837 SFSB_ECOLI_SUGAR_FERMENTATION STIMULATION PROTEIN B (NER-LIKE PROTEIN) pir BVECMP nlp protein - Escherichia coli emb CAA48736.1 (X68873) Ner-like protein, homologous to Ner protein of bacteriophages Mu and D108 [Escherichia coli] gb AA57989.1 (U18997) Ner-like protein [Escherichia coli] gb AAC76220.1 (AE000399) regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu [Escherichia coli K12] gb AAG58322.1 AE005547_8 (AE005547) regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu [Escherichia coli O157:H7]
SEQ ID n° 10314 PL-5605.1	Contig9 from 5088131 to 5088400	m	52%	#N/A
SEQ ID n° 10315 PL-5604.1	Contig9 from 5088397 to 5088627	m	No Hits found	#N/A
SEQ ID n° 10316 PL-5603.1	Contig9 from 5088655 to 5088906	p	No Hits found	#N/A
SEQ ID n° 10317 PL-2135.1	Contig9 from 5089352 to 5090410	m	47%	gb AAG56452.1 AE005371_8 (AE005371) putative integrase for prophage CP-933R [Escherichia coli O157:H7]
				SEQ ID n-2695
				SEQ ID n-3285

SEQ ID n° 10318 PL-5602.1	Contig9 from 5090487 to 5090702	m	No Hits found	#N/A
SEQ ID n° 10319 PL-5601.1	Contig9 from 5090707 to 5090877	m	No Hits found	#N/A
SEQ ID n° 10320 PL-5600.1	Contig9 from 5091142 to 5091243	p	No Hits found	#N/A
SEQ ID n° 10321 PL-5599.1	Contig9 from 5091447 to 5091635	m	No Hits found	#N/A
SEQ ID n° 10322 PL-3477.1	Contig9 from 5091687 to 5092184	m	45%	<p>pir Tl3296 hypothetical protein 8 - Streptococcus phage phi-01205 gb AAC79524.1 (U88974) ORF8 [Streptococcus thermophilus temperate bacteriophage 01205] SEQ ID n-2694</p>
SEQ ID n° 10323 PL-2134.1	Contig9 from 5092181 to 5093941	m	8%	<p>pir T03004 exodeoxyribonuclease_VIII homolog - Salmonella typhimurium gb AAC26062.1 (AF001386) exodeoxyribonuclease VIII [Salmonella typhimurium] SEQ ID n-2284</p>
SEQ ID n° 10324 PL-6939.1	Contig9 from 5093955 to 5094113	m	No Hits found	#N/A
SEQ ID n° 10325 PL-2133.1	Contig9 from 5094120 to 5095145	m	21%	<p>dbj BAB06239.1 (AF001515) transposase related protein (20) [Bacillus halodurans] SEQ ID n-2283</p>
SEQ ID n° 10326 PL-5595.1	Contig9 from 5095321 to 5095665	m	No Hits found	#N/A
SEQ ID n° 10327 PL-5593.1	Contig9 from 5095864 to 5096169	p	No Hits found	#N/A
SEQ ID n° 10328 PL-5592.1	Contig9 from 5096691 to 5097062	m	No Hits found	#N/A

Contig9 from SEQ ID n° 10329 PL-5591.1	5097146 to 5097430	p	37%	pir E82797 conserved hypothetical protein XF0501 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF83311.1 AE003899_3 (AE003899) conserved hypothetical protein [Xylella fastidiosa] gb AAG57034.1 AE005422_9 (AE005422) unknown protein encoded within prophage CP-933U [Escherichia coli O157:H7]	#N/A
Contig9 from SEQ ID n° 10330 PL-5589.1	5097488 to 5097937	p	37%		#N/A
Contig9 from SEQ ID n° 10331 PL-5588.1	5097952 to 5098176	p	No Hits found		#N/A
Contig9 from SEQ ID n° 10332 PL-2132.1	5098179 to 5098931	p	28%	pir T03010 probable replication protein - Salmonella typhimurium gb AAC26071.1 (AF001386) unknown [Salmonella typhimurium] gb AA23700.1 (J04030) dnaC protein [Escherichia coli] gb AAA97260.1 (U14003) CG Site No. 849; alternate gene name dnaD [Escherichia coli] gb AAC77317.1 (AE000507) chromosome replication; initiation and chain elongation [Escherichia coli K12] gb AAG59544.1 AE005667_8 (AE005667) chromosome replication; initiation and chain elongation [Escherichia coli O157:H7] SEQ ID n-2693 ref NP_037740.1 Gp55 [Bacteriophage HK97] gb AAF31133.1 (AF069529) Gp55 [Bacteriophage HK97]	SEQ ID n-2282
Contig9 from SEQ ID n° 10333 PL-3476.1	5098940 to 5099524	p	53%		
Contig9 from SEQ ID n° 10334 PL-2131.1	5099526 to 5100893	p	60%		SEQ ID n-2281
Contig9 from SEQ ID n° 10335 PL-3475.1	5101523 to 5101990	p	No Hits found		SEQ ID n-2692
Contig9 from SEQ ID n° 10336 PL-2130.1	5102006 to 5103205	p	36%	pir T36177 probable DNA-binding protein - Streptomyces coelicolor emb CAB41077.1 (AL049645) putative DNA-binding protein [Streptomyces coelicolor A3(2)] gb AAG56427.1 AE005369_16 (AE005369) unknown protein encoded within prophage CP-933R [Escherichia coli O157:H7]	SEQ ID n-2280
Contig9 from SEQ ID n° 10337 PL-3474.1	5103306 to 5103899	p	64%		SEQ ID n-2691

SEQ ID n° 10338 PL-5586.1	Contig9 from 5103915 to 5104175	p	No Hits found	#N/A
SEQ ID n° 10339 PL-5583.1	Contig9 from 5104200 to 5104358	p	No Hits found	#N/A
SEQ ID n° 10340 PL-5582.1	Contig9 from 5104404 to 5104715	p	63%	emb CAB39993.1 (AJ237660) Q protein [Bacteriophage 21]
SEQ ID n° 10341 PL-5581.1	Contig9 from 5104895 to 5105095	p	49%	gb AAC56133.1 AE005344_9 (AE005344) unknown protein encoded by prophage CP-9330 [Escherichia coli O157:H7]
SEQ ID n° 10342 PL-3473.1	Contig9 from 5105196 to 5105669	p	74%	gb AAC56134.1 AE005344_10 (AE005344) putative DNA adenine methyltransferase encoded by prophage CP-9330 [Escherichia coli O157:H7]
SEQ ID n° 10343 PL-5580.1	Contig9 from 5105845 to 5106213	m	59%	sp Q47588 RDGB ERWCA DNA-BINDING PROTEIN RDGB pir S61399 DNA-binding.protein.rdgb - Erwinia carotovora subsp. carotovora gb AA24866.1 (L32173) DNA-binding protein [Pectobacterium carotovorum] prf 2105355B rdgb gene [Erwinia carotovora carotovora] ref NP_050620.1 gp16 [Bacteriophage Mu] sp Q38494 VG16_BPMU PROTEIN GP16 (E16 PROTEIN) gb AAF01093.1 AF083977_12 (AF083977) gp16 [Bacteriophage Mu]
SEQ ID n° 10344 PL-5579.1	Contig9 from 5106197 to 5106556	m	53%	#N/A
SEQ ID n° 10345 PL-5578.1	Contig9 from 5106735 to 5106926	m	No Hits found	#N/A
SEQ ID n° 10346 PL-2129.1	Contig9 from 5107385 to 5108473	m	47%	gb AAC64124.1 (AF091717) Eha [Salmonella typhi] pir C82157 hypothetical protein VC1799 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94948.1 (AE004256) hypothetical protein [Vibrio cholerae]
SEQ ID n° 10347 PL-2128.1	Contig9 from 5108796 to 5110580	m	52%	SEQ ID n-2277

SEQ ID n-2278

Contig9 from SEQ ID n° 10348 PL-2127.1 5110634 to 5111557	m	47%	pir HB1132 hypothetical protein NMB1002 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF41403.1 (AE002451) hypothetical protein [Neisseria meningitidis MC58]	SEQ ID n° 2276
Contig9 from SEQ ID n° 10349 PL-5576.1 5111610 to 5111918	m	43%	pir F91890 hypothetical protein NMA1223 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB84483.1 (AL162755) hypothetical protein NMA1223 [Neisseria meningitidis Z2491] pir B81133 hypothetical protein NMB1004 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF41405.1 (AE002451) hypothetical protein [Neisseria meningitidis MC58]	#N/A
Contig9 from SEQ ID n° 10350 PL-5575.1 5111974 to 5112159	m	34%	gb AAG56901.1 AE005412.11 (AE005412) unknown protein encoded by prophage CP-933T [Escherichia coli O157:H7]	#N/A
Contig9 from SEQ ID n° 10351 PL-5574.1 5112643	p	48%		#N/A
Contig9 from SEQ ID n° 10352 PL-5573.1 5112679 to 5113023	p	No Hits found		#N/A
Contig9 from SEQ ID n° 10353 PL-5572.1 5113046 to 5113489	p	No Hits found		#N/A
Contig9 from SEQ ID n° 10354 PL-3471.1 5113507 to 5113944	p	No Hits found		#N/A
Contig9 from SEQ ID n° 10355 PL-2126.1 5113992 to 5114762	m	33%	gb AAG50260.1 AF311653_1 (AF311653) probable DNA adenine methylase [Bacteriophage GMSE-1]	SEQ ID n° 2689
Contig9 from SEQ ID n° 10356 PL-5571.1 5115013 to 5115363	p	No Hits found		#N/A

SEQ ID n° 10357 PL-2125.1	Contig9 from 5115396 to 5115983	p	26%	sp P44587 YFHD_HAETN HYPOTHETICAL PROTEIN HI0232 pir H64145 hypothetical protein HI0232 - Haemophilus influenzae (strain Rd KW20) gb AAC21901.1 (U32709) conserved hypothetical protein [Haemophilus influenzae Rd] SEQ ID n-1274	SEQ ID n-1273
SEQ ID n° 10358 PL-2124.1	Contig9 from 5115973 to 5116596	p	No Hits found		
SEQ ID n° 10359 PL-5570.1	Contig9 from 5116593 to 5116925	p	No Hits found		#N/A
SEQ ID n° 10360 PL-5569.1	Contig9 from 5116918 to 5117229	p	No Hits found		#N/A
SEQ ID n° 10361 PL-3470.1	Contig9 from 5117229 to 5117774	p	50%	sp P44223 YE99_HAETN HYPOTHETICAL PROTEIN HI1499 pir H64032 hypothetical protein HI1499 - Haemophilus influenzae (strain Rd KW20) gb AAC23149.1 (U32826) H. influenzae predicted coding region HI1499 [Haemophilus influenzae Rd] ref NP_050632.1 gp28 [Bacteriophage Mu] sp Q9TW6 VG28_BPMU PROTEIN GP28 gb AAF01106.1 AF083977_25 (AF083977) gp28 [Bacteriophage Mu] pir F81811 conserved hypothetical protein NMA1851 [imported] - Neisseria meningitidis (group A strain Z2491) emb CAB85074.1 (AL162757) conserved hypothetical protein [Neisseria meningitidis Z2491] ref NP_050634.1 gp30 [Bacteriophage Mu] sp Q01259 VFF_BPMU F PROTEIN (GPF) (PROTEIN GP30) gb AAF01108.1 AF083977_27 (AF083977) GP30 [Bacteriophage Mu]	SEQ ID n-2688
SEQ ID n° 10362 PL-2123.1	Contig9 from 5117771 to 5119294	p	56%		SEQ ID n-1272
SEQ ID n° 10363 PL-2122.1	Contig9 from 5119294 to 5120787	p	34%		SEQ ID n-1271
SEQ ID n° 10364 PL-2121.1	Contig9 from 5120789 to 5121598	p	51%		SEQ ID n-1270

SEQ ID n° 10365 PL-3469.1	Contig9 from 5121591 to 5122040	p 38%	sp P45255 VPG2_HAEIN MU-LIKE PROPHAGE FLUMU G PROTEIN 2 pir B64130 hypothetical protein HI1568 - Haemophilus influenzae (strain Rd KW20) gb AAC23215.1 (U32831) G protein (muG-2) [Haemophilus influenzae Rd]	SEQ ID n-2686
SEQ ID n° 10366 PL-2120.1	Contig9 from 5122245 to 5123339	p No Hits found		SEQ ID n-2689
SEQ ID n° 10367 PL-2119.1	Contig9 from 5123371 to 5124306	p No Hits found		SEQ ID n-2687
SEQ ID n° 10368 PL-5566.1	Contig9 from 5124320 to 5124670	p No Hits found	#N/A	
SEQ ID n° 10369 PL-3468.1	Contig9 from 5124660 to 5125109	p 28%	sp P44230 VG36_HAEIN MU-LIKE PROPHAGE FLUMU PROTEIN GP36 pir F64033 hypothetical protein HI1508 - Haemophilus influenzae (strain Rd KW20) gb AAC23155.1 (U32827) conserved hypothetical protein [Haemophilus influenzae Rd]	SEQ ID n-2685
SEQ ID n° 10370 PL-3467.1	Contig9 from 5125109 to 5125576	p No Hits found		SEQ ID n-2684
SEQ ID n° 10371 PL-5565.1	Contig9 from 5125573 to 5125785	p No Hits found	#N/A	
SEQ ID n° 10372 PL-2118.1	Contig9 from 5125775 to 5127202	p 88%	dbj BAA76521.1 (AB017338) tail sheath protein [Pectobacterium carotovorum]	SEQ ID n-2266
SEQ ID n° 10373 PL-3466.1	Contig9 from 5127202 to 5127726	p 93%	dbj BAA76522.1 (AB017338) tail core protein [Pectobacterium carotovorum]	SEQ ID n-2693
SEQ ID n° 10374 PL-5563.1	Contig9 from 5127984 to 5128310	p 69%	dbj BAA96857.1 (AB045036) orf4 [Pectobacterium carotovorum subsp. carotovorum]	#N/A

SEQ ID n° 10375 PL-2117.1	Contig9 from 5128393 to 5130945	p	54%	dbj BAA96858.1 (AB045036) tail protein [Pectobacterium carotovorum subsp. carotovorum]	SEQ ID n-3265
SEQ ID n° 10376 PL-2116.1	Contig9 from 5130945 to 5131829	p	66%	dbj BAA96859.1 (AB045036) orf6 [Pectobacterium carotovorum subsp. carotovorum]	SEQ ID n-3264
SEQ ID n° 10377 PL-2115.1	Contig9 from 5132032 to 5133210	p	73%	dbj BAA96860.1 (AB045036) orf7 [Pectobacterium carotovorum subsp. carotovorum]	SEQ ID n-3263
SEQ ID n° 10378 PL-2114.1	Contig9 from 5133207 to 5133812	p	75%	dbj BAA96861.1 (AB045036) tail spike [Pectobacterium carotovorum subsp. carotovorum]	SEQ ID n-3262
SEQ ID n° 10379 PL-5559.1	Contig9 from 5133850 to 5134212	p	74%	dbj BAA76524.1 (AB017338) baseplate [Pectobacterium carotovorum] dbj BAA96862.1 (AB045036) baseplate [Pectobacterium carotovorum subsp. carotovorum] #N/A	
SEQ ID n° 10380 PL-2113.1	Contig9 from 5134203 to 5135306	p	78%	dbj BAA96863.1 (AB045036) baseplate [Pectobacterium carotovorum subsp. carotovorum]	SEQ ID n-3261
SEQ ID n° 10381 PL-2112.1	Contig9 from 5135362 to 5135874	p	54%	dbj BAA76526.1 (AB017338) tail fiber [Pectobacterium carotovorum]	SEQ ID n-3260
SEQ ID n° 10382 PL-2111.1	Contig9 from 5135834 to 5136853	p	25%	dbj BAA76527.2 (AB017338) tail fiber [Pectobacterium carotovorum]	SEQ ID n-3259
SEQ ID n° 10383 PL-5558.1	Contig9 from 5136854 to 5137306	p	46%	ref NP_047855.1 lambda tail fiber assembly protein G [Yersinia pestis] pir T14970 phage lambda-related tail assembly protein G - Yersinia pestis plasmid pMT1 gb AAC82713.1 (AF074611) lambda tail fiber assembly protein G [Yersinia pestis] emb CAB55185.1 (AL117211) hypothetical protein YPM1.03c [Yersinia pestis] #N/A	

sp P18837 SFSB_ECOLI_SUGAR_FERMENTATION STIMULATION PROTEIN B (NER-LIKE PROTEIN) pir BVECNP nlp protein - Escherichia coli emb CAA48736.1 (X68873) Ner-like protein, homologous to Ner protein of bacteriophages Mu and D108 [Escherichia coli] gb AA57989.1 (U18997) Ner-like protein [Escherichia coli] gb AAC76220.1 (AE000399) regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu [Escherichia coli K12] gb AAG58322.1 AE005547_8 (AE005547) regulatory factor of maltose metabolism; similar to Ner repressor protein of phage Mu [Escherichia coli O157:H7]	#N/A		
Contig9 from 5137407 to m 54% 5137694	SEQ ID n° 10384 PL-5556.1		
Contig9 from 5137730 to p No Hits found 5138023	SEQ ID n° 10385 PL-5555.1		
Contig9 from 5138112 to p No Hits found 5138360	SEQ ID n° 10386 PL-5554.1		
Contig9 from 5139176 to p 77% 5139733	SEQ ID n° 10387 PL-3465.1		
Contig9 from 5139777 to m 34% 5140283	SEQ ID n° 10388 PL-3464.1		
DNA adenine methyltransferase encoded by prophage CP-9330 [Escherichia coli O157:H7] sp P09162 YJRAA_ECOLI_HYPOTHETICAL_14.4_KD PROTEIN IN RRPE-META_INTERGENIC_REGION (O127) pir Q3ECE4 hypothetical 14.4K protein (rrfE- meta intergenic region) - Escherichia coli emb CAA26569.1 (X02800) unidentified reading frame (pot. aa 1-127) [Escherichia coli] gb AAC43105.1 (U00006) alternate name yJaa [Escherichia coli] gb AAC76981.1 (AE000474) orf, hypothetical protein [Escherichia coli K12]		SEQ ID n-2682	SEQ ID n-2681

SEQ ID n° 10389 PL-5552.1	Contig9 from 5140339 to 5140521	p	59%	emb CAA09709.1 (AJ011581) gp13 [bacteriophage PS119]	#N/A
SEQ ID n° 10390 PL-2110.1	Contig9 from 5140505 to 5141041	p	66%	ref NP_046950.1 gp54 [Bacteriophage N15] sp O64362 LYCV_BPN15 LYSOZYME (LYSIS PROTEIN) (MURAMIDASE) (ENDOLYSIN) (PROTEIN GP54) pir T13141 lysozyme homolog - phage N15 gb AAC19069.1 (AF064539) gp54 [Bacteriophage N15]	SEQ ID n-2258
SEQ ID n° 10391 PL-3463.1	Contig9 from 5141134 to 5141583	p	41%	sp P77551 RZPR_ECOLI PUTATIVE RZ ENDOPEPTIDASE FROM LAMBDOID PROPHAGE RAC	SEQ ID n-2680
SEQ ID n° 10392 PL-3462.1	Contig9 from 5141714 to 5142232	p	No Hits found		SEQ ID n-2679
SEQ ID n° 10393 PL-2109.1	Contig9 from 5142252 to 5143151	p	No Hits found		SEQ ID n-2256
SEQ ID n° 10394 PL-3461.1	Contig9 from 5143594 to 5143989	m	77%	gb AAG53986.1 AF327444_2 (AF327444) putative transposase B [Erwinia herbicola]	SEQ ID n-2678
SEQ ID n° 10395 PL-5550.1	Contig9 from 5143986 to 5144432	m	75%	gb AAG53985.1 AF327444_1 (AF327444) putative transposase A [Erwinia herbicola]	#N/A
SEQ ID n° 10396 PL-5548.1	Contig9 from 5144545 to 5144862	p	No Hits found		#N/A
SEQ ID n° 10397 PL-2108.1	Contig9 from 5144941 to 5145660	p	No Hits found		#N/A
SEQ ID n° 10398 PL-2107.1	Contig9 from 5145720 to 5146925	p	25%	sp P44184 YE10_HAEMIN HYPOTHETICAL PROTEIN HI1410 pir E64028 hypothetical protein HI1410 - Haemophilus influenzae (strain Rd KW20) gb AAC23058.1 (U32820) H. influenzae predicted coding region HI1410 [Haemophilus influenzae Rd]	SEQ ID n-2255

1141

SEQ ID n° 10399 PL-2106.1	Contig9 from 5146903 to 5148408	p 28%	pir A82664 conserved hypothetical protein XF1571 XF1576 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84380.1 AE003986_10 (AE003986) conserved hypothetical protein [Xylella fastidiosa] gb AAF84485.1 AE003993_4 (AE003993) conserved hypothetical protein [Xylella fastidiosa] sp P71385 YB07_HABIN HYPOTHETICAL PROTEIN H11407 pir B64122 hypothetical protein H11407 - Haemophilus influenzae (strain Rd KW20) gb AAC23048.1 (U32820) tran-related protein [Haemophilus influenzae Rd] pir F82650 hypothetical protein XF1680 XF1575 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84384.1 AE003986_14 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84489.1 AE003993_8 (AE003993) hypothetical protein [Xylella fastidiosa]	SEQ ID n-1254
SEQ ID n° 10400 PL-2105.1	Contig9 from 5148455 to 5149186	p 39%		SEQ ID n-1253
SEQ ID n° 10401 PL-2104.1	Contig9 from 5149204 to 5150529	p 25%		
SEQ ID n° 10402 PL-3460.1	Contig9 from 5150532 to 5151008	p No Hits found		SEQ ID n-1252
SEQ ID n° 10403 PL-2103.1	Contig9 from 5151134 to 5152042	p No Hits found		SEQ ID n-1251
SEQ ID n° 10404 PL-5546.1	Contig9 from 5152043 to 5152369	p No Hits found		#N/A
SEQ ID n° 10405 PL-5545.1	Contig9 from 5152374 to 5152823	p No Hits found		#N/A

Seq ID n° 10406 PL-3459.1	Contig9 from 5152823 to 5153281	p 29%	pir C82651 hypothetical protein XF1685 XF1580 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84389.1 AE003986_19 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84494.1 AE003993_13 (AE003993) hypothetical protein [Xylella fastidiosa]	SEQ ID n-2675
Seq ID n° 10407 PL-5544.1	Contig9 from 5153278 to 5153649	p No Hits found	#N/A	
Seq ID n° 10408 PL-2102.1	Contig9 from 5153610 to 5154191	p No Hits found	SEQ ID n-2250	
Seq ID n° 10409 PL-2101.1	Contig9 from 5154172 to 5155659	-p 37%	pir F82651 hypothetical protein XF1688 XF1583 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84392.1 AE003986_22 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84497.1 AE003993_16 (AE003993) hypothetical protein [Xylella fastidiosa]	SEQ ID n-2249
Seq ID n° 10410 PL-3458.1	Contig9 from 5155659 to 5156096	p No Hits found	SEQ ID n-2674	
Seq ID n° 10411 PL-5543.1	Contig9 from 5156096 to 5156503	p No Hits found	#N/A	
Seq ID n° 10412 PL-2100.1	Contig9 from 5156709 to 5158829	p 19%	pir T09486 hypothetical protein 47 - phage P1 gb AAB88193.1 (AF035607) structural lytic transglycosylase [enterobacteria phage P1]	SEQ ID n-2248
Seq ID n° 10413 PL-2099.1	Contig9 from 5158829 to 5159650	p No Hits found	SEQ ID n-2245	
Seq ID n° 10414 PL-5541.1	Contig9 from 5159647 to 5159952	p No Hits found	#N/A	

Contig9 from SEQ ID n° 10415 PL-2098.1	5159949 to 5160845	p	No Hits found	SEQ ID n-1244
Contig9 from SEQ ID n° 10416 PL-3456.1	5160868 to 5161404	p	No Hits found	SEQ ID n-2672
Contig9 from SEQ ID n° 10417 PL-3455.1	5161868 to 5162401	p	No Hits found	SEQ ID n-2671
Contig9 from SEQ ID n° 10418 PL-5539.1	5162558 to 5162731	p	No Hits found	#N/A
Contig9 from SEQ ID n° 10419 PL-5537.1	5162830 to 5163186	p	No Hits found	#N/A
Contig9 from SEQ ID n° 10420 PL-2097.1	5163252 to 5164427	p	28%	<p>pir [A82649 hypothetical protein XF1704 [imported] - Xylella fastidiosa (strain 9a5c) gb AAE84513.1 AE003994_12 (AE003994) hypothetical protein [Xylella fastidiosa]</p>
Contig9 from SEQ ID n° 10421 PL-2096.1	5164428 to 5165033	p	No Hits found	SEQ ID n-2243
Contig9 from SEQ ID n° 10422 PL-2095.1	5165020 to 5166363	p	19%	<p>ref NP_050653.1 s [Bacteriophage Mu] sp Q9TIV0 VPS_BPMU TAIL FIBER PROTEIN (GPS) gb AAF01127.1 AF083977_46 (AF083977) S [Bacteriophage Mu] ref NP_047855.1 lambda tail fiber assembly protein G [Yersinia pestis] pir T14970 phage lambda-related tail assembly protein G - Yersinia pestis plasmid pMT1 gb AAC82713.1 (AF074611) lambda tail fiber assembly protein G [Yersinia pestis] emb CAB55185.1 (AL117211) hypothetical protein YPMT1.03c [Yersinia pestis]</p>
Contig9 from SEQ ID n° 10423 PL-5536.1	5166364 to 5166810	p	47%	#N/A

1144

Contig9 from SEQ ID n° 10424 PL-5535.1	m	32%	gb AAG59528.1 AE005665_10 (AE005665) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
Contig9 from 5167242				
Contig9 from SEQ ID n° 10425 PL-5534.1	m	No Hits found		#N/A
Contig9 from 5167570			sp P32052 SSRP_ECOLI_SSRA-BINDING PROTEIN (SMALL PROTEIN B) pir JS0701 small protein B, smpB - Escherichia coli dbj BAA02062.1 (D12501) small protein [Escherichia coli] gb AAA79790.1 (U36840) smpB gene product [Escherichia coli] gb AAC75669.1 (AE000347) small protein B [Escherichia coli K12]	SEQ ID n-2670
Contig9 from SEQ ID n° 10427 PL-3453.1	p	80%	gb AAG57729.1 AE005491_9 (AE005491) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-2669
Contig9 from 5169090 to 5169524			pir T08631 hypothetical protein b2618 - Escherichia coli (strain K-12) gb AAA79788.1 (U36840) ORF_f102 [Escherichia coli] gb AAC75667.1 (AE000347) orf, hypothetical protein [Escherichia coli K12]	#N/A
Contig9 from SEQ ID n° 10428 PL-5533.1	p	64%	sp P23089 SMPA_ECOLI_SMALL PROTEIN A PRECURSOR pir T08630 hypothetical protein o133 - Escherichia coli gb AAA79787.1 (U36840) ORF_o133 [Escherichia coli] dbj BAU16502.1 (D90888) SMALL PROTEIN A. [Escherichia coli] pir RQECN recN protein - Escherichia coli gb AAC75665.1 (AE000347) protein used in recombination and DNA repair [Escherichia coli K12]	#N/A
Contig9 from 5170213	m	78%		
Contig9 from SEQ ID n° 10429 PL-5532.1	m	80%		SEQ ID n-2240
Contig9 from 5170452 to 5172113				

Contig9 from 5172202 to 5173080	m	85%	sp P37768 YFJB_ECOLI_HYPOTHETICAL_32.6_KDA PROTEIN IN GRPE-REC INTERGENIC REGION pir B65040 yfjB protein - Escherichia coli (strain K-12) gb AAC75664.1 (AE000347) orf, hypothetical protein [Escherichia coli K12] dbj BAA16500.1 (D90888) similar to [SwissProt Accession Number P37768] [Escherichia coli] SEQ ID n° 10431 PL-2093.1	SEQ ID n-3239
Contig9 from 5173205 to 5173786	p	68%	sp P09372 GRPE_ECOLI_GRPE_PROTEIN (HSP-70 COFACTOR) (HEAT SHOCK PROTEIN B25.3) (HSP24) pir S01240 heat shock protein grpE [heat shock protein b25.3] (hsp24) - Escherichia coli emb CAA30711.1 (X07863) grpE protein (AA 1-197) [Escherichia coli] gb AB32515.1 GrpE-heat shock protein [Escherichia coli, mutant grpE25, Peptide Mutant, 197 aa] gb AAC75663.1 (AE000347) phage lambda replication; host DNA synthesis; heat shock protein; protein repair [Escherichia coli K12] dbj BAAL6498.1 (D90888) heat shock protein B25.3 [Escherichia coli] SEQ ID n° 10432 PL-2092.1	SEQ ID n-2238
Contig9 from 5173855 to 5174535	m	81%	pir C82086 uracil-DNA glycosylase VC2359 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF95502.1 (AE004306) uracil-DNA glycosylase [Vibrio cholerae] SEQ ID n° 10433 PL-2091.1	SEQ ID n-2237
Contig9 from 5175294 to 5176310	p	55%	gb AAC31479.1 (AF067849) phospholipase A [Yersinia enterocolitica (type 0:8)] SEQ ID n° 10434 PL-2090.1	SEQ ID n-2236
Contig9 from 5176443 to 5176913	p	61%	gb AAD29791.1 (U37262) accessory protein [Serratia sp. MK1] #N/A SEQ ID n-3696	
Contig9 from 5177613 to 5178461	p	33%	pir D71094 probable cofactor modifying protein Pyrococcus horikoshii dbj BAA30114.1 (AP000004) 373aa long hypothetical cofactor modifying protein [Pyrococcus horikoshii] SEQ ID n° 10435 PL-3451.2	
Contig9 from 5177613 to 5178461	p	33%	Pyrococcus horikoshii dbj BAA30114.1 (AP000004) 373aa long hypothetical cofactor modifying protein [Pyrococcus horikoshii] SEQ ID n° 10436 PL-853.2	

SEQ ID n° 10437	PL-854.1	Contig9 from 5178463 to 5179602	p	No Hits found	SEQ ID n-3697
SEQ ID n° 10438	PL-855.1	Contig9 from 5179849 to 5180592	p	No Hits found	SEQ ID n-3698
SEQ ID n° 10439	PL-3450.1	Contig9 from 5180608 to 5181138	p	59%	SEQ ID n-2666
SEQ ID n° 10440	PL-856.1	Contig9 from 5181335 to 5182753	p	17%	
SEQ ID n° 10441	PL-7330.1	Contig9 from 5182927 to 5183073	p	No Hits found	SEQ ID n-3699
SEQ ID n° 10442	PL-857.1	Contig9 from 5183242 to 5184351	p	No Hits found	#N/A
SEQ ID n° 10443	PL-858.1	Contig9 from 5184373 to 5184987	p	44%	SEQ ID n-3700
SEQ ID n° 10444	PL-859.1	Contig9 from 5185256 to 5186470	p	50%	SEQ ID n-3701
<p> sp Q13907 ID1L_HUMAN ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (IPP ISOMERASE) (ISOPENTENYL PYROPHOSPHATE ISOMERASE) sp P46377 PASS_RHOFA_HYPOTHETICAL_47.9_KD OXIDOREDUCTASE IN FASCIATION LOCUS (ORF5) pir E55578 hypothetical protein (ipt 3' region) - Rhodococcus fascians plasmid pFID188 emb CAA82745.1 (Z29635) orf5 [Rhodococcus fascians] </p>					
<p> pir A72359 conserved hypothetical protein - Thermotoga maritima (strain MSB8) gb AAD35669.1 AE001733_6 (AE001733) conserved hypothetical protein [Thermotoga maritima] sp P71243 WCAL_ECOLI_PUTATIVE_COLANIC_ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAL pir C64970 hypothetical protein b2044 - Escherichia coli (strain K-12) dbj BAAL5898.1 (D90842) ORF_ID:0352#3; similar to [PIR Accession Number S15296] coli] gb AAC75105.1 (AE000295) putative colanic acid biosynthesis glycosyl transferase [Escherichia coli K12] </p>					SEQ ID n-3702

SEQ ID n° 10445 PL-860.1	Contig9 from 5186477 to 5187181	p	No Hits found	Seq ID n-3704
SEQ ID n° 10446 PL-861.1	Contig9 from 5187219 to 5188109	p	40%	Seq ID n-3705
SEQ ID n° 10447 PL-862.1	Contig9 from 5188485 to 5189498	m	72%	Seq ID n-3706
SEQ ID n° 10448 PL-3449.1	Contig9 from 5189586 to 5190095	p	No Hits found	Seq ID n-2664
SEQ ID n° 10449 PL-863.1	Contig9 from 5190181 to 5190927	p	No Hits found	Seq ID n-3707
SEQ ID n° 10450 PL-864.1	Contig9 from 5191056 to 5192150	p	40%	Seq ID n-3708
SEQ ID n° 10451 PL-865.1	Contig9 from 5192200 to 5193225	p	21%	Seq ID n-3709
SEQ ID n° 10452 PL-3448.1	Contig9 from 5193292 to 5193819	p	49%	Seq ID n-2663
SEQ ID n° 10453 PL-866.1	Contig9 from 5193851 to 5195026	p	39%	Seq ID n-3710
SEQ ID n° 10454 PL-3447.1	Contig9 from 5195584 to 5196102	p	No Hits found	Seq ID n-2662

pir||S39957 succinoglycan biosynthesis
 glycosyltransferase (EC 2.4.1.-) exom
 [validated] - Rhizobium meliloti
 emb|CAA80346.1| (Z22636) Exom [Sinorhizobium
 meliloti]
 ref|NP_073225.1| ransposase of IS630 [Salmonella
 enterica serovar Choleraesuis] dbj|BAA01531.1|
 (D10689) M5 protein [Salmonella choleraesuis]
 dbj|BAE20556.1| (AB040415) ransposase of IS630
 [Salmonella enterica serovar
 Choleraesuis]
 gb|AAC95142.1| (AF075600) ABC translocator
 [Brochothrix campestris]
 dbj|BAB06239.1| (AP001515) transposase related
 protein (20) [Bacillus halodurans]
 sp|P57552|MDLB BUCAI MULTIDRUG RESISTANCE-LIKE
 ATP-BINDING PROTEIN MDLB
 gb|AAC61717.1| (AF081284) chromosomal hemolysin
 D [Escherichia coli]

sp P21507 SRMB_ECOLI ATP-DEPENDENT RNA HELICASE SRMB pir [G65035 ATP-dependent RNA helicase SRMB - Escherichia coli emb CAA32364.1 (X14152) SRMB protein [Escherichia coli] dbj BAO02447.1 (D13169) putative ATP dependent RNA helicase [Escherichia coli] dbj BAO10922.1 (D64044) putative ATP dependent RNA helicase [Escherichia coli] gb AAC75629.1 (AE000344) ATP-dependent RNA helicase [Escherichia coli K12]	74%	m	Contig9 from 5196273 to 5197610	SEQ ID n° 10455 PL-867.1	SEQ ID n-3711
gb AAG57691.1 (AE005488_2 (AE005488) putative enzyme [Escherichia coli O157:H7] pir OXECLD L-aspartate oxidase (EC 1.4.3.16) nadB [validated] - Escherichia coli gb AAC75627.1 (AE000344) quinolinate synthetase, B protein [Escherichia coli K12] dbj BAO10920.1 (D64044) RNA polymerase sigma E [Escherichia coli]	63%	p	Contig9 from 5197893 to 5198627	SEQ ID n° 10456 PL-868.1	SEQ ID n-3712
pir OXECLD L-aspartate oxidase (EC 1.4.3.16) nadB [validated] - Escherichia coli gb AAC75627.1 (AE000344) quinolinate synthetase, B protein [Escherichia coli K12] dbj BAO10920.1 (D64044) RNA polymerase sigma E [Escherichia coli]	85%	m	Contig9 from 5198695 to 5200299	SEQ ID n° 10457 PL-869.1	SEQ ID n-3713
gb AAG57691.1 (AE005488_2 (AE005488) putative enzyme [Escherichia coli O157:H7] pir OXECLD L-aspartate oxidase (EC 1.4.3.16) nadB [validated] - Escherichia coli gb AAC75627.1 (AE000344) quinolinate synthetase, B protein [Escherichia coli K12] dbj BAO10920.1 (D64044) RNA polymerase sigma E [Escherichia coli]	93%	p	Contig9 from 5200503 to 5201072	SEQ ID n° 10458 PL-3445.1	SEQ ID n-2660
sp P38106 RSEA_ECOLI SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN pir [B57255 sigma-E factor negative regulatory protein mclA - Escherichia coli dbj BAO10919.1 (D64044) MCLA protein [Escherichia coli] gb AAH3999.1 (U10148) MCLA [Escherichia coli] gb AAC45315.1 (U37089) RSEA [Escherichia coli] gb AAC75625.1 (AE000343) sigma-E factor, negative regulatory protein [Escherichia coli K12] pir [T02998 sigma-E factor regulatory protein rseB - Salmonella typhimurium gb AAC26064.1 (AF001386) sigma-E factor regulatory protein [Salmonella typhimurium] gb AAG57686.1 (AE005487_10 (AE005487) sigma-E factor, negative regulatory protein [Escherichia coli O157:H7]	72%	p	Contig9 from 5201112 to 5201762	SEQ ID n° 10459 PL-871.1	SEQ ID n-3715
sp P38106 RSEA_ECOLI SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN pir [B57255 sigma-E factor negative regulatory protein mclA - Escherichia coli dbj BAO10919.1 (D64044) MCLA protein [Escherichia coli] gb AAH3999.1 (U10148) MCLA [Escherichia coli] gb AAC45315.1 (U37089) RSEA [Escherichia coli] gb AAC75625.1 (AE000343) sigma-E factor, negative regulatory protein [Escherichia coli K12] pir [T02998 sigma-E factor regulatory protein rseB - Salmonella typhimurium gb AAC26064.1 (AF001386) sigma-E factor regulatory protein [Salmonella typhimurium] gb AAG57686.1 (AE005487_10 (AE005487) sigma-E factor, negative regulatory protein [Escherichia coli O157:H7]	66%	p	Contig9 from 5201768 to 5202724	SEQ ID n° 10460 PL-872.1	SEQ ID n-3716
sp P38106 RSEA_ECOLI SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN pir [B57255 sigma-E factor negative regulatory protein mclA - Escherichia coli dbj BAO10919.1 (D64044) MCLA protein [Escherichia coli] gb AAH3999.1 (U10148) MCLA [Escherichia coli] gb AAC45315.1 (U37089) RSEA [Escherichia coli] gb AAC75625.1 (AE000343) sigma-E factor, negative regulatory protein [Escherichia coli K12] pir [T02998 sigma-E factor regulatory protein rseB - Salmonella typhimurium gb AAC26064.1 (AF001386) sigma-E factor regulatory protein [Salmonella typhimurium] gb AAG57686.1 (AE005487_10 (AE005487) sigma-E factor, negative regulatory protein [Escherichia coli O157:H7]	64%	p	Contig9 from 5202724 to 5203188	SEQ ID n° 10461 PL-3444.1	SEQ ID n-2659

SEQ ID n° 10462 PL-873.1	Contig9 from 5203382 to 5205178	P 91%	sp P07682 LEPA_ECOLI GTP-BINDING PROTEIN LEPA pir BVECLA GTP-binding membrane protein lepa - Escherichia coli gb AAC75622.1 (AE000343) GTP- binding elongation factor, may be inner membrane protein [Escherichia coli K12] gb AAG57685.1 AE005487_9 (AE005487) GTP-binding elongation factor, may be inner membrane protein [Escherichia coli O157:H7] gb AAG57684.1 AE005487_8 (AE005487) leader peptidase (signal peptidase I) [Escherichia coli O157:H7] SEQ ID n-3717
SEQ ID n° 10463 PL-874.1	Contig9 from 5205199 to 5206179	P 73%	sp P05797 RNC_ECOLI RIBONUCLEASE III (RNASE III) pir NREC3 ribonuclease III (EC 3.1.26.3) rnc - Escherichia coli emb CAA26692.1 (X02946) ribonuclease III (rnc) (aa 1-226) [Escherichia coli] dbj BA10914.1 (D64044) ribonuclease III [Escherichia coli] gb AAA79829.1 (U36841) RNase III [Escherichia coli] gb AAC75620.1 (AE000343) RNase III, ds RNA [Escherichia coli K12] gb AAG57682.1 AE005487_6 (AE005487) RNase III, ds RNA [Escherichia coli O157:H7] sp P06616 ERA_ECOLI GTP-BINDING PROTEIN ERA pir S44713 GTP-binding protein era - Escherichia coli pir RGECDT GTP-binding protein era - Escherichia coli pdb 1EGA B Chain B, Crystal Structure of A Widely Conserved Gtpase Era pdb 1EGA A Chain A, Crystal Structure of A Widely Conserved Gtpase Era gb AAA03242.1 (M14658) era [Escherichia coli] dbj BA10913.1 (D64044) GTP binding protein [Escherichia coli] gb AAB34156.1 GTPase, Era [Escherichia coli, Peptide Mutant, 301 aa] gb AAA79828.1 (U36841) GTP-binding protein [Escherichia coli] gb AAC75619.1 (AE000343) GTP-binding protein [Escherichia coli K12] SEQ ID n-3718
SEQ ID n° 10464 PL-875.1	Contig9 from 5206354 to 5207034	P 95%	
SEQ ID n° 10465 PL-876.1	Contig9 from 5207031 to 5207939	P 92%	

SEQ ID n° 10466 PL-877.1	Contig9 from 5207951 to 5208676	p 81%	sp P15027 RECO_ECOLI DNA REPAIR PROTEIN RECO (RECOMBINATION PROTEIN O) pir BVECO DNA repair protein reco - Escherichia coli gb AA24515.1 (M27251) recombination protein [Escherichia coli] gb AA21842.1 (M26416) reco [Escherichia coli] gb BAA10912.1 (D64044) reco protein [Escherichia coli] gb AAC75618.1 (AE000343) protein interacts with RecR and possibly RecF proteins [Escherichia coli K12] gb AAG57680.1 AE005487_4 (AE005487) protein interacts with RecR and possibly RecF proteins [Escherichia coli O157:H7] SEQ ID n° 9721
SEQ ID n° 10467 PL-878.1	Contig9 from 5208871 to 5209602	p 82%	sp P24223 PDXJ_ECOLI PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN PDXJ pir A42293 pyridoxal phosphate biosynthetic protein pdxJ - Escherichia coli gb AA24315.1 (M74526) pdxJ [Escherichia coli] gb AA21845.1 (M76470) pdxJ [Escherichia coli] gb AAA79826.1 (U36841) CG Site No. 416 [Escherichia coli] gb AAC75617.1 (AE000343) pyridoxine biosynthesis [Escherichia coli K12] SEQ ID n° 9722
SEQ ID n° 10468 PL-5523.1	Contig9 from 5209602 to 5209982	p 73%	gb AAG57678.1 AE005487_2 (AE005487) CoA:apo- [acyl-carrier-protein] pantetheinephosphotransferase [Escherichia coli O157:H7] #N/A
SEQ ID n° 10469 PL-5522.1	Contig9 from 5209985 to 5210245	m 85%	gb AAG57676.1 AE005486_7 (AE005486) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 10470 PL-5521.1	Contig9 from 5210713 to 5210814	m 80%	sp P77699 TFAD_ECOLI TAIL FIBER ASSEMBLY PROTEIN HOMOLOG FROM LAMBDROID PROPHAGE DLP12 pir G64788 ybcx protein, phage protein-related Escherichia coli gb AAB40757.1 (U82598) hypothetical protein [Escherichia coli] gb AAC73662.1 (AE000161) orf, hypothetical protein [Escherichia coli K12] #N/A

Contig9 from SEQ ID n° 10471 PL-879.1	m	46%	gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-9723
Contig9 from SEQ ID n° 10472 PL-5519.1	m	62%	ref NP_050998.1 P37 [Bacteriophage APSE-1] sp Q9TIR1 TFA_BPAPS PROBABLE TAIL FIBER ASSEMBLY PROTEIN (P37) gb AAF03980.1 AF157835_37 (AF157835) P37 [Bacteriophage APSE-1]	#N/A
Contig9 from SEQ ID n° 10473 PL-880.1	m	40%	gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-9725
Contig9 from SEQ ID n° 10474 PL-881.1	m	32%	gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-9726
Contig9 from SEQ ID n° 10475 PL-882.1	m	16%	pir G64887 probable tail fiber protein GP37 - Escherichia coli gb AAC74454.1 (AE000234) putative membrane protein [Escherichia coli K12]	SEQ ID n-9727
Contig9 from SEQ ID n° 10476 PL-883.1	m	42%	gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-9728
Contig9 from SEQ ID n° 10477 PL-884.1	m	60%	sp P09153 TFAE_ECOLI TAIL FIBER ASSEMBLY PROTEIN HOMOLOG FROM LAMBDROID PROPHAGE EL4 pir A64861 ycfa protein, phage protein-related - Escherichia coli gb AAC74240.1 (AE000214) orf, hypothetical protein [Escherichia coli K12]	SEQ ID n-9729
Contig9 from SEQ ID n° 10478 PL-3442.1	m	62%	pir S18687 sc/svn protein - Escherichia coli plasmid p15B emb CAA44050.1 (X62121) DNA inversion product [Escherichia coli] gb AAG54576.1 AE005203_5 (AE005203) unknown protein from prophage CP-933H [Escherichia coli O157:H7]	SEQ ID n-2658
Contig9 from SEQ ID n° 10479 PL-5518.1	m	32%	pir C82199 RTX toxin RtxA VC1451 [Imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae]	#N/A
Contig9 from SEQ ID n° 10480 PL-886.1	p	36%		SEQ ID n-9731

SEQ ID n° 10481 PL-3439.1	Contig9 from 5232245 to 5232640	m 77%	gb AAG53986.1 AF327444_2 (AF327444) putative transposase B [Erwinia herbicola]	SEQ ID n-2655
SEQ ID n° 10482 PL-3438.1	Contig9 from 5232637 to 5233083	m 75%	gb AAG53985.1 AF327444_1 (AF327444) putative transposase A [Erwinia herbicola]	SEQ ID n-2654
SEQ ID n° 10483 PL-3437.1	Contig9 from 5233961 to 5234482	p 74%	sp P30134 YFHC_ECOLI_HYPOTHETICAL 20.0 KD PROTEIN IN PURL-DPJ INTERGENIC REGION (ORF178) pir F65033 hypothetical 20.0 kD protein in purL- dpj intergenic region - Escherichia coli (strain K-12) emb CAA51064.1 (X72336) orf 178, gef-resistance, put. membrane protein [Escherichia coli] dbj BAAL0909.1 (D64044) YFHC-ECOLI protein [Escherichia coli] gb AA79821.1 (U36841) alternate name yfhC; orf178 of GenBank Accession Number X72336 [Escherichia coli] gb AAC75612.1 (AE000342) putative deaminase [Escherichia coli K12]	SEQ ID n-2653
SEQ ID n° 10484 PL-888.1	Contig9 from 5234471 to 5236777	m 67%	pir S56346 arginine decarboxylase (EC 4.1.1.19) adi, biodegradative - Escherichia coli gb AAA97017.1 (U14003) adi [Escherichia coli] gb AAC77078.1 (AE000484) biodegradative arginine decarboxylase [Escherichia coli K12]	SEQ ID n-9733
SEQ ID n° 10485 PL-889.1	Contig9 from 5236908 to 5238254	m 66%	emb CAA84588.1 (Z35428) ORF404 [Proteus mirabilis]	SEQ ID n-9734

1153

SP PI5254 PURL_ECOLI		PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (FGAM SYNTHASE) (FGAMS)		(FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT)	
SEQ ID n° 10486 PL-890.1	Contig9 from 5238581 to 5242477	P	88%	gb AAA24456.1 (M19501) formylglycineamide ribonucleotide synthetase (EC 6.3.5.3) [Escherichia coli] gb AAA79819.1 (U36841) phosphoribosylformylglycineamide synthetase [Escherichia coli]	SEQ ID n-9736
SEQ ID n° 10487 PL-5511.1	Contig9 from 5242594 to 5242836	m	44%	pir A83554 hypothetical protein PA0729 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04118.1 AE004508_3 (AE004508) hypothetical protein [Pseudomonas aeruginosa]	#N/A
SEQ ID n° 10488 PL-5510.1	Contig9 from 5242928 to 5243200	m	34%	emb CAB62375.1 (AL117211) hypothetical protein YPMT1.68A [Yersinia pestis]	#N/A
SEQ ID n° 10489 PL-5508.1	Contig9 from 5243561 to 5243848	m	No Hits found		#N/A
SEQ ID n° 10490 PL-891.1	Contig9 from 5243919 to 5245415	P	71%	gb AAG57670.1 AE005486_1 (AE005486) putative 2-component sensor protein [Escherichia coli] O157:H7	SEQ ID n-9737
SEQ ID n° 10491 PL-892.1	Contig9 from 5245509 to 5246264	P	43%	gb AAA79817.1 (U36841) alternate name yfhG; orf1 of GenBank Accession Number S67014 [Escherichia coli]	SEQ ID n-9738

SEQ ID n° 10492	PL-893.1	Contig9 from 5246261 to 5247598	p 92%	sp P211712 YFHA_ECOLI HYPOTHETICAL 49.1 KDA PROTEIN IN GLNB-PURL INTERGENIC REGION (ORFXB) (ORF-2) p12 A65033 hypothetical protein XB (glnB 5' region) - Escherichia coli gb AAC75607.1 (AE000341) putative 2-component transcriptional regulator [Escherichia coli K12] dbj BAAL6462.1 (D90885) nitrogen regulator I homolog [Escherichia coli] gb AAG57668.1 AE005485_6 (AE005485) putative 2- component transcriptional regulator [Escherichia coli O157:H7] SEQ ID n-3739
SEQ ID n° 10493	PL-894.1	Contig9 from 5247665 to 5249287	p 62%	pir C82617 NH3-dependent NAD synthetase XF1961 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84763.1 AE004015_6 (AE004015) NH3-dependent NAD synthetase [Xylella fastidiosa] SEQ ID n-3740
SEQ ID n° 10494	PL-5505.1	Contig9 from 5249303 to 5249641	p 94%	sp P05826 GLNB_ECOLI NITROGEN REGULATORY PROTEIN P-II 1 pir RGECP2 nitrogen regulatory protein P-II.1 - Escherichia coli pdb 2PII Pii, Glnb Product pdb 1PIL Signal Transducing Protein P2 (Product Of Glnb) emb CAA41683.1 (X58872) P. II protein [Escherichia coli] gb AAB28779.1 (S67014) small protein PII, Glnb-transcriptional regulator [Escherichia coli, Peptide, 112 aa] gb AAC75606.1 (AE000341) regulatory protein P-II for glutamine synthetase [Escherichia coli K12] dbj BAAL6461.1 (D90885) regulatory protein P-II [Escherichia coli] prf 1712307B glnB gene [Escherichia coli] #N/A
SEQ ID n° 10495	PL-895.1	Contig9 from 5250002 to 5250886	p 59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]
SEQ ID n° 10496	PL-896.1	Contig9 from 5251308 to 5252381	p 58%	emb CAC04221.1 (AL391515) conserved hypothetical protein [Streptomyces coelicolor A3(2)] SEQ ID n-3742

1155

SEQ ID n° 10497	PL-897.1	Contig9 from 5252381 to 5253772	p	50%	emb CAC04220.1 (AL391515) conserved hypothetical protein [Streptomyces coelicolor A3(2)]	SEQ ID n-9743
SEQ ID n° 10498	PL-898.1	Contig9 from 5254190 to 5255317	p	51%	gb AAG56318.1 AE005360_10 (AE005360) unknown protein associated with Rhs element [Escherichia coli O157:H7]	SEQ ID n-9744
SEQ ID n° 10499	PL-5503.1	Contig9 from 5255391 to 5255651	p	No Hits found		#N/A
SEQ ID n° 10500	PL-899.1	Contig9 from 5255802 to 5256389	p	No Hits found		SEQ ID n-9745
SEQ ID n° 10501	PL-900.1	Contig9 from 5257030 to 5258037	p	39%	pir B83548 hypothetical protein PA0787 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04176.1 AE004513_8 (AE004513) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-9748
SEQ ID n° 10502	PL-901.1	Contig9 from 5258034 to 5258684	p	No Hits found		SEQ ID n-9749
SEQ ID n° 10503	PL-902.1	Contig9 from 5258976 to 5260001	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-9750
SEQ ID n° 10504	PL-7326.1	Contig9 from 5260180 to 5260335	p	No Hits found		#N/A
SEQ ID n° 10505	PL-5495.1	Contig9 from 5260807 to 5261127	p	No Hits found		#N/A
SEQ ID n° 10506	PL-903.1	Contig9 from 5261475 to 5262056	p	85%	sp P05823 TNR0 ECOLI TRANSPOSON TN2501 RESOLVASE pir RPECR5 resolvase - Escherichia coli transposon Tn2501 gb AA27426.1 (M15197) resolvase [Transposon Tn2501]	SEQ ID n-9751

1156

Contig9 from SEQ ID n° 10507 PL-904.1	P	16%	gb AAG55350.1 AE005276_3 (AE005276) Z1205 gene product [Escherichia coli O157:H7]	SEQ ID n-3752
Contig9 from SEQ ID n° 10508 PL-5494.1	P	54%	gb AAG55760.1 AE005312_6 (AE005312) Z1645 gene product [Escherichia coli O157:H7] sp P33596 RECX_ECOLI REGULATORY PROTEIN RECX (ORAA PROTEIN) pir F65049 regulatory protein recX - Escherichia coli gb AAC75740.1 (AE000354) regulator, Orax protein [Escherichia coli K12] dbj BAJ16560.1 (D90892) REGULATORY PROTEIN RECX (ORAA PROTEIN). [Escherichia coli]	#N/A
Contig9 from SEQ ID n° 10509 PL-7325.1	P	No Hits found	sp P26353 HMPA_SALTY FLAVOHEMOPROTEIN (HEMOGLOBIN-LIKE PROTEIN) (FLAVOHEMOGLOBIN) (DIHYDROPTERIDINE REDUCTASE (FERRISIDEROPHORE REDUCTASE B) (NITRIC OXIDE DIOXYGENASE) (NOD) gb AAC24484.1 (AF020388) flavohemoglobin [Salmonella typhimurium] sp P06192 GLYA_SALTY SERINE HYDROXYMETHYLTRANSFERASE (SERINE METHYLASE) (SHMT) pir B48427 glycine hydroxymethyltransferase (EC 2.1.2.1) - Salmonella typhimurium emb CAA33808.1 (X15816) serine hydroxymethyltransferase (AA 1-417) [Salmonella typhimurium]	SEQ ID n-3753
Contig9 from SEQ ID n° 10511 PL-906.1	P	93%	gb AAG57649.1 AE005483_8 (AE005483) MFS (major facilitator superfamily) transporter [Escherichia coli O157:H7]	SEQ ID n-3754
Contig9 from SEQ ID n° 10512 PL-907.1	P	76%		SEQ ID n-3755

SEQ ID n° 10513	PL-908.1	Contig9 from 5268938 to 5269885	p	73%	sp P36674 TRER_SALTY TREHALOSE OPERON REPRESSOR pir A57147 regulatory protein trer - Salmonella typhimurium gb AAA68987.1 (U07843) Submitter comments: Cloned as part of mgta locus. ORF expresses a 37 kda protein. Locus is not regulated by Mg2+. Is homolog of E. coli trer gene, personal communication from Dr. Winfried Boos and also Dr. Kenn Rudd, see GenBank Accession	SEQ ID n-9756
SEQ ID n° 10514	PL-909.1	Contig9 from 5270034 to 5271455	p	88%	gb AAG59437.1 AE005656_5 (AE005656) PTS system enzyme II, trehalose specific [Escherichia coli O157:H7]	SEQ ID n-9757
SEQ ID n° 10515	PL-910.1	Contig9 from 5271555 to 5273216	p	76%	sp P28904 TREC_ECOLI TREHALOSE-6-PHOSPHATE HYDROLASE (ALPHA, ALPHA-PHOSPHOTREHALASE) pir S56465 alpha, alpha-phosphotrehalase (EC 3.2.1.93) - Escherichia coli gb AAA971136.1 (U14003) trehalose-6-phosphate hydrolase [Escherichia coli] gb AAC77196.1 (AE000495) trehalase 6-P hydrolase [Escherichia coli K12] sp P22783 SUHB_ECOLI EXTRAGENIC SUPPRESSOR PROTEIN SUHB pir D65030 myo-inositol-1(or 4)- monophosphatase (EC 3.1.3.25) [validated] - Escherichia coli gb AAC75586.1 (AE000339) enhances synthesis of sigma32 in mutant; extragenic suppressor, may modulate RNase III lethal action [Escherichia coli K12] dbj BAAL6427.1 (D90883) EXTRAGENIC SUPPRESSOR PROTEIN SUHB. [Escherichia coli] dbj BAAL6435.1 (D90884) EXTRAGENIC SUPPRESSOR PROTEIN SUHB. [Escherichia coli] gb AAG57646.1 AE005483_5 (AE005483) putative ATP synthase beta subunit [Escherichia coli O157:H7]	SEQ ID n-9759
SEQ ID n° 10516	PL-911.1	Contig9 from 5273319 to 5274122	m	90%		
SEQ ID n° 10517	PL-912.1	Contig9 from 5274256 to 5274981	p	80%		

SEQ ID n° 10518 PL-3435.1	Contig9 from 5275068 to 5275562	p 78%	sp P77484 YFHP_ECOLI HYPOTHETICAL 17.3 KDA PROTEIN IN HSCA-SUHB INTERGENIC REGION pir B65030 hypothetical protein b2531 - Escherichia coli (strain K-12) gb AAC75584.1 (AE000339) orf, hypothetical protein [Escherichia coli K12] dbj BAAL6425.1 (D90883) similar to [SwissProt Accession Number P44675] [Escherichia coli] gb AAG57645.1 AE005483_4 (AE005483) orf, hypothetical protein [Escherichia coli O157:H7] sp P39171 NIFS_ECOLI NIFS PROTEIN HOMOLOG dbj BAA16424.1 (D90883) UNKNOWN PROTEIN FROM 2D. PAGE (SPOT M92) (FRAGMENT). [Escherichia coli] sp P77310 NIFU_ECOLI NIFU-LIKE PROTEIN pir H65029 hypothetical protein b2529 - Escherichia coli (strain K-12) gb AAC75582.1 (AE000339) orf, hypothetical protein [Escherichia coli K12] dbj BAA16423.1 (D90883) NIFU PROTEIN. [Escherichia coli] gb AAG57643.1 AE005483_2 (AE005483) orf, hypothetical protein [Escherichia coli O157:H7] gb AAK02404.1 (AE006068) unknown [Pasteurella multocida] sp P36540 HSCB_ECOLI CHAPERONE PROTEIN HSCB (HSC20) pir A36958 DnaJ homolog (hsca 5'- region) - Escherichia coli gb AA18299.1 (U01827) ORF-1 [Escherichia coli] gb AAC75580.1 (AE000339) orf, hypothetical protein [Escherichia coli K12] dbj BAA16421.1 (D90883) similar to [SwissProt Accession Number P36540] [Escherichia coli]	SEQ ID n-2652
SEQ ID n° 10519 PL-913.1	Contig9 from 5275612 to 5276826	p 96%		SEQ ID n-3762
SEQ ID n° 10520 PL-5491.1	Contig9 from 5276851 to 5277237	p 90%		
SEQ ID n° 10521 PL-5489.1	Contig9 from 5277347 to 5277670	p 84%		#N/A
SEQ ID n° 10522 PL-3434.1	Contig9 from 5277708 to 5278229	p 76%		#N/A

SEQ ID n°	Contig9 from	Contig9	Contig9 from	SEQ ID n°	Contig9 from	Contig9	Contig9 from	SEQ ID n°	Contig9 from	Contig9	Contig9 from	SEQ ID n°	
10523	PL-914.1	5278241 to 5280091	85%	10524	PL-5488.1	5280094 to 5280429	74%	10525	PL-5487.1	5280448 to 5280648	89%	10526	PL-915.1
<p>sp P36541 HSCA_ECOLI CHAPERONE PROTEIN HSCA (HSC66) pir E5029 heat shock cognate protein 66 - Escherichia coli gb AAC75579.1 (AE000339) heat shock protein, chaperone, member of Hsp70 protein family [Escherichia coli K12] dbj BAA16420.1 (D90883) heat shock cognate protein 66 [Escherichia coli] sp P2528 FER_ECOLI FERREDOXIN, 2FE-2S pir JC1110 ferredoxin [2Fe-2S] - Escherichia coli gb AAA23755.1 (M88654) ferredoxin [Escherichia coli] gb AAC75578.1 (AE000339) [2FE-2S] ferredoxin, electron carrier protein [Escherichia coli K12] dbj BAA16415.1 (D90882) ferredoxin [2Fe-2S] [Escherichia coli] dbj BAA16419.1 (D90883) ferredoxin [2Fe-2S] [Escherichia coli] gb AAG57639.1 (AE005482_6) (AE005482) [2FE-2S] ferredoxin, electron carrier protein [Escherichia coli O157:H7] sp P37096 YFHJ_ECOLI HYPOTHETICAL 7.7 KDA PROTEIN IN PPEB-FDX INTERGENIC REGION pir C65029 hypothetical 7.7 kD protein in fdx 3'region - Escherichia coli (strain K-12) gb AAC75577.1 (AE000339) orf, hypothetical protein [Escherichia coli K12] dbj BAA16414.1 (D90882) similar to [SwissProt Accession Number P37096] [Escherichia coli] dbj BAA16418.1 (D90883) similar to [SwissProt Accession Number P37096] [Escherichia coli] gb AAG57638.1 (AE005482_5) (AE005482) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG57637.1 (AE005482_4) (AE005482) putative peptidase [Escherichia coli O157:H7]</p>				<p>sp P37096 YFHJ_ECOLI HYPOTHETICAL 7.7 KDA PROTEIN IN PPEB-FDX INTERGENIC REGION pir C65029 hypothetical 7.7 kD protein in fdx 3'region - Escherichia coli (strain K-12) gb AAC75577.1 (AE000339) orf, hypothetical protein [Escherichia coli K12] dbj BAA16414.1 (D90882) similar to [SwissProt Accession Number P37096] [Escherichia coli] dbj BAA16418.1 (D90883) similar to [SwissProt Accession Number P37096] [Escherichia coli] gb AAG57638.1 (AE005482_5) (AE005482) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG57637.1 (AE005482_4) (AE005482) putative peptidase [Escherichia coli O157:H7]</p>				<p>sp P37096 YFHJ_ECOLI HYPOTHETICAL 7.7 KDA PROTEIN IN PPEB-FDX INTERGENIC REGION pir C65029 hypothetical 7.7 kD protein in fdx 3'region - Escherichia coli (strain K-12) gb AAC75577.1 (AE000339) orf, hypothetical protein [Escherichia coli K12] dbj BAA16414.1 (D90882) similar to [SwissProt Accession Number P37096] [Escherichia coli] dbj BAA16418.1 (D90883) similar to [SwissProt Accession Number P37096] [Escherichia coli] gb AAG57638.1 (AE005482_5) (AE005482) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG57637.1 (AE005482_4) (AE005482) putative peptidase [Escherichia coli O157:H7]</p>					
10527	PL-5486.1	5282288 to 5282710	59%	10528	PL-5486.1	5282288 to 5282710	59%	10529	PL-5486.1	5282288 to 5282710	59%	10530	PL-5486.1
<p>sp P36541 HSCA_ECOLI CHAPERONE PROTEIN HSCA (HSC66) pir E5029 heat shock cognate protein 66 - Escherichia coli gb AAC75579.1 (AE000339) heat shock protein, chaperone, member of Hsp70 protein family [Escherichia coli K12] dbj BAA16420.1 (D90883) heat shock cognate protein 66 [Escherichia coli] sp P2528 FER_ECOLI FERREDOXIN, 2FE-2S pir JC1110 ferredoxin [2Fe-2S] - Escherichia coli gb AAA23755.1 (M88654) ferredoxin [Escherichia coli] gb AAC75578.1 (AE000339) [2FE-2S] ferredoxin, electron carrier protein [Escherichia coli K12] dbj BAA16415.1 (D90882) ferredoxin [2Fe-2S] [Escherichia coli] dbj BAA16419.1 (D90883) ferredoxin [2Fe-2S] [Escherichia coli] gb AAG57639.1 (AE005482_6) (AE005482) [2FE-2S] ferredoxin, electron carrier protein [Escherichia coli O157:H7] sp P37096 YFHJ_ECOLI HYPOTHETICAL 7.7 KDA PROTEIN IN PPEB-FDX INTERGENIC REGION pir C65029 hypothetical 7.7 kD protein in fdx 3'region - Escherichia coli (strain K-12) gb AAC75577.1 (AE000339) orf, hypothetical protein [Escherichia coli K12] dbj BAA16414.1 (D90882) similar to [SwissProt Accession Number P37096] [Escherichia coli] dbj BAA16418.1 (D90883) similar to [SwissProt Accession Number P37096] [Escherichia coli] gb AAG57638.1 (AE005482_5) (AE005482) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG57637.1 (AE005482_4) (AE005482) putative peptidase [Escherichia coli O157:H7]</p>				<p>sp P37096 YFHJ_ECOLI HYPOTHETICAL 7.7 KDA PROTEIN IN PPEB-FDX INTERGENIC REGION pir C65029 hypothetical 7.7 kD protein in fdx 3'region - Escherichia coli (strain K-12) gb AAC75577.1 (AE000339) orf, hypothetical protein [Escherichia coli K12] dbj BAA16414.1 (D90882) similar to [SwissProt Accession Number P37096] [Escherichia coli] dbj BAA16418.1 (D90883) similar to [SwissProt Accession Number P37096] [Escherichia coli] gb AAG57638.1 (AE005482_5) (AE005482) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG57637.1 (AE005482_4) (AE005482) putative peptidase [Escherichia coli O157:H7]</p>				<p>sp P37096 YFHJ_ECOLI HYPOTHETICAL 7.7 KDA PROTEIN IN PPEB-FDX INTERGENIC REGION pir C65029 hypothetical 7.7 kD protein in fdx 3'region - Escherichia coli (strain K-12) gb AAC75577.1 (AE000339) orf, hypothetical protein [Escherichia coli K12] dbj BAA16414.1 (D90882) similar to [SwissProt Accession Number P37096] [Escherichia coli] dbj BAA16418.1 (D90883) similar to [SwissProt Accession Number P37096] [Escherichia coli] gb AAG57638.1 (AE005482_5) (AE005482) orf, hypothetical protein [Escherichia coli O157:H7] gb AAG57637.1 (AE005482_4) (AE005482) putative peptidase [Escherichia coli O157:H7]</p>					

1160

Contig9 from SEQ ID n° 10528 PL-916.1	5282802 to 5284598	m	71%	pir H82841 conserved hypothetical protein XF0161 [imported] - Xylella fastidiosa (strain 9A5C) - gb AAE82974.1 AE003869_11 (AE003869) conserved hypothetical protein [Xylella fastidiosa]	SEQ ID n-3765
Contig9 from SEQ ID n° 10529 PL-5485.1	5284585 to 5284836	m	No Hits found	#N/A	
Contig9 from SEQ ID n° 10530 PL-5484.1	5284820 to 5285137	m	65%	pir G82841 hypothetical protein XF0160 [imported] - Xylella fastidiosa (strain 9A5C) gb AAE82973.1 AE003869_10 (AE003869) hypothetical protein [Xylella fastidiosa]	#N/A
Contig9 from SEQ ID n° 10531 PL-917.1	5285134 to 5285781	m	40%	pir F82841 hypothetical protein XF0159 [imported] - Xylella fastidiosa (strain 9A5C) gb AAE82972.1 AE003869_9 (AE003869) hypothetical protein [Xylella fastidiosa]	SEQ ID n-3766
Contig9 from SEQ ID n° 10532 PL-5483.1	5285864 to 5286073	m	48%	sp P44191 YE20_HAEMIN HYPOTHETICAL PROTEIN HI1420 pir C64029 hypothetical protein HI1420 - Haemophilus influenzae (strain Rd KW20) gb AAC23070.1 (U32821) H. influenzae predicted coding region HI1420 [Haemophilus influenzae Rd]	#N/A
Contig9 from SEQ ID n° 10533 PL-918.1	5286855 to 5287868	p	72%	ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-3767
Contig9 from SEQ ID n° 10534 PL-919.1	5288236 to 5289852	p	29%	gb AAG00942.1 AF272977_2 (AF272977) transposase [Mycoplasma hyopneumoniae]	SEQ ID n-3768

SEQ ID n° 10535 PL-3433.1	Contig9 from 5289956 to 5290477	p	47%	sp Q07295 PRTA_ERWCH SECRETED PROTEASE A PRECURSOR (PROA) pir S30160 metalloproteinase (EC 3.4.24.-) A - Erwinia chrysanthemi emb CAA49611.1 (X70011) protease A [Erwinia chrysanthemi]	SEQ ID n-2650
SEQ ID n° 10536 PL-920.1	Contig9 from 5290453 to 5291478	m	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-3770
SEQ ID n° 10537 PL-921.1	Contig9 from 5291493 to 5292509	p	68%	pdb 1AKL Alkaline Protease From Pseudomonas Aeruginosa Ifc3080	SEQ ID n-3771
SEQ ID n° 10538 PL-6962.1	Contig9 from 5293418 to 5293564	p	No Hits found	pir T14593 syringomycin synthetase - Pseudomonas syringae pv. syringae gb AAC80285.1 (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae]	#N/A
SEQ ID n° 10539 PL-923.2	Contig9 from 5293684 to 5309334	p	55%	pir F82498 conserved hypothetical protein VCA0107 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96021.1 (AE004353) conserved hypothetical protein [Vibrio cholerae]	SEQ ID n-3772
SEQ ID n° 10540 PL-3431.1	Contig9 from 5310490 to 5310987	p	50%	pir D83439 conserved hypothetical protein PAL658 [imported] - Pseudomonas aeruginosa (strain PAO1)	SEQ ID n-2649
SEQ ID n° 10541 PL-924.1	Contig9 from 5311019 to 5312545	p	58%	gb AAG05047.1 AE004593_9 (AE004593) conserved hypothetical protein [Pseudomonas aeruginosa] pir E82499 hypothetical protein VCA0114 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96028.1 (AE004353) hypothetical protein [Vibrio cholerae]	SEQ ID n-3773
SEQ ID n° 10542 PL-925.1	Contig9 from 5312561 to 5313910	p	44%		SEQ ID n-3774
SEQ ID n° 10543 PL-5475.1	Contig9 from 5313907 to 5314299	p	No Hits found		#N/A

Contig9 from SEQ ID n° 10544 PL-926.1	5314349 to 5315854	m	53%	ref NP_053113.1 orf51 [Escherichia coli] dbj BA084886.1 (AB024946) orf51 [Escherichia coli]	SEQ ID n-3775
Contig9 from SEQ ID n° 10545 PL-5473.1	5315918 to 5316253	m	73%	gb AAG55308.1 AE005273.1 (AE005273) unknown in ISEC8 [Escherichia coli O157:H7] gb AAG55717.1 AE005309.7 (AE005309) unknown in ISEC8 [Escherichia coli O157:H7]	#N/A
Contig9 from SEQ ID n° 10546 PL-5472.1	5316247 to 5316612	m	No Hits found		#N/A
Contig9 from SEQ ID n° 10547 PL-927.1	5316874 to 5318652	p	10%	gb AAD39495.1 AF145799.1 (AF145799) immunogenic 23 kDa lipoprotein PG3 [Porphyromonas gingivalis] pir B83613 secreted protein Hcp PA0263 [imported] - Pseudomonas aeruginosa (strain PA01) pir C83455 secreted protein Hcp PA1512 [imported] - Pseudomonas aeruginosa (strain PA01) pir G82987 secreted protein Hcp PA5267 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03652.1 AE004464_5 (AE004464) secreted protein Hcp [Pseudomonas aeruginosa] gb AAG04901.1 AE004580_1 (AE004580) secreted protein Hcp [Pseudomonas aeruginosa] gb AAG08652.1 AE004939_4 (AE004939) secreted protein Hcp [Pseudomonas aeruginosa] pir A83613 conserved hypothetical protein PA0262 [imported] - Pseudomonas aeruginosa (strain PA01)	SEQ ID n-3776
Contig9 from SEQ ID n° 10548 PL-3427.1	5318671 to 5319162	p	50%	gb AAG03651.1 AE004464_4 (AE004464) conserved hypothetical protein [Pseudomonas aeruginosa] pir B83458 hypothetical protein PA1510 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04899.1 AE004579_11 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2647
Contig9 from SEQ ID n° 10549 PL-928.1	5319339 to 5321867	p	42%	gb AAG03651.1 AE004464_4 (AE004464) conserved hypothetical protein [Pseudomonas aeruginosa] pir B83458 hypothetical protein PA1510 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04899.1 AE004579_11 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-3777
Contig9 from SEQ ID n° 10550 PL-929.1	5321870 to 5323480	p	48%		SEQ ID n-3778

SEQ ID n° 10551	PL-930.1	Contig9 from 5323473 to 5324564	P	21%	pir A83458 hypothetical protein PA1509 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04898.1 AE004579_10 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-9780
SEQ ID n° 10552	PL-931.1	Contig9 from 5324686 to 5325792	P	No Hits found		SEQ ID n-9781
SEQ ID n° 10553	PL-5464.1	Contig9 from 5325880 to 5326113	P	No Hits found	#N/A	
SEQ ID n° 10554	PL-932.1	Contig9 from 5326334 to 5327452	P	No Hits found		SEQ ID n-9782
SEQ ID n° 10555	PL-933.1	Contig9 from 5327449 to 5330820	P	26%	pir G83637 hypothetical protein PA0077 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03467.1 AE004446_15 (AE004446) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-9783
SEQ ID n° 10556	PL-934.1	Contig9 from 5331556 to 5333955	P	43%	pir C83458 conserved hypothetical protein PA1511 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04900.1 AE004579_12 (AE004579) conserved hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-9784
SEQ ID n° 10557	PL-935.1	Contig9 from 5333959 to 5334741	P	41%	pir F83234 hypothetical protein PA3293 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06681.1 AE004751_7 (AE004751) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-9785
SEQ ID n° 10558	PL-3422.1	Contig9 from 5334751 to 5335266	P	45%	pir D83234 hypothetical protein PA3291 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06679.1 AE004751_5 (AE004751) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2645

1164

Contig9 from SEQ ID n° 10559 PL-3421.1 5335318 to 5335830	p	48%	pir D83234 hypothetical protein PA3291 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06679.1 AE004751_5 (AE004751) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2644
Contig9 from SEQ ID n° 10560 PL-3420.1 5335882 to 5336394	p	45%	pir D83234 hypothetical protein PA3291 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06679.1 AE004751_5 (AE004751) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2643
Contig9 from SEQ ID n° 10561 PL-936.1 5336382 to 5338871	p	49%	pir C83234 hypothetical protein PA3290 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06678.1 AE004751_4 (AE004751) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-3786
Contig9 from SEQ ID n° 10562 PL-937.1 5339122 to 5340273	p	No Hits found		SEQ ID n-3787
Contig9 from SEQ ID n° 10563 PL-938.1 5340290 to 5343640	p	27%	pir H83437 hypothetical protein PA1669 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05058.1 AE004594_10 (AE004594) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-3788
Contig9 from SEQ ID n° 10564 PL-6958.1 5343737 to 5343853	p	No Hits found		#N/A
Contig9 from SEQ ID n° 10565 PL-939.1 5344479 to 5347004	p	45%	pir C83458 conserved hypothetical protein PA1511 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04900.1 AE004579_12 (AE004579) conserved hypothetical protein [Pseudomonas aeruginosa] pir B83458 hypothetical protein PA1510 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04899.1 AE004579_11 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-3789
Contig9 from SEQ ID n° 10566 PL-940.1 5347005 to 5348621	p	43%		SEQ ID n-3791

1165

SEQ ID n° 10567 PL-941.1	Contig9 from 5348720 to 5349724	p 33%	pir A83458 hypothetical protein PA1509 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG04898.1 AE004579.10 (AE004579) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-3792
SEQ ID n° 10568 PL-5457.1	Contig9 from 5350058 to 5350297	p No Hits found		#N/A
SEQ ID n° 10569 PL-942.1	Contig9 from 5350317 to 5351396	p No Hits found		SEQ ID n-3793
SEQ ID n° 10570 PL-943.1	Contig9 from 5351393 to 5354764	p 26%	pir G83637 hypothetical protein PA0077 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG03467.1 AE004446.15 (AE004446) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-3794
SEQ ID n° 10571 PL-5455.1	Contig9 from 5354837 to 5354977	p No Hits found		#N/A
SEQ ID n° 10572 PL-5454.1	Contig9 from 5355242 to 5355478	m No Hits found		#N/A
SEQ ID n° 10573 PL-3416.1	Contig9 from 5355552 to 5356064	p 46%	pir E83234 hypothetical protein PA3292 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06680.1 AE004751.6 (AE004751) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2641
SEQ ID n° 10574 PL-3415.1	Contig9 from 5356116 to 5356628	p 46%	pir D83234 hypothetical protein PA3291. [imported] - Pseudomonas aeruginosa (strain PAO1) gb AAG06679.1 AE004751.5 (AE004751) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-2640

Contig9 from SEQ ID n° 10575 PL-944.1 5356616 to 5359093	p	49%	pir C83234 hypothetical protein PA3290 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG06678.1 AE004751.4 (AE004751) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-9795
Contig9 from SEQ ID n° 10576 PL-945.1 5359137 to 5360120	p	No Hits found		SEQ ID n-9796
Contig9 from SEQ ID n° 10577 PL-946.1 5360647 to 5362407	p	48%	pir A82499 hypothetical protein VCA0110 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96024.1 (AE004353) hypothetical protein [Vibrio cholerae]	SEQ ID n-9797
Contig9 from SEQ ID n° 10578 PL-947.1 5362371 to 5363459	p	38%	gb AAG54528.1 AE005198_9 (AE005198) Z0259 gene product [Escherichia coli O157:H7]	SEQ ID n-9798
Contig9 from SEQ ID n° 10579 PL-3414.1 5363437 to 5363976	p	32%	pir E83634 hypothetical protein PA0080 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG03470.1 AE004447_3 (AE004447) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-9839
Contig9 from SEQ ID n° 10580 PL-5451.1 5363981 to 5364409	p	34%	pir E83439 hypothetical protein PA1659 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05048.1 AE004593_10 (AE004593) hypothetical protein [Pseudomonas aeruginosa]	#N/A
Contig9 from SEQ ID n° 10581 PL-948.1 5364734 to 5365402	m	37%	pir C83477 probable transcription regulator PA1347 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-9799
Contig9 from SEQ ID n° 10582 PL-949.1 5365715 to 5366401	m	43%	pir B82381 transcription regulator LuxR family VCA1078 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF96971.1 (AE004433) transcriptional regulator, LuxR family [Vibrio cholerae]	SEQ ID n-9800

Contig9 from 5366443 to 5367130	SEQ ID n° 10583 PL-950.1	m	34%	pir C83477 probable transcription regulator PA1347 [imported] - Pseudomonas aeruginosa (strain PAO1) gb AA04736.1 AE004564_5 (AE004564) probable transcriptional regulator [Pseudomonas aeruginosa]	SEQ ID n-3802
Contig9 from 5368090 to 5368731	SEQ ID n° 10584 PL-951.1	p	No Hits found	pir C82199 RTX toxin RTXA VC1451 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RTXA [Vibrio cholerae]	SEQ ID n-3803
Contig9 from 5369876 to 5380462	SEQ ID n° 10585 PL-952.1	p	33%		SEQ ID n-3804
Contig9 from 5380956 to 5381516	SEQ ID n° 10586 PL-953.1	p	No Hits found		SEQ ID n-3805
Contig9 from 5381516 to 5381917	SEQ ID n° 10587 PL-5444.1	p	No Hits found		#N/A
Contig9 from 5382436 to 5383989	SEQ ID n° 10588 PL-954.1	m	51%	ref NP_066697.1 hypothetical protein [Agrobacterium rhizogenes] dbj BAB16235.1 (AP002086) hypothetical protein [Agrobacterium rhizogenes]	SEQ ID n-3806
Contig9 from 5384213 to 5384320	SEQ ID n° 10589 PL-5441.1	p	No Hits found		#N/A
Contig9 from 5384475 to 5385491	SEQ ID n° 10590 PL-955.1	p	71%	pir F64674 aliphatic amidase - Helicobacter pylori (strain 26695) gb AAD08283.1 (AE000629) aliphatic amidase (aimE) [Helicobacter pylori 26695]	SEQ ID n-3807
Contig9 from 5385982 to 5386920	SEQ ID n° 10591 PL-956.1	p	71%	gb AAF81206.1 AF247502_1 (AF247502) Ytl2 [Salmonella dublin]	SEQ ID n-3808
Contig9 from 5387100 to 5387354	SEQ ID n° 10592 PL-5439.1	m	74%	sp P46147 YEFM_ECOLI HYPOTHETICAL 9.3 KD PROTEIN IN SBCB-HISL INTERGENIC REGION	#N/A

SEQ ID n° 10593 PL-5438.1	Contig9 from 5387618 to 5387950	p 62%	gb AAG22120.1 (AY008264) hypothetical protein [Yersinia enterocolitica]	#N/A
SEQ ID n° 10594 PL-957.1	Contig9 from 5388578 to 5395762	p 63%	pir C82199 RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94608.1 (AE004223) RTX toxin RtxA [Vibrio cholerae]	SEQ ID n-3809
SEQ ID n° 10595 PL-958.1	Contig9 from 5395750 to 5396634	p 59%	gb AAC26596.1 (U83995) putative protease [Porphyromonas gingivalis]	SEQ ID n-3810
SEQ ID n° 10596 PL-959.1	Contig9 from 5396739 to 5399705	p 79%	gb AAD21057.1 (AF119150) RtxA protein [Vibrio cholerae]	SEQ ID n-3811
SEQ ID n° 10597 PL-960.1	Contig9 from 5399772 to 5400563	m 70%	gb AAG55009.1 AE005246_9 (AE005246) orf, hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-3813
SEQ ID n° 10598 PL-961.1	Contig9 from 5401024 to 5402277	p 94%	sp P37312 DCTA_ECOLI C4-DICARBOXYLATE TRANSPORT PROTEIN pir S47749 C4-dicarboxylate transport protein dctA - Escherichia coli gb AAB18505.1 (U00039) CG site No. 872 [Escherichia coli] gb AAC76553.1 (AE000429) uptake of C4- dicarboxylic acids [Escherichia coli K12]	SEQ ID n-3814
SEQ ID n° 10599 PL-5435.1	Contig9 from 5402832 to 5403086	p No Hits found		#N/A
SEQ ID n° 10600 PL-962.1	Contig9 from 5403649 to 5404401	p 71%	sp P43262 VACJ_SHIFL VACJ LIPOPROTEIN PRECURSOR dbj BAA03799.1 (D16293) VacJ [Shigella flexneri]	SEQ ID n-3815
SEQ ID n° 10601 PL-963.1	Contig9 from 5404605 to 5405948	m 78%	gb AAG17182.1 AF191030_1 (AF191030) outer membrane protein FadL [Enterobacter cloacae]	SEQ ID n-3816

Contig9 from SEQ ID n° 10602 PL-964.1 5407837	P	84%	sp P76503 YFCY_ECOLI PROBABLE 3-KETOACYL-COA THIOLASE (ACETYL-COA ACYLTRANSFERASE) (BETA-KETO THIOLASE) pir D65007 hypothetical protein b2342 - Escherichia coli (strain K-12) gb AAC75402.1 (AE000322) putative acyltransferase [Escherichia coli K12] SEQ ID n-3817
Contig9 from SEQ ID n° 10603 PL-965.1 5407789 to 5410020	P	72%	gb AA057469.1 AE005465_9 (AE005465) putative enzyme [Escherichia coli O157:H7] SEQ ID n-3818
Contig9 from SEQ ID n° 10604 PL-966.1 5410427 to 5410909	P	56%	sp P76502 SLXA_ECOLI PHOSPHOHISTIDINE PHOSPHATASE SIXA (RX6) pir B65007 hypothetical protein b2340 - Escherichia coli (strain K-12) gb AAC75400.1 (AE000322) orf, hypothetical protein [Escherichia coli K12] dbj BAA24878.1 (D86298) RX6 [Escherichia coli] SEQ ID n-3819
Contig9 from SEQ ID n° 10605 PL-3410.1 5410930 to 5411466	M	87%	sp P77458 YFCN_ECOLI HYPOTHETICAL 21.0 KDA PROTEIN IN AROC-SIXA INTERGENIC REGION pir A65006 hypothetical protein b2331 - Escherichia coli (strain K-12) gb AAC75391.1 (AE000321) orf, hypothetical protein [Escherichia coli K12] dbj BAA16189.1 (D90864) similar to [SwissProt Accession Number P44126] [Escherichia coli] SEQ ID n-2638
Contig9 from SEQ ID n° 10606 PL-967.1 5411742 to 5412989	P	63%	pir H82228.imidazolonepropionase VC1205 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94364.1 (AE004200) imidazolonepropionase [Vibrio cholerae] sp P19452 HUTG_KLEAE FORMINOGUTAMASE (FORMINOGUTAMATE HYDROLASE) (HISTIDINE UTILIZATION PROTEIN G) pir A36730 hutG protein - Klebsiella pneumoniae (fragment) gb AAA25074.1 (M34604) histidine utilization repressor G [Klebsiella aerogenes] SEQ ID n-3821
Contig9 from SEQ ID n° 10607 PL-968.1 5413000 to 5413956	P	50%	

1170

SEQ ID n° 10608 PL-969.1	Contig9 from 5414062 to 5414793	p 69%	sp P12380 HUTC_KLEAE HISTIDINE UTILIZATION REPRESSOR pir B36730 repressor protein hutc - Klebsiella pneumoniae gb AA25075.1 (M34604) histidine utilization repressor C (hutc) [Klebsiella aerogenes] SEQ ID n-9822
SEQ ID n° 10609 PL-5434.1	Contig9 from 5414828 to 5415010	m 43%	sp Q11169 Y505_MYCTU HYPOTHETICAL 39.5 KDA PROTEIN RV0505C pir D70746 probable PHOSPHOSERINE PHOSPHATASE - Mycobacterium tuberculosis (strain H37RV) emb CAB00931.1 (Z77162) serB [Mycobacterium tuberculosis] #N/A
SEQ ID n° 10610 PL-970.1	Contig9 from 5415762 to 5417441	p 88%	pir E83007 urocanase PA5100 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG08485.1 AE004923_1 (AE004923) urocanase [Pseudomonas aeruginosa] SEQ ID n-9824
SEQ ID n° 10611 PL-971.1	Contig9 from 5417450 to 5418994	p 84%	sp P21310 HUTH_PSEPU HISTIDINE AMMONIA-LYASE (HISTIDASE) pir P83009 probable amino acid permease PA5097 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG08482.1 AE004922_7 (AE004922) probable amino acid permease [Pseudomonas aeruginosa] SEQ ID n-9825
SEQ ID n° 10612 PL-972.1	Contig9 from 5419082 to 5420476	p 78%	sp P39199 YFCB_ECOLI HYPOTHETICAL ADENINE- SPECIFIC METHYLASE YFCB pir H65005 site- specific DNA-methyltransferase (adenine- specific) (ac 2.1.1.72), hypothetical, aroC 3'region - Escherichia coli (strain K-12) gb AAC75390.1 (AE000321) putative adenine-specific methylase [Escherichia coli K12] dbj BAAL6188.1 (D90864) similar to [SwissProt Accession Number P39199] [Escherichia coli] SEQ ID n-9827
SEQ ID n° 10613 PL-973.1	Contig9 from 5420696 to 5421640	p 88%	gb AAG57458.1 AE005464_9 (AE005464) chorismate synthase [Escherichia coli O157:H7] SEQ ID n-9828

1171

SEQ ID n° 10615-PL-975.1	Contig9 from 5422889 to 5423692	p	73%	sp P14008 YFCA_ECOLI_HYPOTHETICAL_28.6_KDA PROTEIN IN FABB-MEPA INTERGENIC REGION pir S08346 hypothetical 28.6 K protein (mepa 3' region) - Escherichia coli emb CAA34783.1 (x16909) unidentified ORF (269 AA) [Escherichia coli] gb AAC75387.1 (AE000321) putative structural protein [Escherichia coli K12] dbj BAA16183.1 (D90863) similar to [PIR Accession Number S08346] [Escherichia coli] gb AAG57456.1 AE005464_7 (AE005464) putative structural protein [Escherichia coli O157:H7]	SEQ ID n-3829
SEQ ID n° 10616 PL-3408.1	Contig9 from 5423715 to 5424266	p	83%	dbj BAA16182.1 (D90863) similar to [SwissProt Accession Number P44255] [Escherichia coli]	SEQ ID n-2636
SEQ ID n° 10617 PL-5433.1	Contig9 from 5424288 to 5424566	p	71%	sp P76496 YFCL_ECOLI_HYPOTHETICAL_10.0_KD PROTEIN IN FABB-MEPA INTERGENIC REGION pir C65005 hypothetical protein b2325 - Escherichia coli (strain K-12) gb AAC75385.1 (AE000321) orf, hypothetical protein [Escherichia coli K12] gb AAG57454.1 AE005464_5 (AE005464) orf, hypothetical protein [Escherichia coli O157:H7]	#N/A
SEQ ID n° 10618 PL-976.1	Contig9 from 5424641 to 5426683	m	69%	pir B65005 hypothetical protein b2324 - Escherichia coli (strain K-12) gb AAC75384.1 (AE000321) putative peptidase [Escherichia coli K12] dbj BAA16181.1 (D90863) similar to [SwissProt Accession Number P44246] [Escherichia coli]	SEQ ID n-3830
SEQ ID n° 10619 PL-5432.1	Contig9 from 5426735 to 5426848	p	No Hits found		#N/A

SEQ ID n° 10620	PL-977.1	Contig9 from 5427421 to 5428635	p	88%	<p>pdb 1DD8 A Chain A, Crystal Structure Of Beta-Ketoacyl-[acyl Carrier Protein] Synthase I From Escherichia Coli pdb 1DD8 B Chain B, Crystal Structure Of Beta-Ketoacyl-[acyl Carrier Protein] From Escherichia Coli pdb 1DD8 C Chain C, Crystal Structure Of Beta-Ketoacyl-[acyl Carrier Protein] Synthase I From Escherichia Coli pdb 1DD8 D Chain D, Crystal Structure Of Beta-Ketoacyl-[acyl Carrier Protein] Synthase I From Escherichia Coli</p>	SEQ ID n-3831
SEQ ID n° 10621	PL-978.1	Contig9 from 5429122 to 5430642	m	90%	<p>gb AAG31207.1 AF020810_8 (AF020810) TctA [Salmonella enterica]</p>	SEQ ID n-3832
SEQ ID n° 10622	PL-5430.1	Contig9 from 5430653 to 5431084	m	76%	<p>gb AAG31206.1 AF020810_7 (AF020810) TctB [Salmonella enterica]</p>	#N/A
SEQ ID n° 10623	PL-979.1	Contig9 from 5431098 to 5432078	m	83%	<p>gb AAG31205.1 AF020810_6 (AF020810) TctC [Salmonella enterica]</p>	SEQ ID n-3833
SEQ ID n° 10624	PL-980.1	Contig9 from 5432455 to 5433111	p	No Hits found	<p>sp P22104 TCTD_SALTY TRANSCRIPTIONAL REGULATORY PROTEIN TCTD pir A33861 trans-activating transcription regulator tctD - Salmonella typhimurium gb AA27232.1 (M28368) membrane associated regulatory protein [Salmonella typhimurium] gb AAG31204.1 AF020810_5 (AF020810) TctD [Salmonella enterica]</p>	SEQ ID n-3835
SEQ ID n° 10625	PL-981.1	Contig9 from 5433564 to 5434241	p	76%	<p>gb AAG31203.1 AF020810_4 (AF020810) TctE [Salmonella enterica]</p>	SEQ ID n-3836
SEQ ID n° 10626	PL-982.1	Contig9 from 5434228 to 5435649	p	73%	<p>[Salmonella enterica]</p>	SEQ ID n-3837

SEQ ID n° 10627 PL-983.1	Contig9 from 5435646 to 5436533	m 61%	pir [a83109 hypothetical protein PA4287 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07675.1 AE004845_1 (AE004845) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-3838
SEQ ID n° 10628 PL-5427.3	Contig9 from 5437292 to 5437546	p NO Hits found		#N/A
SEQ ID n° 10629 PL-5426.1	Contig9 from 5437638 to 5437880	p 52%	gb AAC38631.1 (AF047028) insecticidal toxin complex protein TccZ [Photorhabdus luminescens]	#N/A
SEQ ID n° 10630 PL-984.1	Contig9 from 5438344 to 5439471	p 80%	sp P05459 PDXB_ECOLI ERYTHRONATE-4-PHOSPHATE DEHYDROGENASE pir [DEECP] probable erythronate- 4-phosphate dehydrogenase (EC 1.1.1.-) - Escherichia coli gb AAA24308.1 (M29962) erythronate-4-phosphate dehydrogenase [Escherichia coli] gb AAB36530.1 (U76961) 4- phosphoerythronate dehydrogenase [Escherichia coli] gb AAC75380.1 (AE000321) erythronate-4- phosphate dehydrogenase [Escherichia coli K12] dbj BAAL6177.1 (D90863) probable erythronate-4-phosphate dehydrogenase (EC 1.1.1.-) [Escherichia coli]	SEQ ID n-3839
SEQ ID n° 10631 PL-985.1	Contig9 from 5439523 to 5440533	p 79%	sp P08390 USG_ECOLI USG-1 PROTEIN pir [QOECH3 probable dehydrogenase (EC 1.2.1.-) usg1 - Escherichia coli emb CAP26521.1 (X02743) usg protein (aa 1-337) [Escherichia coli] gb AAC75379.1 (AE000320) putative PTS system enzyme II A component [Escherichia coli K12] dbj BAAL6176.1 (D90863) usg1 protein [Escherichia coli]	SEQ ID n-3840
SEQ ID n° 10632 PL-986.1	Contig9 from 5440530 to 5441369	p 79%	gb AAG57447.1 AE005463_10 (AE005463) pseudouridylylate synthase I [Escherichia coli O157:H7]	SEQ ID n-3841

Contig9 from SEQ ID n° 10633 PL-987.1	5441404 to 5442105	p 79%	<p>gb AAG57446.1 AE005463_9 (AE005463) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3842</p> <p>sp P08193 ACCD_ECOLI ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA (ACCASE BETA CHAIN) pir XMECHD acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase beta chain [validated] - Escherichia coli gb AAC75376.1 (AE000320) acetylCoA carboxylase, carboxyltransferase component, beta subunit [Escherichia coli K12] dbj BAA16173.1 (D90863) acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase beta chain [Escherichia coli]</p>	SEQ ID n-3843
Contig9 from SEQ ID n° 10634 PL-988.1	5442208 to 5443152	p 80%	<p>gb AAG57445.1 AE005463_8 (AE005463) acetylCoA carboxylase, carboxyltransferase component, beta subunit [Escherichia coli O157:H7] sp P08192 FOLC_ECOLI FOLC BIFUNCTIONAL PROTEIN [INCLUDES: FOLYLPOLYGLUTAMATE SYNTHASE (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS); DIHYDROFOLATE SYNTHASE] pir SYECFG tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17) / dihydrofolate synthase (EC 6.3.2.12) - Escherichia coli gb AAC75375.1 (AE000320) dihydrofolate:folylpolyglutamate synthetase; [Escherichia coli K12] dbj BAA16164.1 (D90862) FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) / DIHYDROFOLATE SYNTHASE (EC 6.3.2.12). [Escherichia coli] dbj BAA16172.1 (D90863) FOLYLPOLYGLUTAMATE SYNTHASE (EC 6.3.2.17) (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) / DIHYDROFOLATE SYNTHASE (EC 6.3.2.12). [Escherichia coli]</p>	SEQ ID n-3844
Contig9 from SEQ ID n° 10635 PL-989.1	5443145 to 5444443	p 70%		

Contig9 from SEQ ID n° 10635 PL-990.1	p 62%	<u>5445116</u>
Contig9 from SEQ ID n° 10637 PL-3407.1	p 90%	<u>5445837</u>
<hr/>		
Contig9 from SEQ ID n° 10638 PL-991.1	p 86%	<u>5447369</u>
<hr/>		
Contig9 from SEQ ID n° 10639 PL-992.1	p 84%	<u>5448000</u>
<hr/>		

gb|AAG57443.1|AE005463_6 (AE005463) putative lipoprotein [Escherichia coli O157:H7]

gb|AAG57442.1|AE005463_5 (AE005463) membrane protein required for colicin V production [Escherichia coli O157:H7]
sp|F0U496|PUR1_ECOLI

AMIDOPHOSPHORIBOSYLTRANSFERASE (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPATASE) pir||XQEC

amidophosphoribosyltransferase (EC 2.4.2.14) [validated] - Escherichia coli
gb|AAC75372.1|(AE000320)

amidophosphoribosyltransferase = PRPP amidotransferase [Escherichia coli K12]

sp|P09550|UBIX_ECOLI 3-OCTAPRENYL-4-HYDROXYBENZOATE CARBOXY-LYASE (POLYPRENYL P-HYDROXYBENZOATE DECARBOXYLASE) pir||XMECD 3-octaprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.1.-) - Escherichia coli
gb|AAC75371.1|(AE000320) 3-octaprenyl-4-hydroxybenzoate carboxy-lyase [Escherichia coli K12] dbj|BAAL6157.1|(D90862) 3-OCTAPRENYL-4-HYDROXYBENZOATE CARBOXY-LYASE (EC 4.1.1.1.-) (POLYPRENYL P-HYDROXYBENZOATE DECARBOXYLASE).

[Escherichia coli] gb|AAG57440.1|AE005463_3 (AE005463) 3-octaprenyl-4-hydroxybenzoate carboxy-lyase [Escherichia coli O157:H7]

SEQ ID n-9846

SEQ ID n-9835

SEQ ID n-9847

SEQ ID n-9848

1176

SEQ ID n° 10640 PL-993.1	Contig9 from 5447981 to 5448895	m	74%	sp P77775 YFCH_ECOLI_HYPOTHETICAL_32.7_KDA PROTEIN IN FOLX-HISP INTERGENIC REGION pir P65002 hypothetical protein_b2304_- Escherichia coli (strain K-12) gb AAC75364.1 (AE000319) putative sugar nucleotide epimerase [Escherichia coli K12] dbj BAAL6141.1 (D90861) similar to [SwissProt Accession Number Q10403] [Escherichia coli] dbj BAAL6150.1 (D90862) similar to [SwissProt Accession Number Q10403] [Escherichia coli]	SEQ ID n-3849
SEQ ID n° 10641 PL-994.1	Contig9 from 5449048 to 5449668	m	64%	gb AAE57431.1 AE005462_6 (AE005462) putative S- transferase [Escherichia coli O157:H7]	SEQ ID n-9850
SEQ ID n° 10642 PL-995.1	Contig9 from 5449838 to 5451367	m	No Hits found		SEQ ID n-9851
SEQ ID n° 10643 PL-5420.1	Contig9 from 5451437 to 5451847	m	35%	gb AAG01468.1 AF282857_17 (AF282857) WtsF [Pantoea stewartii subsp. stewartii]	#N/A
SEQ ID n° 10644 PL-5419.1	Contig9 from 5451964 to 5452068	m	No Hits found	ref NP_073235.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAA01531.1 (D10689) M5 protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	#N/A
SEQ ID n° 10645 PL-996.1	Contig9 from 5452289 to 5453329	m	73%	pir P82202 hypothetical protein VC1418 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAF94575.1 (AE004220) hypothetical protein [Vibrio cholerae]	SEQ ID n-3852
SEQ ID n° 10646 PL-997.1	Contig9 from 5454013 to 5455890	p	29%		SEQ ID n-9853

SEQ ID n° 10647 PL-998.1	Contig9 from 5456372 to 5456938	p	71%	pir A65002 hypothetical protein b2299 - Escherichia coli (strain K-12) gb AAC75359.1 (AE00319) putative regulator [Escherichia coli K12] gb AAG57428.1 AE005462_3 (AE005462) putative regulator [Escherichia coli O157:H7] dbj BAB07353.1 (AP001519) transcriptional regulator (AraC/XylS family) [Bacillus halodurans]	SEQ ID n-3854
SEQ ID n° 10648 PL-5417.1	Contig9 from 5457108 to 5457392	m	40%	#N/A	
SEQ ID n° 10649 PL-999.1	Contig9 from 5457979 to 5458749	p	22%	gb AAG58551.1 AE005568_1 (AE005568) orf; hypothetical protein [Escherichia coli O157:H7]	SEQ ID n-3855
SEQ ID n° 10650 PL-3406.1	Contig9 from 5458926 to 5459450	p	No Hits found		SEQ ID n-2634
SEQ ID n° 10651 PL-3405.1	Contig9 from 5459560 to 5460039	m	66%	gb AAG54517.1 AE005197_6 (AE005197) Z0248 gene product [Escherichia coli O157:H7]	SEQ ID n-2633
SEQ ID n° 10652 PL-5415.1	Contig9 from 5460282 to 5460434	p	No Hits found	#N/A	
SEQ ID n° 10653 PL-5413.1	Contig9 from 5460726 to 5461040	p	32%	pir E82456 conserved hypothetical protein VCA0477 [imported] - Vibrio cholerae (group O1 strain N16961) gb AAE96381.1 (AE004379) conserved hypothetical protein [Vibrio cholerae]	#N/A
SEQ ID n° 10654 PL-5412.1	Contig9 from 5461031 to 5461210	p	No Hits found	#N/A	

SEQ ID n° 10655 PL-5411.1	Contig9 from 5461213 to 5461617	P 45%	sp Q47157 YAFO_ECOLI_HYPOTHETICAL_15.5_KD PROTEIN IN DIMP-PRFH INTERGENIC REGION pir B64748 yafo protein - Escherichia coli dbj BAA07595.1 (D38582) yafo [Escherichia coli] gb AAB08653.1 (U70214) hypothetical [Escherichia coli] gb AAC73337.1 (AE000131) orf, hypothetical protein [Escherichia coli K12] dbj BAA77902.1 (D83536) Hypothetical 11.2 kd protein in dimp-prfh intergenic region. [Escherichia coli] #N/A
SEQ ID n° 10656 PL-3404.1	Contig9 from 5462019 to 5462447	P 62%	pir F75337 transposase - Deinococcus radiodurans (strain R1) gb AAP11477.1 AE002031_6 (AE002031) transposase [Deinococcus radiodurans] SEQ ID n-2632
SEQ ID n° 10657 PL-5409.1	Contig9 from 5462523 to 5462822	M 72%	sp P76144 YNEC_ECOLI_HYPOTHETICAL_11.3_KD PROTEIN IN HIPB-UXAB INTERGENIC REGION pir A64906 hypothetical protein b1518 - Escherichia coli gb AAC74591.1 (AE000249) orf, hypothetical protein [Escherichia coli K12] gb AAG56248.1 AE005353_3 (AE005353) orf, hypothetical protein [Escherichia coli O157:H7] #N/A
SEQ ID n° 10658 PL-1000.1	Contig9 from 5462834 to 5463709	M 91%	sp P76143 YNEB_ECOLI_PUTATIVE_ALDOLASE_YNEB pir H64905 conserved hypothetical protein b1517 - Escherichia coli gb AAC74590.1 (AE000249) orf, hypothetical protein [Escherichia coli K12] SEQ ID n-45 gb AAG56250.1 AE005353_5 (AE005353) putative LACI-type transcriptional regulator
SEQ ID n° 10659 PL-1001.1	Contig9 from 5463778 to 5464797	M 79%	[Escherichia coli O157:H7] sp P77651 YDEZ_ECOLI_HYPOTHETICAL_ABC TRANSPORTER PERMEASE PROTEIN YDEZ pir F64905 probable sugar transport permease protein b1515 Escherichia coli dbj BAAL5202.1 (D90794) Ribose transport system permease protein RbsC. [Escherichia coli] gb AAC74588.1 (AE000249) putative transport system permease protein [Escherichia coli K12] SEQ ID n-47
SEQ ID n° 10660 PL-1002.1	Contig9 from 5464860 to 5465861	M 87%	

Contig9 from 5465861 to 5466862	m	86%	sp P77672 YDEY_ECOLI_HYPOTHETICAL_ABC TRANSPORTER_PERMEASE_PROTEIN_YDEY_pir E64905 probable sugar transport permease protein b1514 Escherichia coli dbj BAA15201.1 (D90794) L- arabinose transport system permease protein AraH. [Escherichia coli] gb AAC74587.1 (AE000249) putative transport system permease protein [Escherichia coli K12]	SEQ ID n-48
Contig9 from 5466856 to 5468391	m	77%	sp P77257 EGO_ECOLI_PUTATIVE_ABC_TRANSPORTER_ATP. BINDING_PROTEIN_EGO (EG010A) pir D64905 probable sugar transport ATP-binding protein b1513 - Escherichia coli dbj BAA15200.1 (D90794) Ribose transport ATP- binding protein RbsA. [Escherichia coli] gb AAC74586.1 (AE000249) putative ATP- binding component of a transport system [Escherichia coli K12] gb AAC61747.1 (AF089855) aerobic growth essential protein [Escherichia coli] gb AAG56254.1 AE005353_9 (AE005353) putative transcriptional regulator, sorC family [Escherichia coli O157:H7]	SEQ ID n-49
Contig9 from 5468617 to 5469624	p	75%	gb AAG56255.1 AE005353_10 (AE005353) putative kinase [Escherichia coli O157:H7]	SEQ ID n-50
Contig9 from 5471432	p	84%		SEQ ID n-51
Contig9 from 5471627 to 5471764	p	No Hits found		#N/A
Contig9 from 5472216 to 5473241	p	21%	dbj BAB06239.1 (AP001515) transposase related protein (20) [Bacillus halodurans]	SEQ ID n-52
Contig9 from 5473316 to 5474377	p	No Hits found		SEQ ID n-53

SEQ ID n° 10668 PL-1009.1	Contig9 from 5474539 to 5475750	p	46%	gb AAA25769.1 (M29728) citrate synthase [Pseudomonas aeruginosa]	SEQ ID n-94
SEQ ID n° 10669 PL-1010.1	Contig9 from 5475747 to 5477111	p	No Hits found		SEQ ID n-96
SEQ ID n° 10670 PL-1011.1	Contig9 from 5477136 to 5478302	p	30%	pir E69804 multidrug resistance protein homolog yfis - Bacillus subtilis emb CAB12667.1 (Z99108) similar to multidrug resistance protein [Bacillus subtilis] dbj BAA24459.1 (D85082) Yfis [Bacillus subtilis] pir B83121 probable AMP-binding enzyme PA4198 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG07585.1 AE004836_4 (AE004836) probable AMP-binding enzyme [Pseudomonas aeruginosa] sp Q51955 PCAK_PSEPU 4-HYDROXYBENZOATE TRANSPORTER gb AAA85137.1 (U10895) PCAK [Pseudomonas putida]	SEQ ID n-97
SEQ ID n° 10671 PL-1012.1	Contig9 from 5478295 to 5479905	p	55%		SEQ ID n-98
SEQ ID n° 10672 PL-1013.1	Contig9 from 5480215 to 5481537	p	65%		SEQ ID n-99
SEQ ID n° 10673 PL-5401.1	Contig9 from 5482174 to 5482512	p	No Hits found		#N/A
SEQ ID n° 10674 PL-5400.1	Contig9 from 5482717 to 5482956	m	46%	ref NP_047874.1 putative transposase [Yersinia pestis] pir T14989 probable transposase - Yersinia pestis plasmid pMT1 gb AAC82732.1 (AF074611) putative transposase [Yersinia pestis] emb CAB55253.1 (AL117211) hypothetical protein YPMT1.71 [Yersinia pestis] gb AAF81206.1 AF247502_1 (AF247502) Yt12 [Salmonella dublin]	#N/A
SEQ ID n° 10675 PL-1014.1	Contig9 from 5483098 to 5484072	m	69%		SEQ ID n-60
SEQ ID n° 10676 PL-5399.1	Contig9 from 5484550 to 5484651	m	45%	gb AAC54517.1 AE005197_6 (AE005197) Z0248 gene product [Escherichia coli O157:H7]	#N/A

SEQ ID n° 10677 PL-7314.1	Contig9 from 5485703 to 5485828	m	No Hits found	#N/A
SEQ ID n° 10678 PL-1015.1	Contig9 from 5485998 to 5495933	p	60%	SEQ ID n-61
SEQ ID n° 10679 PL-1017.1	Contig9 from 5497034 to 5504188	m	10%	SEQ ID n-62
SEQ ID n° 10680 PL-1018.1	Contig9 from 5504308 to 5506467	m	71%	SEQ ID n-63
SEQ ID n° 10681 PL-1019.1	Contig9 from 5506467 to 5507855	m	58%	SEQ ID n-64
SEQ ID n° 10682 PL-1020.1	Contig9 from 5507855 to 5509975	m	71%	SEQ ID n-65
SEQ ID n° 10683 PL-5385.1	Contig9 from 5510308 to 5510505	p	No Hits found	#N/A
SEQ ID n° 10684 PL-1021.1	Contig9 from 5511969 to 5528342	p	55%	SEQ ID n-87
SEQ ID n° 10685 PL-5381.1	Contig9 from 5529840 to 5529971	p	No Hits found	#N/A

gb|AAG61082.1|AF322013_201 (AF322013) ID930
 [Bradyrhizobium japonicum]
 pir||A37052 toxin A - Clostridium difficile
 gb|AA23283.1| (M30307) toxin A [Clostridium
 difficile]
 pir||F82198 probable toxin secretion transporter
 VC1446 [imported] - Vibrio cholerae
 (group O1 strain N16961) gb|AAF94603.1|
 (AE004223) toxin secretion transporter, putative
 [Vibrio cholerae]
 pir||G82198 RTX toxin transporter VC1447
 [imported] - Vibrio cholerae (group
 O1 strain N16961) gb|AAD21060.1| (AF119150)
 RTX protein [Vibrio cholerae] gb|AAF94604.1|
 (AE004223) RTX toxin transporter [Vibrio
 cholerae]
 pir||H82198 RTX toxin transporter VC1448
 [imported] - Vibrio cholerae (group
 O1 strain N16961) gb|AAF94605.1| (AE004223) RTX
 toxin transporter [Vibrio cholerae]
 pir||T14593 syringomycin synthetase -
 Pseudomonas syringae pv. syringae
 gb|AAC80285.1| (AF047828) syringomycin
 synthetase [Pseudomonas syringae pv.
 syringae]

SEQ ID n° 10686 PL-5380.1	Contig9 from 5530311 to 5530478	p	No Hits found		#N/A
SEQ ID n° 10687 PL-1024.1	Contig9 from 5530494 to 5534990	p	36%	gb AAG54900.1 AE005236_1 (AE005236) Z0705 gene product [Escherichia coli O157:H7]	SEQ ID n°90
SEQ ID n° 10688 PL-5377.1	Contig9 from 5534995 to 5535342	p	No Hits found		#N/A
SEQ ID n° 10689 PL-5376.1	Contig9 from 5535389 to 5535706	m	No Hits found		#N/A
SEQ ID n° 10690 PL-5375.1	Contig9 from 5535968 to 5536198	p	No Hits found		#N/A
SEQ ID n° 10691 PL-5374.1	Contig9 from 5536208 to 5536588	p	No Hits found		#N/A
SEQ ID n° 10692 PL-1025.1	Contig9 from 5536774 to 5538279	m	53%	ref NP_053113.1 orf51 [Escherichia coli] dbj BAAB4886.1 (AB024946) orf51 [Escherichia coli]	SEQ ID n°71
SEQ ID n° 10693 PL-5371.1	Contig9 from 5538343 to 5538678	m	73%	gb AAG55308.1 AE005273_1 (AE005273) unknown in ISEC8 [Escherichia coli O157:H7] gb AAG55717.1 AE005309_7 (AE005309) unknown in ISEC8 [Escherichia coli O157:H7]	#N/A
SEQ ID n° 10694 PL-5370.1	Contig9 from 5538672 to 5538974	m	No Hits found		#N/A
SEQ ID n° 10695 PL-5369.1	Contig9 from 5539044 to 5539412	p	No Hits found		#N/A
SEQ ID n° 10696 PL-5368.1	Contig9 from 5539400 to 5539648	p	No Hits found		#N/A

SEQ ID n°	Contig9 from	m	No Hits found	#N/A	SEQ ID n~72
10697 PL-5367.1	5539998 to 5540102				
10698 PL-1026.1	5541741 to 5542949	p	78%		
10699 PL-1027.1	5542971 to 5544002	p	69%		
10700 PL-1028.1	5544005 to 5545480	p	75%		
10701 PL-1029.1	5545531 to 5546874	p	74%		

gb|AAB51148.1| (U90416) N-(alpha)-
 acetylornithine-(delta)-aminotransferase
 [Escherichia coli]
 sp|P76218|ASTA_ECOLI ARGININE N-
 SUCCINYLTRANSFERASE (AOST) pir||C64934
 hypothetical protein b1747 - Escherichia coli
 (strain K-12) gb|AAC74817.1| (AE000269) orf,
 hypothetical protein [Escherichia coli K12]
 gb|AAG56733.1|AE005397_10 (AE005397) orf,
 hypothetical protein [Escherichia coli O157:H7]
 pir||T46996 hypothetical protein arud [imported]
 - Yersinia pestis emb|CAA21339.1| (AL031866)
 ORF16, len:505 aa, aruD, probable
 succinylglutamate 5-semialdehyde
 dehydrogenase, belongs to Pseudomonas
 aeruginosa aru gene cluster, highly similar to
 many, eg: AruD Pseudomonas
 aeruginosa, Fasta scores: opt: 2117,
 E(): 0, 63.5% identity in >
 pir||T46995 hypothetical protein aruB [imported]
 - Yersinia pestis emb|CAA21338.1| (AL031866)
 ORF15, len: 447 aa, aruB, probable
 succinylarginine dihydrolase, belongs
 to Pseudomonas aeruginosa aru gene
 cluster similar to many eg. Pseudomonas
 aeruginosa O50175, Fasta scores opt:
 1764, E(): 0, 60.8% identity in 446
 aa overlapand E. coli>

SEQ ID n~75

SEQ ID n° 10702 PL-1030.1	Contig9 from 5546887 to 5547864	p 63%	pir T46994 hypothetical protein aruE [imported] - Yersinia pestis emb CAA21337.1 (AL031866) ORF14, len:330 aa, aruE, probable succinylglutamate desuccinylase, belongs to Pseudomonas aeruginosa aru gene cluster similar to many, eg. AF011922.8 Pseudomonas aeruginosa aruB gene, Fasta scores: opt: 697, E():0, 38.0% identity in 324 aa o> sp P39312 CYCA_ECOLI D-SERINE/D-ALANINE/GLYCINE TRANSPORTER pir S56433 D-serine/D- alanine/glycine transporter - Escherichia coli gb AA97104.1 (U14003) ORF_0470 [Escherichia coli] gb AAC77165.1 (AE000492) transport of D- alanine, D-serine, and glycine [Escherichia coli K12] gb AAC59406.1 AE005653_7 (AE005653) transport of D-alanine, D-serine, and glycine [Escherichia coli O157:H7]	SEQ ID n-77
SEQ ID n° 10703 PL-1031.1	Contig9 from 5547969 to 5549423	p 68%	pir A71652 iron-sulfur cofactor synthesis protein RP486 - Rickettsia prowazekii emb CAA14939.1 (AJ235272) NIFS PROTEIN HOMOLOG (spl1) [Rickettsia prowazekii] gb AAD28459.1 AF127374_14 (AF127374) MitM [Streptomyces lavendulae]	SEQ ID n-79
SEQ ID n° 10704 PL-1032.1	Contig9 from 5550320 to 5551204	p No Hits found		SEQ ID n-79
SEQ ID n° 10705 PL-1033.1	Contig9 from 5551204 to 5552370	p 56%		SEQ ID n-80
SEQ ID n° 10706 PL-1034.1	Contig9 from 5552382 to 5553206	p 42%		SEQ ID n-81
SEQ ID n° 10707 PL-1035.2	Contig9 from 5553870 to 5554499	p No Hits found		SEQ ID n-82
SEQ ID n° 10708 PL-3215.3	Contig9 from 5555306 to 5555950	p No Hits found		#N/A

1185

Contig9 from SEQ ID n° 10709 PL-3216.1 5556069 to 5557082	p	72%	ref NP_073225.1 ransposase of IS630 [Salmonella enterica serovar Choleraesuis] dbj BAAC01531.1 (D10689) M5_protein [Salmonella choleraesuis] dbj BAB20556.1 (AB040415) ransposase of IS630 [Salmonella enterica serovar Choleraesuis]	SEQ ID n-2469
Contig9 from SEQ ID n° 10710 PL-5362.2 5557619 to 5558293	p	24%	pir S73104 DNA-directed RNA polymerase (EC 2.7.7.6) III large chain RPC1 - Euplotes octocarinatus (fragment) emb CAA47897.1 (X67660) DNA-directed RNA polymerase [Euplotes octocarinatus]	#N/A
Contig9 from SEQ ID n° 10711 PL-2492.1 5558899 to 5559555	p	No Hits found		SEQ ID n-2676
Contig9 from SEQ ID n° 10712 PL-2491.1 5559864 to 5562005	m	90%	gb AAG57426.1 AE005462_1 (AE005462) phosphotransacetylase [Escherichia coli O157:H7] sp P15046 ACKA_ECOLI ACETATE KINASE (ACETOKINASE) pir KIECAA acetate kinase (EC 2.7.2.1) - Escherichia coli gb AAA23406.1 (M22956) acetate kinase (EC 2.7.2.1) [Escherichia coli] gb AAC75356.1 (AE000318) acetate kinase [Escherichia coli K12] dbj BAAL6135.1 (D90861) acetate kinase (EC 2.7.2.1) [Escherichia coli]	SEQ ID n-2675
Contig9 from SEQ ID n° 10713 PL-2490.1 5562077 to 5563279	m	88%	pir E65001 hypothetical protein b2295 - Escherichia coli (strain K-12) gb AAC75355.1 (AE000318) orf, hypothetical protein [Escherichia coli K12] dbj BAAL6130.1 (D90860) similar to [SwissProt Accession Number P44127] [Escherichia coli] dbj BAAL6134.1 (D90861) similar to [SwissProt Accession Number P44127] [Escherichia coli]	SEQ ID n-2674
Contig9 from SEQ ID n° 10714 PL-4001.1 5563669 to 5564124	p	72%	gb AAG57421.1 AE005461_6 (AE005461) putative transport protein [Escherichia coli O157:H7]	SEQ ID n-3157
Contig9 from SEQ ID n° 10715 PL-2489.1 5564302 to 5566134	p	82%		SEQ ID n-2672

SEQ ID n° 10716 PL-2488.1	Contig9 from 5566131 to 5566730	m 85%	gb AAG57420.1 AE005461_5 (AE005461) putative alpha helix protein [Escherichia coli O157:H7] SEQ ID n-2671
SEQ ID n° 10717 PL-2487.1	Contig9 from 5567638 to 5568852	m 86%	sp P77727 YFBQ_ECOLI PROBABLE AMINOTRANSFERASE YFBQ pir H65000 probable transaminase (EC 2.6.1.1-) b2290 [similarity] - Escherichia coli (strain K-12) gb AAC75350.1 (AE000318) putative aminotransferase [Escherichia coli K12] dbj BAAL6127.1 (D90860) ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPART) [Escherichia coli] SEQ ID n-2670
SEQ ID n° 10718 PL-2486.1	Contig9 from 5569661 to 5570590	p 77%	gb AAG57418.1 AE005461_3 (AE005461) NADH dehydrogenase transcriptional regulator, LysR family [Escherichia coli O157:H7] SEQ ID n-2669
SEQ ID n° 10719 PL-5358.1	Contig9 from 5571294 to 5571743	p 85%	sp O85273 NUOA_ERWCA NADH DEHYDROGENASE I CHAIN A (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN gb AAC38640.1 (AF057063) NADH dehydrogenase chain A [Pectobacterium carotovorum subsp. carotovorum] #N/A
SEQ ID n° 10720 PL-2485.1	Contig9 from 5571761 to 5572435	p 93%	sp O85274 NUOB_ERWCA NADH DEHYDROGENASE I CHAIN B (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2) (NUO2) gb AAC38641.1 (AF057063) NADH dehydrogenase chain B [Pectobacterium carotovorum subsp. carotovorum] SEQ ID n-2668
SEQ ID n° 10721 PL-2484.1	Contig9 from 5572554 to 5574353	p 93%	sp P33599 NUCD_ECOLI NADH DEHYDROGENASE I CHAIN C/D (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3/4) (NUO3/NUO4) pir D65000 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I, chain C-D - Escherichia coli
SEQ ID n° 10722 PL-3999.1	Contig9 from 5574356 to 5574904	p 75%	gb AAC75346.1 (AE000317) NADH dehydrogenase I chain C, D [Escherichia coli K12] sp P33903 NUOE_SALTY NADH DEHYDROGENASE I CHAIN E (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5) (NUO5) gb AAAL6061.1 (L22504) NADH dehydrogenase subunit [Salmonella typhimurium] SEQ ID n-3153

SEQ ID n° 10723 PL-2483.1	Contig9 from 5574901 to 5576265	p 90%	sp P31979 NUO6_ECOLI NADH DEHYDROGENASE I CHAIN F (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6) (NUO6) pir B65000 NADH dehydrogenase. (ubiquinone) (EC 1.6.5.3) I chain F - Escherichia coli gb AAC75344.1 (AE000317) NADH dehydrogenase I chain F [Escherichia coli K12] dbj BAAL6113.1 (D90859) NADH DEHYDROGENASE I CHAIN F (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6) (NUO6). [Escherichia coli] dbj BAAL6118.1 (D90860) NADH DEHYDROGENASE I CHAIN F (EC 1.6.5.3) (NADH- UBIQUINONE OXIDOREDUCTASE CHAIN 6) (NUO6). [Escherichia coli] sp P33900 NUOG_SALTY NADH DEHYDROGENASE I CHAIN G (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN G) (NUO7) sp P33603 NUOH_ECOLI NADH DEHYDROGENASE I CHAIN H (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN H) (NUO8) pir H64999 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain H - Escherichia coli gb AAC75342.1 (AE000317) NADH dehydrogenase I chain H [Escherichia coli K12] dbj BAAL6110.1 (D90859) NADH DEHYDROGENASE I CHAIN H (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 8) (NUO8). [Escherichia coli] gb AAG57411.1 AE005460_5 (AE005460) NADH dehydrogenase I chain H [Escherichia coli. O157:H7] dbj BAAL6109.1 (D90859) NADH DEHYDROGENASE I CHAIN I (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 9) (NUO9). [Escherichia coli] SEQ ID n-2666 SEQ ID n-2665 SEQ ID n-2664 SEQ ID n-9152
SEQ ID n° 10724 PL-2482.1	Contig9 from 5576332 to 5579067	p 85%	
SEQ ID n° 10725 PL-2481.1	Contig9 from 5579064 to 5580041	p 93%	
SEQ ID n° 10726 PL-3995.1	Contig9 from 5580056 to 5580598	p 94%	

1188

SEQ ID n° 10727 PL-3994.1	Contig9 from 5580611 to 5581156	p 80%	sp P33605 NUOJ_ECOLI_NADH_DEHYDROGENASE_I_CHAIN J (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN J) (NUO10) pir [F64999_NADH_dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain J - Escherichia coli gb AAC75340.1 (AE000317) NADH dehydrogenase I chain J [Escherichia coli K12] dbj BAAL6108.1 (D90859) NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain J [Escherichia coli] gb AAG57409.1 AE005460_3 (AE005460) NADH dehydrogenase I chain J [Escherichia coli O157:H7] dbj BAAL6107.1 (D90859) NADH DEHYDROGENASE I CHAIN K (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11). [Escherichia coli] gb AAG57407.1 AE005460_1 (AE005460) NADH dehydrogenase I chain L [Escherichia coli O157:H7] sp P31978 NUOM_ECOLI_NADH_DEHYDROGENASE_I_CHAIN M (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN M) (NUO13) pir [C64999_NADH_dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Escherichia coli gb AAC75337.1 (AE000317) NADH dehydrogenase I chain M [Escherichia coli K12] dbj BAAL6105.1 (D90859) NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [Escherichia coli] gb AAG57406.1 AE005459_9 (AE005459) NADH dehydrogenase I chain M [Escherichia coli O157:H7]	SEQ ID n-3151
SEQ ID n° 10728 PL-5351.1	Contig9 from 5581153 to 5581455	p 91%	#N/A	
SEQ ID n° 10729 PL-2480.1	Contig9 from 5581452 to 5583299	p 87%	SEQ ID n-2663	
SEQ ID n° 10730 PL-2479.1	Contig9 from 5583320 to 5584840	p 89%	SEQ ID n-3661	

SEQ ID n°	Contig9 from	P	%	Accession	SEQ ID n°
10731 PL-2478.1	5584847 to 5586304	77%		sp P33608 NUON_ECOLI NADH DEHYDROGENASE I CHAIN N (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 14) (NUO14) pir B64999 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain N - Escherichia coli gb AAC75336.1 (AE000317) NADH dehydrogenase I chain N [Escherichia coli K12] dbj BAAL16103.1 (D90858) NADH DEHYDROGENASE I CHAIN N (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 14) (NUO14). [Escherichia coli] dbj BAAL16104.1 (D90859) NADH DEHYDROGENASE I CHAIN N (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 14) (NUO14). [Escherichia coli] gb AAF53604.1 (AE003655) CLIP-190 gene product [alt 1] [Drosophila melanogaster] gb AAF53605.1 (AE003655) CLIP-190 gene product [alt 2] [Drosophila melanogaster] pir Tl8372 repeat organellar protein - Plasmodium chabaudi gb AAC63403.1 (U43145) repeat organellar protein [Plasmodium chabaudi] sp P38051 MENF_ECOLI MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE dbj BAAL6092.1 (D90857) MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE [EC 5.4.99.6]. [Escherichia coli] dbj BAAL6099.1 (D90858) MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE (EC 5.4.99.6). [Escherichia coli] emb CAA90702.1 (Z50849) isochorismate synthase [Escherichia coli] dbj BAAL6089.1 (D90857) 2-SUCCINYL-6-HYDROXY-2, 4-CYCLOHEXADIENE-1-CARBOXYLATE SYNTHASE (SHCHC SYNTHASE) / 2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71) (ALPHA-KETOGLUTARATE DECARBOXYLASE) (KDC). [Escherichia coli]	SEQ ID n-2650
10732 PL-2477.1	5586487 to 5587548	46%			SEQ ID n-2659
10733 PL-2476.1	5587595 to 5588809	42%			SEQ ID n-2658
10734 PL-2475.1	5589873 to 5591192	62%			
10735 PL-2474.1	5591297 to 5592991	78%			SEQ ID n-2657

Contig9 from SEQ ID n° 10736 PL-2473.1 5592952 to 5593824	p	50%	gb AAG57396.1 AE005458_13 (AE005458) putative enzyme [Escherichia coli O157:H7] sp P27290 MENB_ECOLI NAPHTHOATE SYNTHASE (DIHYDROXYNAPHTHOIC ACID SYNTHETASE) (DHNA SYNTHETASE) pir A42714 naphthoate synthase, DHNA synthase, MenB=menaquinone biosynthesis enzyme/mitochondrial enoyl-CoA hydratase homolog - Escherichia coli pir D64997 naphthoate synthase (EC 4.1.3.36) [validated] - Escherichia coli gb AA23682.1 (M93421) DHNA synthase [Escherichia coli] gb AAC75322.1 (AE000316) dihydroxynaphthoic acid synthetase [Escherichia coli K12] dbj BAAL6086.1 (D90857) naphthoate synthase, DHNA synthase, MenB=menaquinone biosynthesis enzyme/mitochondrial enoyl-CoA hydratase homolog [Escherichia coli] SEQ ID n-2654	SEQ ID n-2655
Contig9 from SEQ ID n° 10737 PL-2472.1 5593766 to 5594623	p	91%	dbj BAA16085.1 (D90857) O-SUCCINYLBENZOATE-COA SYNTHASE (OSB SYNTHASE) CARBOXYPHENYL)-4-OXYBUTYRIC ACID SYNTHASE). (4-(2'- [Escherichia coli] SEQ ID n-2652	SEQ ID n-2652
Contig9 from SEQ ID n° 10738 PL-2470.1 5594623 to 5595594	p	79%	dbj BAA16080.1 (D90856) O-SUCCINYLBENZOIC ACID- COA LIGASE (EC 5.2.1.26) (OSB-COA SYNTHETASE) (O-SUCCINYLBENZOATE-COA SYNTHASE). [Escherichia coli] SEQ ID n-2650	SEQ ID n-2650
Contig9 from SEQ ID n° 10739 PL-2469.1 5595582 to 5596982	p	67%	sp P42321 CATA_PROMI CATALASE pir A58663 catalase (EC 1.11.1.6) [validated] - Proteus mirabilis emb CAB93973.1 (AJ400964) catalase [Proteus mirabilis] emb CAB93976.1 (AJ400965) catalase [Proteus mirabilis] SEQ ID n-2649	SEQ ID n-2649
Contig9 from SEQ ID n° 10741 PL-3993.1 5598794 to 5599336	p	65%	gb AAG57381.1 AE005457_7 (AE005457) orf, hypothetical protein [Escherichia coli O157:H7] SEQ ID n-3150	SEQ ID n-3150

SEQ ID n° 10742 PL-2467.1	Contig9 from 5593383 to 5600588	m 81%	sp P18199 TYRP_ECOLI TYROSINE-SPECIFIC TRANSPORT PROTEIN (TYROSINE PERMEASE) pir [GRECY tyrosine- specific transport protein - Escherichia coli dbj BAAL5730.1 (D90832) Tyrosine-specific transport protein (Tyrosine permease). [Escherichia coli] gb AAC74977.1 (AE000284) tyrosine-specific transport system [Escherichia coli K12]	SEQ ID n° 1648
SEQ ID n° 10743 PL-2466.1	Contig9 from 5600892 to 5602571	p 60%	gb AAC31980.1 (L39897) HecB [Pectobacterium chrysanthemi]	SEQ ID n° 1647
SEQ ID n° 10744 PL-2465.1	Contig9 from 5602632 to 5607719	p 27%	pir [C83339 hypothetical protein PA2462 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05850.1 AE004673_10 (AE004673) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n° 1646
SEQ ID n° 10745 PL-3992.1	Contig9 from 5607719 to 5608255	p No Hits found		SEQ ID n° 9149
SEQ ID n° 10746 PL-5347.1	Contig9 from 5608482 to 5608826	p 65%	pir [E81193 hypothetical protein NMB0489 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF40924.1 (AE002405) hypothetical protein [Neisseria meningitidis MC58]	#N/A
SEQ ID n° 10747 PL-3991.1	Contig9 from 5608826 to 5609326	p 48%	pir [G81077 hypothetical protein NMB1489 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF41845.1 (AE002498) hypothetical protein [Neisseria meningitidis MC58]	SEQ ID n° 9148
SEQ ID n° 10748 PL-3990.1	Contig9 from 5609490 to 5609996	p 55%	pir [G81077 hypothetical protein NMB1489 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF41845.1 (AE002498) hypothetical protein [Neisseria meningitidis MC58]	SEQ ID n° 9147

Contig9 from 5610160 to 5610666	SEQ ID n° 10749 PL-3989.1	p	53%	pir [G81077 hypothetical protein NMB1489 [imported] - Neisseria meningitidis (group_B strain MD58) gb AAF41845.1 (AE002498) hypothetical protein [Neisseria meningitidis MC58]	SEQ ID n° 3145
Contig9 from 5610908 to 5611921	SEQ ID n° 10750 PL-2464.1	m	37%	-----dbj BAB07562.1 (AP001520) oxidoreductase [Bacillus halodurans]	SEQ ID n° 3645
Contig9 from 5612251 to 5612490	SEQ ID n° 10751 PL-5344.1	p	77%	sp P55510 Y4JJ_RHISN PUTATIVE PLASMID STABILITY PROTEIN Y4JJ pir T28637 probable plasmid stability protein Y4JJ - Rhizobium sp. plasmid pNGR234a gb AAB91722.1 (AE000080) Y4JJ [Rhizobium sp. NGR234]	#N/A
Contig9 from 5612487 to 5612906	SEQ ID n° 10752 PL-5342.1	p	75%	sp P55511 Y4JK_RHISN PUTATIVE PLASMID STABILITY PROTEIN Y4JK pir T28638 probable plasmid stability protein Y4JK - Rhizobium sp. plasmid pNGR234a gb AAB91723.1 (AE000080) Y4JK [Rhizobium sp. NGR234]	#N/A
Contig9 from 5613078 to 5613686	SEQ ID n° 10753 PL-2463.1	p	No Hits found		SEQ ID n° 3644
Contig9 from 5613686 to 5614066	SEQ ID n° 10754 PL-5341.1	p	No Hits found		#N/A
Contig9 from 5614188 to 5614454	SEQ ID n° 10755 PL-5340.1	m	52%	gb AAG57365.1 AE005456.2 (AE005456) orf, hypothetical protein [Escherichia coli O157:H7] sp P37427 RIR2_SALTY RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 BETA CHAIN (RIBONUCLEOTIDE REDUCTASE 1) (B2 PROTEIN) (R2 PROTEIN) emb CAA51453.1 (X72948) nrdB [Salmonella typhimurium]	#N/A
Contig9 from 5614454 to 5615584	SEQ ID n° 10756 PL-2462.1	m	93%		SEQ ID n° 3643

SEQ ID n° 10762 PL-2456.1	Contig9 from 5625694 to 5627370	m 67%	gb AAC82660.1 (AF071215) regulator of swarming behavior precursor [Proteus mirabilis]	SEQ ID n-2636
SEQ ID n° 10763 PL-2455.1	Contig9 from 5627324 to 5628385	m 64%	gb AAC82660.1 (AF071215) regulator of swarming behavior precursor [Proteus mirabilis]	SEQ ID n-2635
SEQ ID n° 10764 PL-2454.1	Contig9 from 5628996 to 5629622	m 45%	ref NP_053304.1 Hypothetical gene [Agrobacterium tumefaciens] dbj BA087689.1 (AB016260) Hypothetical gene [Agrobacterium tumefaciens]	SEQ ID n-2634
SEQ ID n° 10765 PL-2453.1	Contig9 from 5629772 to 5630740	m 44%	ref NP_057878.1 crystallin, mu [Mus musculus] sp O54983 CRYM_MOUSE MU-CRYSTALLIN HOMOLOG gb AAB94770.1 (AF039391) mu-crystallin [Mus musculus]	SEQ ID n-2633
SEQ ID n° 10766 PL-3986.1	Contig9 from 5630741 to 5631283	m 45%	pir D83354 hypothetical protein PA2331 [imported] - Pseudomonas aeruginosa (strain PA01) gb AAG05719.1 AE004659_5 (AE004659) hypothetical protein [Pseudomonas aeruginosa]	SEQ ID n-3144
SEQ ID n° 10767 PL-3985.1	Contig9 from 5631352 to 5631930	m 45%	sp P39638 YWF_BACSU HYPOTHETICAL 23.3 KD PROTEIN IN ROCC-PTA INTERGENIC REGION pir S39735 ywfB protein - Bacillus subtilis emb CAA51636.1 (X73124) ipa-80d [Bacillus subtilis] emb CAB15801.1 (Z99123) alternate gene name: ipa-80d [Bacillus subtilis]	SEQ ID n-3143
SEQ ID n° 10768 PL-2452.1	Contig9 from 5631952 to 5632899	m 55%	sp O67733 ILVE_AQUAE PROBABLE BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (BCAT) pir C70463 branched-chain amino acid aminotransferase - Aquifex aeolicus gb AAC07697.1 (AE000762) branched-chain amino acid aminotransferase [Aquifex aeolicus]	SEQ ID n-2632
SEQ ID n° 10769 PL-2451.1	Contig9 from 5632896 to 5634299	m 48%	pir D82622 coenzyme F390 synthetase XF1916 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84722.1 AE004011_7 (AE004011) coenzyme F390 synthetase [Xylella fastidiosa]	SEQ ID n-2631

Contig9 from	SEQ ID n° 10770 PL-5333.1	5634313 to	5634735	m	No Hits found	#N/A
Contig9 from	SEQ ID n° 10771 PL-5332.1	5634725 to	5635102	m	32%	sp P37977 YRPX_STRCO HYPOTHETICAL 11.1 KD PROTEIN IN RPOX 5'REGION pir 569775 hypothetical protein - Streptomyces coelicolor gb AA33051.1 (L11648) putative [Streptomyces coelicolor A3(2)]
Contig9 from	SEQ ID n° 10772 PL-5329.1	5637077 to	5637496	p	65%	ref NP_050966.1 P5 [Bacteriophage APSE-1] sp Q9T1U3 REGQ_BRAPS PROBABLE ANTITERMINATION PROTEIN Q (P5) gb AAF03999.1 AF157835_56 (AF157835) P5 [Bacteriophage APSE-1]
Contig9 from	SEQ ID n° 10773 PL-2450.1	5638016 to	5638579	p	No Hits found	SEQ ID n-1630 pir F82651 hypothetical protein XF1688 XF1583 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84392.1 AE003986_22 (AE003986) hypothetical protein [Xylella fastidiosa] gb AAF84497.1 AE003993_16 (AE003993) hypothetical protein [Xylella fastidiosa]
Contig9 from	SEQ ID n° 10774 PL-2449.1	5638583 to	5640052	p	53%	emb CAC02585.1 (AL390114) hypothetical protein LML2.920 [Leishmania major]
Contig9 from	SEQ ID n° 10775 PL-5328.1	5640062 to	5640502	p	43%	#N/A ref NP_049909.1 structural protein P5 [Alteromonas phage PM2] gb AAD43555.1 AF155037_18 (AF155037) structural protein P5 [Alteromonas phage PM2]
Contig9 from	SEQ ID n° 10776 PL-5327.1	5640610 to	5641026	p	No Hits found	#N/A
Contig9 from	SEQ ID n° 10777 PL-2448.1	5641219 to	5642988	p	12%	SEQ ID n-1627
Contig9 from	SEQ ID n° 10778 PL-5324.1	5643581 to	5643886	p	No Hits found	#N/A

1196

SEQ ID n° 10779 PL-2446.1	Contig9 from 5643977 to 5644933	p 43%	pir D82661 hypothetical protein XF1593 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84402.1 AE003987_6 (AE003987) hypothetical protein [Xylella fastidiosa]	SEQ ID n-1626
SEQ ID n° 10780 PL-2445.1	Contig9 from 5644930 to 5645685	p 46%	pir E82661 hypothetical protein XF1594 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84403.1 AE003987_7 (AE003987) hypothetical protein [Xylella fastidiosa]	SEQ ID n-1625
SEQ ID n° 10781 PL-5323.1	Contig9 from 5645775 to 5646029	p 44%	pir F82661 hypothetical protein XF1595 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84404.1 AE003987_8 (AE003987) hypothetical protein [Xylella fastidiosa]	#N/A
SEQ ID n° 10782 PL-2444.1	Contig9 from 5646022 to 5647215	p 40%	pir A82649 hypothetical protein XF1704 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84513.1 AE003994_12 (AE003994) hypothetical protein [Xylella fastidiosa]	SEQ ID n-1624
SEQ ID n° 10783 PL-3984.1	Contig9 from 5647284 to 5647784	p 36%	pir B82649 hypothetical protein XF1705 [imported] - Xylella fastidiosa (strain 9a5c) gb AAF84514.1 AE003994_13 (AE003994) hypothetical protein [Xylella fastidiosa]	SEQ ID n-3142
SEQ ID n° 10784 PL-2443.5	Contig9 from 5647787 to 5648893	p 41%	dbj E8B35073.1 (AF002555) putative tail fiber protein [Escherichia coli O157:H7]	#N/A

REVENDICATIONS

1. Séquence nucléotidique isolée issue du génome de *Photorhabdus luminescens*, caractérisée en ce qu'elle comprend une séquence choisie parmi les
5 séquences SEQ ID N° 1 à SEQ ID N° 41 et les séquences SEQ ID N° 5826 à SEQ ID N° 5834.

2. Séquence nucléotidique isolée issue du génome *Photorhabdus luminescens*, caractérisée en ce qu'elle est choisie parmi :

- 10 a) une séquence nucléotidique comportant au moins 75 % d'identité avec une séquence choisie parmi les séquences SEQ ID N° 1 à SEQ ID N° 41 ou les séquences SEQ ID N° 5826 à SEQ ID N° 5834 ;
- b) une séquence nucléotidique comprenant un fragment représentatif d'une séquence choisie parmi les séquences SEQ ID N° 1 à SEQ ID N° 41 ou les séquences SEQ ID N° 5826 à SEQ ID N° 5834,
- 15 c) une séquence nucléotidique complémentaire d'une séquence nucléotidique telle que définie en a) ou b),
- d) une séquence nucléotidique de l'ARN correspondant à l'une des séquences telles que définies en a), b) ou c) ;
- e) une séquence nucléotidique telle que définie en a), b), c) ou d) modifiée.

20 3. Séquence nucléotidique selon la revendication 2, caractérisée en ce qu'il s'agit d'une séquence comprise dans une des séquences SEQ ID N° 1 à SEQ ID N° 41 ou dans les séquences SEQ ID N° 5826 à SEQ ID N° 5834, et en ce qu'elle code pour un polypeptide choisi parmi les polypeptides de séquence SEQ ID N° 42 à SEQ ID N° 3855 ou parmi les polypeptides de séquence codé par une séquence SEQ ID N° 5835 à
25 SEQ ID N° 10784 .

4. Séquence nucléotidique selon la revendication 3, caractérisée :

- a) en ce qu'elle code pour un polypeptide choisi parmi les polypeptides de séquence
30 SEQ ID N° 61, SEQ ID N° 62, SEQ ID N° 67, SEQ ID N° 171, SEQ ID N° 221, SEQ ID N° 268, SEQ ID N° 288, SEQ ID N° 380, SEQ ID N° 426, SEQ ID N° 438, SEQ ID N° 448, SEQ ID N° 453, SEQ ID N° 455, SEQ ID N° 456, SEQ ID N° 458, SEQ ID N° 501, SEQ ID N° 516, SEQ ID N° 530, SEQ ID N° 542, SEQ ID N° 551, SEQ ID N° 720, SEQ ID N° 761, SEQ ID N° 762, SEQ ID N° 814, SEQ ID N° 859, SEQ ID N° 860, SEQ ID N° 861, SEQ ID N° 862, SEQ ID N° 869, SEQ ID N° 1079, SEQ ID N° 1168, SEQ ID N° 1174, SEQ ID N° 1176, SEQ ID N° 1413, SEQ ID N° 1414, SEQ

- ID N° 1415, SEQ ID N° 1416, SEQ ID N° 1417, SEQ ID N° 1457, SEQ ID N° 1651, SEQ ID N° 1856, SEQ ID N° 1869, SEQ ID N° 2021, SEQ ID N° 2080, SEQ ID N° 2152, SEQ ID N° 2162, SEQ ID N° 2173, SEQ ID N° 2251, SEQ ID N° 2295, SEQ ID N° 2306, SEQ ID N° 2317, SEQ ID N° 2328, SEQ ID N° 2340, SEQ ID N° 2342, 5 SEQ ID N° 2351, SEQ ID N° 2500, SEQ ID N° 3228, SEQ ID N° 3230, SEQ ID N° 3311, SEQ ID N° 3317, SEQ ID N° 3318, SEQ ID N° 3319, SEQ ID N° 3320, SEQ ID N° 3322, SEQ ID N° 3323, SEQ ID N° 3326, SEQ ID N° 3327, SEQ ID N° 3328, SEQ ID N° 3375, SEQ ID N° 3376, SEQ ID N° 3377, SEQ ID N° 3378, SEQ ID N° 3422, SEQ ID N° 3489, SEQ ID N° 3503, SEQ ID N° 3609, SEQ ID N° 3623, SEQ 10 ID N° 3624, SEQ ID N° 3772, SEQ ID N° 3783, SEQ ID N° 3788 et SEQ ID N° 3794 ;
- ou
- b) en ce qu'elle est choisie parmi les séquences SEQ ID N° 5835 à SEQ ID N° 10784 homologues aux séquences telles que définies en a) comme indiquées à la dernière colonne du tableau II.
- 15 5. Séquence nucléotidique, caractérisée en ce qu'elle comprend une séquence nucléotidique choisie parmi :
- a) une séquence nucléotidique selon la revendication 3 ou 4 ;
- b) une séquence nucléotidique comportant au moins 75 % d'identité avec une séquence nucléotidique selon la revendication 3 ou 4;
- 20 c) une séquence nucléotidique complémentaire ou d'ARN correspondant à une séquence telle que définie en a) ou b) ;
- d) une séquence nucléotidique d'un fragment représentatif d'une séquence telle que définie en a) ou c) ; et
- e) une séquence telle que définie en a), ou c) modifiée.
- 25 6. Polypeptide codé par une séquence nucléotidique selon l'une des revendications 2 à 5.
7. Polypeptide selon la revendication 6, caractérisé :
- a) en ce qu'il est choisi parmi les polypeptides de séquence SEQ ID N° 61, SEQ ID N° 62, SEQ ID N° 67, SEQ ID N° 171, SEQ ID N° 221, SEQ ID N° 268, SEQ ID N° 288, 30 SEQ ID N° 380, SEQ ID N° 426, SEQ ID N° 438, SEQ ID N° 448, SEQ ID N° 453, SEQ ID N° 455, SEQ ID N° 456, SEQ ID N° 458, SEQ ID N° 501, SEQ ID N° 516, SEQ ID N° 530, SEQ ID N° 542, SEQ ID N° 551, SEQ ID N° 720, SEQ ID N° 761, SEQ ID N° 762, SEQ ID N° 814, SEQ ID N° 859, SEQ ID N° 860, SEQ ID N° 861, SEQ ID N° 862, SEQ ID N° 869, SEQ ID N° 1079, SEQ ID N° 1168, SEQ ID N° 1174,

SEQ ID N° 1176, SEQ ID N° 1413, SEQ ID N° 1414, SEQ ID N° 1415, SEQ ID N° 1416, SEQ ID N° 1417, SEQ ID N° 1457, SEQ ID N° 1651, SEQ ID N° 1856, SEQ ID N° 1869, SEQ ID N° 2021, SEQ ID N° 2080, SEQ ID N° 2152, SEQ ID N° 2162, SEQ ID N° 2173, SEQ ID N° 2251, SEQ ID N° 2295, SEQ ID N° 2306, SEQ ID N° 2317,
5 SEQ ID N° 2328, SEQ ID N° 2340, SEQ ID N° 2342, SEQ ID N° 2351, SEQ ID N° 2500, SEQ ID N° 3228, SEQ ID N° 3230, SEQ ID N° 3311, SEQ ID N° 3317, SEQ ID N° 3318, SEQ ID N° 3319, SEQ ID N° 3320, SEQ ID N° 3322, SEQ ID N° 3323, SEQ ID N° 3326, SEQ ID N° 3327, SEQ ID N° 3328, SEQ ID N° 3375, SEQ ID N° 3376, SEQ ID N° 3377, SEQ ID N° 3378, SEQ ID N° 3422, SEQ ID N° 3489, SEQ ID N°
10 3503, SEQ ID N° 3609, SEQ ID N° 3623, SEQ ID N° 3624, SEQ ID N° 3772, SEQ ID N° 3783, SEQ ID N° 3788 et SEQ ID N° 3794 ;

ou

b) choisie parmi les polypeptides codés par les séquences SEQ ID N° 5835 à SEQ ID N° 10784 homologues aux séquences telles que définies en a) comme indiquées à la
15 dernière colonne du tableau II.

8. Polypeptide caractérisé en ce qu'il comprend un polypeptide choisi parmi :

- a) un polypeptide selon l'une des revendications 6 et 7 ;
- b) un polypeptide présentant au moins 80 % d'identité avec un polypeptide de séquence
20 SEQ ID N° 42 à SEQ ID N° 3855 ou avec un polypeptide codé par une séquence SEQ ID N° 5835 à SEQ ID N° 10784;
- c) un fragment d'au moins 5 acides aminés d'un polypeptide de séquence SEQ ID N° 42 à SEQ ID N° 3855 ou d'un polypeptide codé par une séquence SEQ ID N° 5835 à SEQ ID N° 10784 ;
- 25 d) un fragment biologiquement actif d'un polypeptide de séquence SEQ ID N° 42 à SEQ ID N° 3855 ou d'un polypeptide codé par une séquence SEQ ID N° 5835 à SEQ ID N° 10784 ; et
- e) un polypeptide de séquence SEQ ID N° 42 à SEQ ID N° 3855 ou un polypeptide codé par une séquence SEQ ID N° 5835 à SEQ ID N° 10784, ou tel que défini en c)
30 ou d) modifié.

9. Séquence nucléotidique codant pour un polypeptide selon l'une des revendications 6 à 8.

10. Séquence nucléotidique selon l'une des revendications 2 à 5 et 9, caractérisée en ce qu'elle code pour un polypeptide de *P. luminescens* à activité de type

toxine et/ou antibiotique, ou impliqué dans la synthèse de ces toxines et/ou antibiotiques.

11. Polypeptide selon l'une des revendications 6 à 8, caractérisé en ce qu'il s'agit d'un polypeptide de *P. luminescens* à activité de type toxine et/ou antibiotique, ou impliqué dans la synthèse de ces toxines et/ou antibiotiques, ou l'un de ses fragments.

12. Séquence nucléotidique selon l'une des revendications 1 à 5, 9 et 10 ou séquence de polypeptide selon l'une des revendications 6 à 8 et 11, caractérisée en ce que ladite séquence est enregistrée sur un support d'enregistrement dont la forme et la nature facilitent la lecture, l'analyse et/ou l'exploitation de ladite ou desdites séquences.

13. Séquence nucléotidique ou séquence de polypeptide selon la revendication 12, caractérisée en ce que le support d'enregistrement est un CD-ROM, une disquette informatique ou un serveur informatique.

14. Support d'enregistrement caractérisé en ce qu'y est enregistrée une séquence nucléotidique ou de polypeptide selon la revendication 12 ou 13.

15. 15. Utilisation d'un support selon la revendication 14 pour le choix d'amorces ou de sondes nucléotidiques pour la détermination de gènes dans des souches proches de *P. luminescens*.

16. Utilisation d'un support selon la revendication 14 pour l'étude du polymorphisme génétique de souches proches de *P. luminescens*.

20. 17. Utilisation d'un support selon la revendication 14, pour l'étude d'autres génomes en particulier pour l'annotation automatique de gènes provenant d'autres génomes.

18. Séquence nucléotidique utilisable comme amorce ou comme sonde, caractérisée en ce que ladite séquence est choisie parmi les séquences nucléotidiques selon l'une des revendications 1 à 5, 9 et 10.

19. Séquence nucléotidique selon la revendication 18, caractérisée en ce qu'elle est marquée par un composé radioactif ou par un composé non radioactif.

20. Séquence nucléotidique selon l'une des revendications 18 et 19, caractérisée en ce qu'elle est immobilisée sur un support, de manière covalente ou non-covalente.

21. Séquence nucléotidique selon la revendication 20, caractérisée en ce qu'elle est immobilisée sur un support tel qu'un filtre à haute densité ou une puce à ADN.

22. Séquence nucléotidique selon l'une des revendications 18 à 21 pour la détection et/ou l'amplification de séquences nucléiques.

23. Puce à ADN ou filtre, caractérisé en ce qu'il contient au moins une séquence nucléotidique selon la revendication 21.

5 24. Puce à ADN ou filtre selon la revendication 23, caractérisé en ce qu'il contient en outre au moins une séquence nucléotidique d'une cellule de plante, d'un animal ou d'un micro-organisme autre que *P. luminescens*, immobilisée sur le support de ladite puce.

10 25. Puce à ADN ou filtre selon la revendication 24, caractérisé en ce que ladite cellule ou micro-organisme autre est choisi parmi une cellule ou micro-organisme sensible à une toxine ou un antibiotique produit par *P. luminescens*, une bactérie du genre *Photorhabdus*, et un variant de *P. luminescens*.

15 26. Kit ou nécessaire pour la détection et/ou la quantification de l'expression d'au moins un gène de *P. luminescens*, caractérisé en ce qu'il comprend une puce à ADN ou un filtre selon l'une des revendications 23 à 25.

27. Vecteur de clonage, et/ou d'expression, caractérisé en ce qu'il contient une séquence nucléotidique selon l'une des revendications 1 à 5, 9 et 10.

20 28. Vecteur de clonage, et/ou d'expression selon la revendication 27, caractérisé en ce qu'il contient une séquence nucléotidique choisi parmi les séquences SEQ ID N° 3856 à SEQ ID N° 5825, les séquences SEQ ID N° 5835 à SEQ ID N° 10784, ou leur fragment issu du génome de *P. luminescens*.

25 29. Cellule hôte, caractérisée en ce qu'elle est transformée par un vecteur selon la revendication 27 ou 28.

25 30. Végétal ou animal, excepté l'Homme, comprenant une cellule transformée selon la revendication 29.

31. Procédé de préparation d'un polypeptide, caractérisé en ce que l'on cultive une cellule transformée par un vecteur selon la revendication 29 dans des conditions permettant l'expression dudit polypeptide et que l'on récupère ledit polypeptide recombinant.

30 32. Polypeptide recombinant susceptible d'être obtenu par un procédé selon la revendication 31.

33. Procédé de préparation d'un polypeptide selon l'une des revendications 6 à 8, 11 et 32, caractérisé en ce que l'on effectue une synthèse chimique dudit polypeptide.

34. Anticorps monoclonal ou polyclonal, ses fragments, ou anticorps chimérique, caractérisé en ce qu'il est capable de reconnaître spécifiquement un polypeptide selon l'une des revendications 6 à 8, 11 et 32.

5 35. Anticorps selon la revendication 34, caractérisé en ce qu'il s'agit d'un anticorps marqué.

36. Procédé pour la détection et/ou l'identification de bactéries appartenant à l'espèce *P. luminescens* dans un échantillon biologique, caractérisé en ce qu'il comprend les étapes suivantes :

- 10 a) mise en contact de l'échantillon biologique avec un anticorps selon l'une des revendications 34 et 35 ;
b) mise en évidence du complexe antigène-anticorps éventuellement formé.

15 37. Procédé pour la détection de l'expression d'un gène de *P. luminescens*, caractérisé en ce que l'on met en contact une souche de *P. luminescens*, avec un anticorps selon la revendication 34 ou 35, et que l'on détecte le complexe antigène/anticorps éventuellement formé.

38. Kit ou nécessaire pour la mise en œuvre d'un procédé selon la revendication 36 ou 37, caractérisé en ce qu'il comprend les éléments suivants :

- 20 a) un anticorps selon l'une des revendications 34 et 35 ;
b) éventuellement, les réactifs pour la constitution du milieu propice à la réaction immunologique ;
c) éventuellement, les réactifs permettant la mise en évidence des complexes antigène-anticorps produits par la réaction immunologique.

25 39. Polypeptide selon l'une des revendications 6 à 8, 11 et 32, ou anticorps selon l'une des revendications 34 et 35, caractérisé en ce qu'il est immobilisé sur un support, notamment une puce à protéine.

40. Puce à protéine, caractérisée en ce qu'elle contient au moins un polypeptide selon l'une des revendications 6 à 8, 11 et 32, ou au moins un anticorps selon l'une des revendications 34 et 35, immobilisé sur le support de ladite puce.

30 41. Puce à protéine selon la revendication 40, caractérisée en ce qu'elle contient en outre au moins un polypeptide d'une cellule de plante, d'un animal ou d'un micro-organisme autre que *P. luminescens*, immobilisée sur le support de ladite puce.

42. Puce à protéine selon la revendication 41, caractérisée en ce que ladite cellule ou micro-organisme autre est choisi parmi une cellule ou micro-organisme sensible à une toxine ou un antibiotique produit par *P. luminescens*.

43. Kit ou nécessaire pour la détection et/ou la quantification de l'expression d'au moins un gène de *P. luminescens*, caractérisé en ce qu'il comprend une puce à protéine selon l'une des revendications 40 à 42.

5 44. Procédé de détection et/ou d'identification de bactéries appartenant à l'espèce *P. luminescens* dans un échantillon biologique, caractérisé en ce qu'il met en œuvre une séquence nucléotidique selon l'une des revendications 1 à 5, 9, 10, 18 et 19.

45. Procédé selon la revendication 44, caractérisé en ce qu'il comporte les étapes suivantes :

- 10 a) éventuellement, isolement de l'ADN à partir de l'échantillon biologique à analyser, ou obtention d'un ADNc à partir de l'ARN de l'échantillon biologique ;
- b) amplification spécifique de l'ADN de bactéries appartenant à l'espèce *P. luminescens* à l'aide d'au moins une amorce selon l'une des revendications 18 et 19 ;
- c) mise en évidence des produits d'amplification.

15 46. Kit ou nécessaire pour la détection et/ou l'identification de bactéries appartenant à l'espèce *P. luminescens*, caractérisé en ce qu'il comprend les éléments suivants :

- a) une sonde et/ou amorce nucléotidique selon l'une des revendications 18 à 20 ;
- b) éventuellement, les réactifs nécessaires à la mise en œuvre d'une réaction d'hybridation ;
- 20 c) éventuellement, les réactifs nécessaires à une réaction d'amplification de l'ADN.

47. Utilisation d'une séquence nucléotidique selon l'une des revendications 1 à 5, 9 et 10, d'un polypeptide selon l'une des revendications 6 à 8, 11 et 32, d'un anticorps selon l'une des revendications 34 et 35, et/ou d'une cellule selon la revendications 29, pour la sélection de composé organique ou inorganique capable de
25 moduler, de réguler, d'induire ou d'inhiber l'expression de gènes d'une cellule végétale ou animal, ou d'un micro-organisme autre que *P. luminescens*, dont on veut modifier la résistance ou la sensibilité à au moins une toxine ou antibiotique produit par *P. luminescens*.

30 48. Composition comprenant un composé choisi parmi les composés suivants :

- a) une séquence nucléotidique selon l'une des revendications 1 à 5, 9 et 10 ;
- b) un polypeptide selon l'une des revendications 6 à 8, 11 et 32 ;
- c) un vecteur selon la revendication 27 ou 28 ; et
- d) un anticorps selon la revendication 34 ou 35.

49. Composition pharmaceutique selon la revendication 48, éventuellement en association avec un véhicule pharmaceutiquement acceptable.
50. Composition biopesticide selon la revendication 48.
51. Utilisation d'une cellule selon la revendication 29, ou d'un vecteur selon l'une des revendications 27 et 28, pour la préparation de toxine ou d'antibiotique.
52. Banque génomique d'une bactérie du genre *Phototrhhabdus*.
53. Banque d'ADN génomique d'une bactérie du genre *Phototrhhabdus* selon la revendication 52, caractérisée en ce que ladite banque d'ADN est clonée dans un plasmide.
54. Banque d'ADN génomique selon la revendication 52 ou 53, caractérisée en ce que ladite bactérie est *P. luminescens* ou *P. luminescens* souche TT01.
55. Banque selon la revendication 52 ou 53, caractérisée en ce qu'il s'agit de la banque déposée à la CNCM le 12 mai 2000 sous le N° I-2478.
56. Procédé d'identification d'au moins une séquence nucléotidique de *P. luminescens* non présente dans le génome d'une autre espèce de bactérie, notamment pathogène, et/ou d'identification d'au moins une séquence nucléotidique d'un génome d'une bactérie, notamment pathogène, d'une autre espèce que *P. luminescens* et non présente dans le génome de *P. luminescens*, caractérisée en ce qu'elle comprend les étapes suivantes :
- a) on aligne les séquences nucléotidiques de *P. luminescens* selon l'une des revendications 1 à 5, 9 et 10 ou contenues dans une banque génomique selon l'une des revendications 54 et 55, avec les séquences génomiques de l'autre espèce de bactérie ; et
- b) on traite les données obtenues par cet alignement pour isoler et identifier lesdites séquences uniquement présentes dans l'un ou l'autre génome.

THIS PAGE BLANK (USPTO)